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(71) Applicants (*for all designated States except US*):
AGRICULTURE VICTORIA SERVICES PTY LTD
[AU/AU]; 475 Mickleham Road, Attwood, Victoria 3049
(AU). **AGRESEARCH LIMITED** [NZ/NZ]; 5th Floor,
Tower Block, Ruakura Research Centre, East Street,
Hamilton (NZ).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **SPANGENBERG**,
German [UY/AU]; 56 Arthur Street, Bundoora, Victoria
3083 (AU). **SAWBRIDGE, Timothy, Ivor** [GB/AU]; 174
Keele Street, Collingwood, Victoria 3066 (AU). **ONG**,
Eng, Kok [MY/AU]; 19 Overland Drive, Vermont South,
Victoria 3133 (AU). **EMMERLING, Michael** [DE/AU];
249 Nepean Street, Greensborough, Victoria 3088 (AU).

(74) Agent: **FREEHILLS CARTER SMITH BEADLE**;
Level 43, 101 Collins Street, Melbourne, Victoria 3000
(AU).

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(54) Title: MANIPULATION OF FLAVONOID BIOSYNTHESIS IN PLANTS

(57) Abstract: The present invention relates to nucleic acids and nucleic acid fragments encoding amino acid sequences for flavonoid biosynthetic enzymes in plants, and the use thereof for the modification of flavonoid biosynthesis in plants. More particularly, the flavonoid biosynthetic enzyme is selected from the group consisting of chalcone isomerase (CHI), chalcone synthase (CHS), chalcone reductase (CHR), dihydroflavonol 4-reductase (DFR), leucoanthocyanidin reductase (LCR), flavonoid 3', 5' hydrolase (F3'5'H), flavanone 3-hydroxylase (F3H), flavonoid 3'-hydroxylase (F3'H), phenylalanine ammonia-lyase (PAL) and vestitone reductase (VR), and functionally active fragments and variants thereof.



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MANIPULATION OF FLAVONOID BIOSYNTHESIS IN PLANTS

The present invention relates to nucleic acids and nucleic acid fragments encoding amino acid sequences for flavonoid biosynthetic enzymes in plants, and the use thereof for the modification of flavonoid biosynthesis in plants.

5 Flavonoids constitute a relatively diverse family of aromatic molecules that are derived from phenylalanine and malonyl-coenzyme A (CoA, via the fatty acid pathway). These compounds include six major subgroups that are found in most higher plants: the chalcones, flavones, flavonols, flavandiols, anthocyanins and condensed tannins (or proanthocyanidins). A seventh group, the aurones, is
10 widespread, but not ubiquitous.

 Some plant species also synthesize specialised forms of flavonoids, such as the isoflavonoids that are found in legumes and a small number of non-legume plants. Similarly, sorghum, maize and gloxinia are among the few species known to synthesize 3-deoxyanthocyanins (or phlobaphenes in the polymerised form).
15 The stilbenes which are closely related to flavonoids, are synthesised by another group of unrelated species that includes grape, peanut and pine.

 Besides providing pigmentation to flowers, fruits, seeds, and leaves, flavonoids also have key roles in signalling between plants and microbes, in male fertility of some species, in defense as antimicrobial agents and feeding
20 deterrents, and in UV protection.

 Flavonoids also have significant activities when ingested by animals, and there is great interest in their potential health benefits, particularly for compounds such as isoflavonoids, which have been linked to anticancer benefits, and stilbenes that are believed to contribute to reduced heart disease.

25 The major branch pathways of flavonoid biosynthesis start with general phenylpropanoid metabolism and lead to the nine major subgroups: the colorless chalcones, aurones, isoflavonoids, flavones, flavonols, flavandiols, anthocyanins, condensed tannins, and phlobaphene pigments. The enzyme phenylalanine

ammonia-lyase (PAL) of the general phenylpropanoid pathway will lead to the production of cinnamic acid. Cinnamate-4-hydroxylase (C4H) will produce p-coumaric acid which will be converted through the action of 4-coumaroyl:CoA-ligase (4CL) to the production of 4-coumaroyl-CoA and malonyl-CoA. The first
5 committed step in flavonoid biosynthesis is catalyzed by chalcone synthase (CHS), which uses malonyl CoA and 4-coumaroyl CoA as substrates. Chalcone reductase (CHR) balances the production of 5-hydroxy- or 5-deoxyflavonoids. The next enzyme, chalcone isomerase (CHI) catalyses ring closure to form a flavanone, but the reaction can also occur spontaneously. Other enzymes in the
10 pathway are: flavanone 3-hydroxylase (F3H), dihydroflavonol 4-reductase (DFR), flavonoid 3'-hydroxylase (F3'H) and flavonoid 3', 5' hydroxylase (F3'5'H).

The *Arabidopsis* BANYULS gene encodes a DFR-like protein that may be a leucoanthocyanidin reductase (LCR) that catalyzes an early step in condensed tannin biosynthesis. Condensed tannins are plant polyphenols with protein-
15 precipitating and antioxidant properties, synthesized by the flavonoid pathway. Their chemical properties include protein binding, metal chelation, anti-oxidation, and UV-light absorption. As a result condensed tannins inhibit viruses, micro-organisms, insects, fungal pathogens, and monogastric digestion. Moderate amounts of tannins improve forage quality by disrupting protein foam and
20 conferring protection from rumen pasture bloat. Bloat is a digestive disorder that occurs on some highly nutritious forage legumes such as alfalfa (*Medicago sativa*) and white clover (*Trifolium repens*). Moderate amounts of tannin can also reduce digestion rates in the rumen and can reduce parasitic load sufficiently to increase the titre of amino acids and small peptides in the small intestine without
25 compromising total digestion.

Vestitone reductase (VR) is the penultimate enzyme in medicarpin biosynthesis. Medicarpin, a phytoalexin, has been associated with plant resistance to fungal pathogens.

While nucleic acid sequences encoding some flavonoid biosynthetic
30 enzymes CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR have been isolated for certain species of plants, there remains a need for materials useful in

modifying flavonoid biosynthesis; in modifying protein binding, metal chelation, anti-oxidation, and UV-light absorption; in modifying plant pigment production; in modifying plant defense to biotic stresses such as viruses, micro-organisms, insects or fungal pathogens; in modifying forage quality, for example by disrupting protein foam and/or conferring protection from rumen pasture bloat, particularly in forage legumes and grasses, including alfalfa, medics, clovers, ryegrasses and fescues, and for methods for their use.

It is an object of the present invention to overcome, or at least alleviate, one or more of the difficulties or deficiencies associated with the prior art.

10 In one aspect, the present invention provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding the flavonoid biosynthetic enzymes CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species and functionally active fragments and variants thereof.

15 The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of proteins which are related to CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR and functionally active fragments and variants thereof. Such proteins are referred to herein as CHI-like, CHS-like, CHR-like, DFR-like, LCR-like, F3'5'H-like, 20 F3H-like, F3'H-like, PAL-like and VR-like, respectively.

The individual or simultaneous enhancement or otherwise manipulation of CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and/or VR or like gene activities in plants may enhance or otherwise alter flavonoid biosynthesis; may enhance or otherwise alter the plant capacity for protein binding, metal chelation, anti-oxidation or UV-light absorption; may enhance or reduce or otherwise alter plant pigment production; may modify plant defense to biotic stresses such as viruses, micro-organisms, insects or fungal pathogens; and/or may modify forage quality, for example by disrupting protein foam and/or conferring protection from rumen pasture bloat.

The individual or simultaneous enhancement or otherwise manipulation of CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and/or VR or like gene activities in plants has significant consequences for a range of applications in, for example, plant production and plant protection. For example, it has applications in
5 increasing plant tolerance and plant defense to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; in improving plant forage quality, for example by disrupting protein foam and in conferring protection from rumen pasture bloat; in reducing digestion rates in the rumen and reducing parasitic load; in the production of plant compounds leading to health benefits, such as
10 isoflavonoids, which have been linked to anticancer benefits, and stilbenes that are believed to contribute to reduced heart disease.

Methods for the manipulation of CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and/or VR or like gene activities in plants, including legumes such as clovers (*Trifolium* species), lucerne (*Medicago sativa*) and grass species such as
15 ryegrasses (*Lolium* species) and fescues (*Festuca* species) may facilitate the production of, for example, forage legumes and forage grasses and other crops with enhanced tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; altered pigmentation in flowers; forage legumes with enhanced herbage quality and bloat-safety; crops with enhanced isoflavonoid
20 content leading to health benefits.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*). White clover (*Trifolium repens* L.) and perennial ryegrass (*Lolium perenne* L.) are key pasture legumes and grasses,
30 respectively, in temperate climates throughout the world. Perennial ryegrass is also an important turf grass.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof.

5 The term “isolated” means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid present in a living plant is not isolated, but the same nucleic acid separated from some or all of the coexisting materials in the natural system, is isolated. Such nucleic acids could be part of a vector and/or
10 such nucleic acids could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment.

Such nucleic acids or nucleic acid fragments could be assembled to form a consensus contig. As used herein, the term “consensus contig” refers to a nucleotide sequence that is assembled from two or more constituent nucleotide
15 sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acids or nucleic acid fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acids or nucleic acid fragments, the sequences (and thus their
20 corresponding nucleic acids or nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a CHI or CHI-like protein includes a nucleotide sequence selected from the group consisting of
25 (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 10, 12, 122 and 127 hereto (Sequence ID Nos: 1, 3 to 7, 8, 10 to 12, 13, 15 and 16, 17, 19 to 22, 307, and 309, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a CHS or CHS-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 13, 15, 16, 18, 19, 21, 22, 24, 25, 27, 28, 30, 31, 33, 34, 137, 142, 147, 152, 157 and 162 hereto (Sequence ID Nos: 23, 25 to 63, 64, 66 to 68, 69, 71 to 77, 78, 80 to 90, 91, 93 and 94, 95, 97 to 100, 101, 103 to 105, 106, 313, 315, 317, 319, 321, and 323, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a CHR or CHR-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 36, 38, 40, 41, 43 and 132 hereto (Sequence ID Nos: 108, 110, 112 to 116, 117, 119 to 134, and 311, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a DFR or DFR-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 44, 46, 47, 49, 50, 52, 54, 55, 57, 59, 61, 62, 64, 101, 103, 104, 106, 117 and 167 hereto (Sequence ID Nos: 135, 137 to 146, 147, 149 to 152, 153, 155, 157 and 158, 159, 161, 163, 165 to 167, 168, 170 to 184, 286, 288 to 292, 293, 295 to 297, 305, and 325, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an LCR or LCR-like protein includes a nucleotide sequence selected from the group

consisting of (a) sequences shown in Figures 65 and 67 hereto (Sequence ID Nos: 185 and 187 to 193, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an F3'5'H or F3'5'H-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 68, 70 and 72 hereto (Sequence ID Nos: 194, 196, and 198 to 201, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an F3H or F3H-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 73, 75, 76, 78, 107, 109, 111 and 172 hereto (Sequence ID Nos: 202, 204 to 244, 245, 247, 298, 300 to 302, 303, and 327, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an F3'H or F3'H-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 80 and 82 hereto (Sequence ID Nos: 249, and 251 and 252, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an PAL or PAL-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 83, 85, 86, 88, 89, 91, 93, 95, 97, 177, 182 and 187 hereto (Sequence ID Nos: 253, 255 to 257, 258, 260 to 267, 268, 270, 272, 274, 276 and 277, 329, 331, and 333, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an VR or VR-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 98, 100 and 192 hereto (Sequence ID Nos: 278, 280 to 285, and 335, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

By "functionally active" in relation to nucleic acids it is meant that the fragment or variant (such as an analogue, derivative or mutant) encodes a polypeptide which is capable of modifying flavonoid biosynthesis in a plant. Such variants include naturally occurring allelic variants and non-naturally occurring variants. Additions, deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the relevant part of the above mentioned nucleotide sequence, more preferably at least approximately 90% identity, even more preferably at least approximately 95% identity, most preferably at least approximately 98% homology. Such functionally active variants and fragments include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least

10 nucleotides, more preferably at least 15 nucleotides, most preferably at least 20 nucleotides.

Nucleic acids or nucleic acid fragments encoding at least a portion of several CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR have been
5 isolated and identified. The nucleic acids or nucleic acid fragments of the present invention may be used to isolate cDNAs and genes encoding homologous proteins from the same or other plant species. Isolation of homologous genes using sequence-dependent protocols, such as methods of nucleic acid hybridisation, and methods of DNA and RNA amplification as exemplified by various uses of nucleic
10 acid amplification technologies (e.g. polymerase chain reaction, ligase chain reaction), is well known in the art.

For example, genes encoding other CHI or CHI-like, CHS or CHS-like, CHR or CHR-like, DFR or DFR-like, LCR or LCR-like, F3'5'H or F3'5'H-like, F3H or F3H-like, F3'H or F3'H-like, PAL or PAL-like and VR or VR-like proteins, either as
15 cDNAs or genomic DNAs, may be isolated directly by using all or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant employing the methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized
20 by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labelling, nick translation, or end-labelling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers may be designed and used to amplify a part or all of the sequences of the present
25 invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full-length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, short segments of the nucleic acids or nucleic acid fragments of
30 the present invention may be used in amplification protocols to amplify longer nucleic acids or nucleic acid fragments encoding homologous genes from DNA or

RNA. For example, polymerase chain reaction may be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol [Frohman *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:8998, the entire disclosure of which is incorporated herein by reference] to generate cDNAs by using PCR to amplify 5 copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or 5' cDNA fragments may be isolated [Ohara *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:5673; Loh *et al.* (1989) *Science* 243:217, the entire disclosures of which are incorporated herein by reference]. Products generated by the 3' and 5' RACE 10 procedures may be combined to generate full-length cDNAs. 15

In a second aspect of the present invention there is provided a substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of CHI and CHI-like, CHS and CHS-like, CHR and CHR-like, DFR and DFR-like, 20 LCR and LCR-like, F3'5'H and F3'5'H-like, F3H and F3H-like, F3'H and F3'H-like, PAL and PAL-like, VR and VR-like; and functionally active fragments and variants thereof.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*). 25 30

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated CHI or CHI-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 2, 5, 8, 11, 123 and 128 hereto (Sequence ID Nos: 2, 9, 14, 18, 308, and 310, respectively),
5 and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated CHS or CHS-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 14, 17, 20, 23, 26, 29, 32, 35, 138, 143, 148, 153, 158 and 163 hereto
10 (Sequence ID Nos: 24, 65, 70, 79, 92, 96, 102, 107, 314, 316, 318, 320, 322, and 324, respectively), and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated CHR or CHR-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in
15 Figures 37, 39, 42 and 133 hereto (Sequence ID Nos: 109, 111, 118, and 312, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated DFR or DFR-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in
20 Figures 45, 48, 51, 53, 56, 58, 60, 63, 102, 105, 118 and 168 hereto (Sequence ID Nos: 136, 148, 54, 156, 160, 162, 164, 169, 287, 294, 306, and 326, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated LCR or LCR-like polypeptide includes an amino
25 acid sequence shown in Figure 66 hereto (Sequence ID No: 186), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated F3'5'H or F3'5'H-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown

in Figures 69 and 71 hereto (Sequence ID Nos: 195 and 197, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated F3H or F3H-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in
5 Figures 74, 77, 79, 108, 112 and 173 hereto (Sequence ID Nos: 203, 246, 248, 299, 304, and 328, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the
10 substantially purified or isolated F3'H or F3'H-like polypeptide includes an amino acid sequence shown in Figure 81 hereto (Sequence ID No: 250), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated PAL or PAL-like polypeptide includes an amino
15 acid sequence selected from the group consisting of the sequences shown in Figures 84, 87, 90, 92, 94, 96, 178, 183 and 188 hereto (Sequence ID Nos: 254, 259, 269, 271, 273, 275, 330, 332, and 334, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the
20 substantially purified or isolated VR or VR-like polypeptide includes an amino acid sequence shown in Figures 99 and 193 hereto (Sequence ID Nos: 279 and 336, respectively), and functionally active fragments and variants thereof.

By "functionally active" in relation to polypeptides it is meant that the fragment or variant has one or more of the biological properties of the proteins
25 CHI, CHI-like, CHS, CHS-like, CHR, CHR-like, DFR, DFR-like, LCR, LCR-like, F3'5'H, F3'5'H-like, F3H, F3H-like, F3'H, F3'H-like, PAL, PAL-like, VR and VR-like, respectively. Additions, deletions, substitutions and derivatizations of one or more of the amino acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally

active fragment or variant has at least approximately 60% identity to the relevant part of the above mentioned amino acid sequence, more preferably at least approximately 80% identity, even more preferably at least approximately 90% identity most preferably at least approximately 95% homology. Such functionally
5 active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, most preferably at least 20 amino acids.

In a further embodiment of this aspect of the invention, there is provided a
10 polypeptide recombinantly produced from a nucleic acid or nucleic acid fragment according to the present invention. Techniques for recombinantly producing polypeptides are well known to those skilled in the art.

Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA
15 expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins including the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA
20 clones of interest.

A genotype is the genetic constitution of an individual or group. Variations in genotype are important in commercial breeding programs, in determining parentage, in diagnostics and fingerprinting, and the like. Genotypes can be readily described in terms of genetic markers. A genetic marker identifies a
25 specific region or locus in the genome. The more genetic markers, the finer defined is the genotype. A genetic marker becomes particularly useful when it is allelic between organisms because it then may serve to unambiguously identify an individual. Furthermore, a genetic marker becomes particularly useful when it is based on nucleic acid sequence information that can unambiguously establish a
30 genotype of an individual and when the function encoded by such nucleic acid is known and is associated with a specific trait. Such nucleic acids and/or nucleotide

sequence information including single nucleotide polymorphisms (SNPs), variations in single nucleotides between allelic forms of such nucleotide sequence, may be used as perfect markers or candidate genes for the given trait.

Applicants have identified a number of SNPs of the nucleic acids or nucleic acid fragments of the present invention. These are indicated (marked with grey on the black background) in the figures that show multiple alignments of nucleotide sequences of nucleic acid fragments contributing to consensus contig sequences. See for example, Figures 3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 40, 43, 46, 49, 54, 61, 64, 67, 72, 75, 82, 85, 88, 97, 100, 103, 106 and 109 hereto (Sequence ID Nos: 3 to 7, 10 to 12, 15 and 16, 19 to 22, 25 to 63, 66 to 68, 71 to 77, 80 to 90, 93 and 94, 97 to 100, 103 to 105, 112 to 116, 119 to 134, 137 to 146, 149 to 152, 157 and 158, 165 to 167, 170 to 184, 187 to 193, 198 to 201, 204 to 244, 251 and 252, 255 to 257, 260 to 267, 276 and 277, 280 to 285, 288 to 292, 295 to 297, and 300 to 302, respectively).

Accordingly, in a further aspect of the present invention, there is provided a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid or nucleic acid fragment according to the present invention or complements or sequences antisense thereto, and functionally active fragments and variants thereof.

In a still further aspect of the present invention there is provided a method of isolating a nucleic acid or nucleic acid fragment of the present invention including a SNP, said method including sequencing nucleic acid fragments from a nucleic acid library.

The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid or nucleic acid fragments may be isolated from a recombinant plasmid or may be amplified, for example using polymerase chain reaction.

The sequencing may be performed by techniques known to those skilled in the art.

In a still further aspect of the present invention, there is provided use of the nucleic acids or nucleic acid fragments of the present invention including SNPs,
5 and/or nucleotide sequence information thereof, as molecular genetic markers.

In a still further aspect of the present invention there is provided use of a nucleic acid or nucleic acid fragment of the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the
10 present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence
15 information thereof may be used as molecular genetic markers in plant improvement in relation to plant tolerance to biotic stresses such as viruses, micro-organisms, insects, fungal pathogens; in relation to forage quality; in relation to bloat safety; in relation to condensed tannin content; in relation to plant pigmentation. Even more particularly, sequence information revealing SNPs in
20 allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging and mapping and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues.

In a still further aspect of the present invention there is provided a construct
25 including a nucleic acid or nucleic acid fragment according to the present invention.

The term "construct" as used herein refers to an artificially assembled or isolated nucleic acid molecule which includes the gene of interest. In general a construct may include the gene or genes of interest, a marker gene which in some

cases can also be the gene of interest and appropriate regulatory sequences. It should be appreciated that the inclusion of regulatory sequences in a construct is optional, for example, such sequences may not be required in situations where the regulatory sequences of a host cell are to be used. The term construct includes
5 vectors but should not be seen as being limited thereto.

In a still further aspect of the present invention there is provided a vector including a nucleic acid or nucleic acid fragment according to the present invention.

The term "vector" as used herein encompasses both cloning and
10 expression vectors. Vectors are often recombinant molecules containing nucleic acid molecules from several sources.

In a preferred embodiment of this aspect of the invention, the vector may include a regulatory element such as a promoter, a nucleic acid or nucleic acid fragment according to the present invention and a terminator; said regulatory
15 element, nucleic acid or nucleic acid fragment and terminator being operatively linked.

By "operatively linked" is meant that said regulatory element is capable of causing expression of said nucleic acid or nucleic acid fragment in a plant cell and said terminator is capable of terminating expression of said nucleic acid or nucleic
20 acid fragment in a plant cell. Preferably, said regulatory element is upstream of said nucleic acid or nucleic acid fragment and said terminator is downstream of said nucleic acid or nucleic acid fragment.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, non-
25 chromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from *Agrobacterium tumefaciens*, derivatives of the Ri plasmid from *Agrobacterium rhizogenes*; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids

and phage DNA. However, any other vector may be used as long as it is replicable, integrative or viable in the plant cell.

The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they
5 are functional in the target plant cell.

Preferably the regulatory element is a promoter. A variety of promoters which may be employed in the vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the desired tissue specificity of the vector, and whether constitutive or inducible
10 expression is desired and the nature of the plant cell to be transformed (eg. monocotyledon or dicotyledon). Particularly suitable constitutive promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) promoter and derivatives thereof, the maize Ubiquitin promoter, and the rice Actin promoter.

A variety of terminators which may be employed in the vectors of the
15 present invention are also well known to those skilled in the art. The terminator may be from the same gene as the promoter sequence or a different gene. Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (*nos*), the octopine synthase (*ocs*) and the *rbcS* genes.

20 The vector, in addition to the regulatory element, the nucleic acid or nucleic acid fragment of the present invention and the terminator, may include further elements necessary for expression of the nucleic acid or nucleic acid fragment, in different combinations, for example vector backbone, origin of replication (*ori*), multiple cloning sites, spacer sequences, enhancers, introns (such as the maize
25 Ubiquitin *Ubi* intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (*npt2*) gene, the hygromycin phosphotransferase (*hph*) gene, the phosphinothricin acetyltransferase (*bar* or *pat*) gene and the gentamycin acetyl transferase (*aacC1*) gene], and reporter genes [such as beta-glucuronidase (GUS) gene (*gusA*) and green fluorescent protein

(gfp)]. The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector
5 in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, northern and Western blot hybridisation analyses.

Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid or
10 nucleic acid fragment. Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such techniques include the use of linkers, such as synthetic linkers, for example including one or more restriction enzyme sites.

The constructs and vectors of the present invention may be incorporated
15 into a variety of plants, including monocotyledons (such as grasses from the genera *Lolium*, *Festuca*, *Paspalum*, *Pennisetum*, *Panicum* and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley), dicotyledons (such as *Arabidopsis*, tobacco, clovers, medics, eucalyptus, potato, sugarbeet, canola, soybean, chickpea) and gymnosperms. In a preferred embodiment, the constructs
20 and vectors may be used to transform monocotyledons, preferably grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species), more preferably perennial ryegrass, including forage- and turf-type cultivars. In an alternate preferred embodiment, the constructs and vectors may be used to transform dicotyledons, preferably forage legume species such as clovers
25 (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*). Clovers, alfalfa and medics are key pasture legumes in temperate climates throughout the world.

Techniques for incorporating the constructs and vectors of the present
30 invention into plant cells (for example by transduction, transfection or

transformation) are well known to those skilled in the art. Such techniques include *Agrobacterium* mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into immature embryos and high velocity projectile introduction to cells, tissues, calli,
5 immature and mature embryos. The choice of technique will depend largely on the type of plant to be transformed.

Cells incorporating the constructs and vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to regenerate transformed plants, using techniques well known in the art. The culture
10 conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

In a further aspect of the present invention there is provided a plant cell,
15 plant, plant seed or other plant part, including, e.g. transformed with, a construct, vector, nucleic acid or nucleic acid fragment of the present invention.

The plant cell, plant, plant seed or other plant part may be from any suitable species, including monocotyledons, dicotyledons and gymnosperms. In a preferred embodiment the plant cell, plant, plant seed or other plant part may be
20 from a monocotyledon, preferably a grass species, more preferably a ryegrass (*Lolium* species) or fescue (*Festuca* species), even more preferably perennial ryegrass, including both forage- and turf-type cultivars. In an alternate preferred embodiment the plant cell, plant, plant seed or other plant part may be from a dicotyledon, preferably forage legume species such as clovers (*Trifolium* species)
25 and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*).

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant cell of the present invention.

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant of the present invention.

In a further aspect of the present invention there is provided a method of modifying flavonoid biosynthesis in a plant; said method including introducing
5 into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or a vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying protein binding, metal chelation, anti-oxidation, and/or UV-light absorption in a plant, said method including introducing into said plant an effective
10 amount of a nucleic acid or nucleic acid fragment, construct and/or a vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying pigment production in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct
15 and/or a vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying plant defense to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or a
20 vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying forage quality of a plant by disrupting protein foam and/or conferring protection from rumen pasture bloat, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct
25 and/or a vector according to the present invention.

By "an effective amount" it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, or a plant, plant seed or other plant part derived therefrom. Such amounts can be readily determined by an appropriately

skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is incorporated herein by reference.

Using the methods and materials of the present invention, flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety; and/or isoflavonoid content leading to health benefits, may be increased or otherwise modified, for example by incorporating additional copies of a sense nucleic acid or nucleic acid fragment of the present invention. They may be decreased or otherwise modified, for example by incorporating an antisense nucleic acid or nucleic acid fragment of the present invention.

The present invention will now be more fully described with reference to the accompanying Examples and drawings. It should be understood, however, that the description following is illustrative only and should not be taken in any way as a restriction on the generality of the invention described above.

In the Figures

Figure 1 shows the consensus contig nucleotide sequence of TrCH1a (Sequence ID No: 1).

Figure 2 shows the deduced amino acid sequence of TrCH1a (Sequence ID No: 2).

Figure 3 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCH1a (Sequence ID Nos: 3 to 7).

Figure 4 shows the consensus contig nucleotide sequence of TrCH1b (Sequence ID No: 8).

Figure 5 shows the deduced amino acid sequence of TrCH1b (Sequence ID No: 9).

Figure 6 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCH1b (Sequence ID Nos: 10 to 12).

Figure 7 shows the consensus contig nucleotide sequence of TrCH1c (Sequence
5 ID No: 13).

Figure 8 shows the deduced amino acid sequence of TrCH1c (Sequence ID No: 14).

Figure 9 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCH1c (Sequence ID Nos: 15 and
10 16).

Figure 10 shows the consensus contig nucleotide sequence of TrCH1d (Sequence ID No: 17).

Figure 11 shows the deduced amino acid sequence of TrCH1d (Sequence ID No: 18).

Figure 12 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCH1d (Sequence ID Nos: 19 to 22).

Figure 13 shows the consensus contig nucleotide sequence of TrCHSa (Sequence ID No: 23).

Figure 14 shows the deduced amino acid sequence of TrCHSa (Sequence ID No: 24).

Figure 15 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSa (Sequence ID Nos: 25 to 63).

Figure 16 shows the consensus contig nucleotide sequence of TrCHSb (Sequence ID No: 64).

Figure 17 shows the deduced amino acid sequence of TrCHSb (Sequence ID No: 65).

- 5 Figure 18 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSb (Sequence ID Nos: 66 to 68).

Figure 19 shows the consensus contig nucleotide sequence of TrCHSc (Sequence ID No: 69).

- 10 Figure 20 shows the deduced amino acid sequence of TrCHSc (Sequence ID No: 70).

Figure 21 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSc (Sequence ID Nos: 71 to 77).

- 15 Figure 22 shows the consensus contig nucleotide sequence of TrCHSd (Sequence ID No: 78).

Figure 23 shows the deduced amino acid sequence of TrCHSd (Sequence ID No: 79).

- 20 Figure 24 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSd (Sequence ID Nos: 80 to 90).

Figure 25 shows the consensus contig nucleotide sequence of TrCHSe (Sequence ID No: 91).

- 25 Figure 26 shows the deduced amino acid sequence of TrCHSe (Sequence ID No: 92).

Figure 27 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSe (Sequence ID Nos: 93 and 94).

Figure 28 shows the consensus contig nucleotide sequence of TrCHSf (Sequence
5 ID No: 95).

Figure 29 shows the deduced amino acid sequence of TrCHSf (Sequence ID No: 96).

Figure 30 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSf (Sequence ID Nos: 97 to
10 100).

Figure 31 shows the consensus contig nucleotide sequence of TrCHSg (Sequence ID No: 101).

Figure 32 shows the deduced amino acid sequence of TrCHSg (Sequence ID No: 102).

Figure 33 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSg (Sequence ID Nos: 103 to
15 105).

Figure 34 shows the consensus contig nucleotide sequence of TrCHSh (Sequence ID No: 106).

Figure 35 shows the deduced amino acid sequence of TrCHSh (Sequence ID No: 107).

Figure 36 shows the nucleotide sequence of TrCHRa (Sequence ID No: 108).

Figure 37 shows the deduced amino acid sequence of TrCHRa (Sequence ID No: 109).

Figure 38 shows the consensus contig nucleotide sequence of TrCHRB (Sequence ID No: 110).

Figure 39 shows the deduced amino acid sequence of TrCHRB (Sequence ID No: 111).

- 5 Figure 40 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHRB (Sequence ID Nos: 112 to 116).

Figure 41 shows the consensus contig nucleotide sequence of TrCHRC (Sequence ID No: 117).

- 10 Figure 42 shows the deduced amino acid sequence of TrCHRC (Sequence ID No: 118).

Figure 43 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHRC (Sequence ID Nos: 119 to 134).

- 15 Figure 44 shows the consensus contig nucleotide sequence of TrDFRa (Sequence ID No: 135).

Figure 45 shows the deduced amino acid sequence of TrDFRa (Sequence ID No: 136).

- 20 Figure 46 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRa (Sequence ID Nos: 137 to 146).

Figure 47 shows the consensus contig nucleotide sequence of TrDFRb (Sequence ID No: 147).

- 25 Figure 48 shows the deduced amino acid sequence of TrDFRb (Sequence ID No: 148).

Figure 49 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRb (Sequence ID Nos: 149 to 152).

Figure 50 shows the nucleotide sequence of TrDFRc (Sequence ID No: 153).

- 5 Figure 51 shows the deduced amino acid sequence of TrDFRc (Sequence ID No: 154).

Figure 52 shows the consensus contig nucleotide sequence of TrDFRd (Sequence ID No: 155).

- 10 Figure 53 shows the deduced amino acid sequence of TrDFRd (Sequence ID No: 156).

Figure 54 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRd (Sequence ID Nos: 157 and 158).

Figure 55 shows the nucleotide sequence of TrDFRe (Sequence ID No: 159).

- 15 Figure 56 shows the deduced amino acid sequence of TrDFRe (Sequence ID No: 160).

Figure 57 shows the nucleotide sequence of TrDFRf (Sequence ID No: 161).

Figure 58 shows the deduced amino acid sequence of TrDFRf (Sequence ID No: 162).

- 20 Figure 59 shows the consensus contig nucleotide sequence of TrDFRg (Sequence ID No: 163).

Figure 60 shows the deduced amino acid sequence of TrDFRg (Sequence ID No: 164).

Figure 61 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRg (Sequence ID Nos: 165 to 167).

Figure 62 shows the consensus contig nucleotide sequence of TrDFRh (Sequence
5 ID No: 168).

Figure 63 shows the deduced amino acid sequence of TrDFRh (Sequence ID No: 169).

Figure 64 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRh (Sequence ID Nos: 170 to
10 184).

Figure 65 shows the consensus contig nucleotide sequence of TrLCRa (Sequence ID No: 185).

Figure 66 shows the deduced amino acid sequence of TrLCRa (Sequence ID No: 186).

Figure 67 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrLCRa (Sequence ID Nos: 187 to 193).

Figure 68 shows the nucleotide sequence of TrF3'5'Ha (Sequence ID No: 194).

Figure 69 shows the deduced amino acid sequence of TrF3'5'Ha (Sequence ID
20 No: 195).

Figure 70 shows the consensus contig nucleotide sequence of TrF3'5'Hb (Sequence ID No: 196).

Figure 71 shows the deduced amino acid sequence of TrF3'5'Hb (Sequence ID No: 197).

Figure 72 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrF3'5'Hb (Sequence ID Nos: 198 to 201).

Figure 73 shows the consensus contig nucleotide sequence of TrF3Ha (Sequence ID No: 202).

Figure 74 shows the deduced amino acid sequence of TrF3Ha (Sequence ID No: 203).

Figure 75 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrF3Ha (Sequence ID Nos: 204 to 244).

Figure 76 shows the nucleotide sequence of TrF3Hb (Sequence ID No: 245).

Figure 77 shows the deduced amino acid sequence of TrF3Hb (Sequence ID No: 246).

Figure 78 shows the nucleotide sequence of TrF3Hc (Sequence ID No: 247).

Figure 79 shows the deduced amino acid sequence of TrF3Hc (Sequence ID No: 248).

Figure 80 shows the consensus contig nucleotide sequence of TrF3'Ha (Sequence ID No: 249).

Figure 81 shows the deduced amino acid sequence of TrF3'Ha (Sequence ID No: 250).

Figure 82 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrF3'Ha (Sequence ID Nos: 251 and 252).

Figure 83 shows the consensus contig nucleotide sequence of TrPALa (Sequence ID No: 253).

Figure 84 shows the deduced amino acid sequence of TrPALa (Sequence ID No: 254).

- 5 Figure 85 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPALa (Sequence ID Nos: 255 to 257).

Figure 86 shows the consensus contig nucleotide sequence of TrPALb (Sequence ID No: 258).

- 10 Figure 87 shows the deduced amino acid sequence of TrPALb (Sequence ID No: 259).

Figure 88 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPALb (Sequence ID Nos: 260 to 267).

- 15 Figure 89 shows the nucleotide sequence of TrPALc (Sequence ID No: 268).

Figure 90 shows the deduced amino acid sequence of TrPALc (Sequence ID No: 269).

Figure 91 shows the nucleotide sequence of TrPALd (Sequence ID No: 270).

- 20 Figure 92 shows the deduced amino acid sequence of TrPALd (Sequence ID No: 271).

Figure 93 shows the nucleotide sequence of TrPALe (Sequence ID No: 272).

Figure 94 shows the deduced amino acid sequence of TrPALe (Sequence ID No: 273).

Figure 95 shows the consensus contig nucleotide sequence of TrPALf (Sequence ID No: 274).

Figure 96 shows the deduced amino acid sequence of TrPALf (Sequence ID No: 275).

- 5 Figure 97 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPALf (Sequence ID Nos: 276 and 277).

Figure 98 shows the consensus contig nucleotide sequence of TrVRa (Sequence ID No: 278).

- 10 Figure 99 shows the deduced amino acid sequence of TrVRa (Sequence ID No: 279).

Figure 100 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrVRa (Sequence ID Nos: 280 to 285).

- 15 Figure 101 shows the consensus contig nucleotide sequence of LpDFRa (Sequence ID No: 286).

Figure 102 shows the deduced amino acid sequence of LpDFRa (Sequence ID No: 287).

- 20 Figure 103 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpDFRa (Sequence ID Nos: 288 to 292).

Figure 104 shows the consensus contig nucleotide sequence of LpDFRb (Sequence ID No: 293).

- 25 Figure 105 shows the deduced amino acid sequence of LpDFRb (Sequence ID No: 294).

Figure 106 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpDFRb (Sequence ID Nos: 295 to 297).

Figure 107 shows the consensus contig nucleotide sequence of LpF3Ha
5 (Sequence ID No: 298).

Figure 108 shows the deduced amino acid sequence of LpF3Ha (Sequence ID No: 299).

Figure 109 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpF3Ha (Sequence ID Nos: 300 to
10 302).

Figure 110 shows a plasmid map of the cDNA encoding perennial ryegrass F3OH.

Figure 111 shows the full nucleotide sequence of perennial ryegrass F3OH cDNA (Sequence ID No: 303).

Figure 112 shows the deduced amino acid sequence of perennial ryegrass F3OH
15 cDNA (Sequence ID No: 304).

Figure 113 shows plasmid maps of sense and antisense constructs of LpF3OH in pDH51 transformation vector.

Figure 114 shows plasmid maps of sense and antisense constructs of LpF3OH in pPZP221:35S² binary transformation vector.

20 Figure 115 shows screening by Southern hybridisation for RFLPs using LpF3OH as a probe.

Figure 116 shows a plasmid map of the cDNA encoding white clover BANa.

Figure 117 shows the full nucleotide sequence of white clover BANa cDNA (Sequence ID No: 305).

Figure 118 shows the deduced amino acid sequence of white clover BANa cDNA (Sequence ID No: 306).

Figure 119 shows plasmid maps of sense and antisense constructs of TrBANa in pDH51 transformation vector.

- 5 Figure 120 shows plasmid maps of sense and antisense constructs of TrBANa in pPZP221:35S² binary transformation vector.

Figure 121 shows a plasmid map of the cDNA encoding white clover CH1a.

Figure 122 shows the full nucleotide sequence of white clover CH1a cDNA (Sequence ID No: 307).

- 10 Figure 123 shows the deduced amino acid sequence of white clover CH1a cDNA (Sequence ID No: 308).

Figure 124 shows plasmid maps of sense and antisense constructs of TrCH1a in pDH51 transformation vector.

- 15 Figure 125 shows plasmid maps of sense and antisense constructs of TrCH1a in pPZP221:35S² binary transformation vector.

Figure 126 shows a plasmid map of the cDNA encoding white clover CH1d.

Figure 127 shows the full nucleotide sequence of white clover CH1d cDNA (Sequence ID No: 309).

- 20 Figure 128 shows the deduced amino acid sequence of white clover CH1d cDNA (Sequence ID No: 310).

Figure 129 shows plasmid maps of sense and antisense constructs of TrCH1d in pDH51 transformation vector.

Figure 130 shows plasmid maps of sense and antisense constructs of TrCHId in pPZP221:35S² binary transformation vector.

Figure 131 shows a plasmid map of the cDNA encoding white clover CHRc.

Figure 132 shows the full nucleotide sequence of white clover CHRc cDNA
5 (Sequence ID No: 311).

Figure 133 shows the deduced amino acid sequence of white clover CHRc cDNA (Sequence ID No: 312).

Figure 134 shows plasmid maps of sense and antisense constructs of TrCHRc in pDH51 transformation vector.

10 Figure 135 shows plasmid maps of sense and antisense constructs of TrCHRc in pPZP221:35S² binary transformation vector.

Figure 136 shows a plasmid map of the cDNA encoding white clover CHSa1.

Figure 137 shows the full nucleotide sequence of white clover CHSa1 cDNA (Sequence ID No: 313).

15 Figure 138 shows the deduced amino acid sequence of white clover CHSa1 cDNA (Sequence ID No: 314).

Figure 139 shows plasmid maps of sense and antisense constructs of TrCHSa1 in pDH51 transformation vector.

Figure 140 shows plasmid maps of sense and antisense constructs of TrCHSa1 in
20 pPZP221:35S² binary transformation vector.

Figure 141 shows a plasmid map of the cDNA encoding white clover CHSa3.

Figure 142 shows the full nucleotide sequence of white clover CHSa3 cDNA (Sequence ID No: 315).

Figure 143 shows the deduced amino acid sequence of white clover CHSa3 cDNA (Sequence ID No: 316).

Figure 144 shows plasmid maps of sense and antisense constructs of TrCHSa3 in pDH51 transformation vector.

- 5 Figure 145 shows plasmid maps of sense and antisense constructs of TrCHSa3 in pPZP221:35S² binary transformation vector.

Figure 146 shows a plasmid map of the cDNA encoding white clover CHSc.

Figure 147 shows the full nucleotide sequence of white clover CHSc cDNA (Sequence ID No: 317).

- 10 Figure 148 shows the deduced amino acid sequence of white clover CHSc cDNA (Sequence ID No: 318).

Figure 149 shows plasmid maps of sense and antisense constructs of TrCHSc in pDH51 transformation vector.

- Figure 150 shows plasmid maps of sense and antisense constructs of TrCHSc in
15 pPZP221:35S² binary transformation vector.

Figure 151 shows a plasmid map of the cDNA encoding white clover CHSd2.

Figure 152 shows the full nucleotide sequence of white clover CHSd2 cDNA (Sequence ID No: 319).

- Figure 153 shows the deduced amino acid sequence of white clover CHSd2 cDNA
20 (Sequence ID No: 320).

Figure 154 shows plasmid maps of sense and antisense constructs of TrCHSd2 in pDH51 transformation vector.

Figure 155 shows plasmid maps of sense and antisense constructs of TrCHSd2 in pPZP221:35S² binary transformation vector.

Figure 156 shows a plasmid map of the cDNA encoding white clover CHSf.

Figure 157 shows the full nucleotide sequence of white clover CHSf cDNA
5 (Sequence ID No: 321).

Figure 158 shows the deduced amino acid sequence of white clover CHSf cDNA (Sequence ID No: 322).

Figure 159 shows plasmid maps of sense and antisense constructs of TrCHSf in pDH51 transformation vector.

10 Figure 160 shows plasmid maps of sense and antisense constructs of TrCHSf in pPZP221:35S² binary transformation vector.

Figure 161 shows a plasmid map of the cDNA encoding white clover CHSh.

Figure 162 shows the full nucleotide sequence of white clover CHSh cDNA (Sequence ID No: 323).

15 Figure 163 shows the deduced amino acid sequence of white clover CHSh cDNA (Sequence ID No: 324).

Figure 164 shows plasmid maps of sense and antisense constructs of TrCHSh in pDH51 transformation vector.

Figure 165 shows plasmid maps of sense and antisense constructs of TrCHSh in
20 pPZP221:35S² binary transformation vector.

Figure 166 shows a plasmid map of the cDNA encoding white clover DFRd.

Figure 167 shows the full nucleotide sequence of white clover DFRd cDNA (Sequence ID No: 325).

Figure 168 shows the deduced amino acid sequence of white clover DFRd cDNA (Sequence ID No: 326).

Figure 169 shows plasmid maps of sense and antisense constructs of TrDFRd in pDH51 transformation vector.

- 5 Figure 170 shows plasmid maps of sense and antisense constructs of TrDFRd in pPZP221:35S² binary transformation vector.

Figure 171 shows a plasmid map of the cDNA encoding white clover F3Ha.

Figure 172 shows the full nucleotide sequence of white clover F3Ha cDNA (Sequence ID No: 327).

- 10 Figure 173 shows the deduced amino acid sequence of white clover F3Ha cDNA (Sequence ID No: 328).

Figure 174 shows plasmid maps of sense and antisense constructs of TrF3Ha in pDH51 transformation vector.

- Figure 175 shows plasmid maps of sense and antisense constructs of TrF3Ha in
15 pPZP221:35S² binary transformation vector.

Figure 176 shows a plasmid map of the cDNA encoding white clover PALa.

Figure 177 shows the full nucleotide sequence of white clover PALa cDNA (Sequence ID No: 329).

- Figure 178 shows the deduced amino acid sequence of white clover PALa cDNA
20 (Sequence ID No: 330).

Figure 179 shows plasmid maps of sense and antisense constructs of TrPALa in pDH51 transformation vector.

Figure 180 shows plasmid maps of sense and antisense constructs of TrPALa in pPZP221:35S² binary transformation vector.

Figure 181 shows a plasmid map of the cDNA encoding white clover PALb.

Figure 182 shows the full nucleotide sequence of white clover PALb cDNA
5 (Sequence ID No: 331).

Figure 183 shows the deduced amino acid sequence of white clover PALb cDNA (Sequence ID No: 332).

Figure 184 shows plasmid maps of sense and antisense constructs of TrPALb in pDH51 transformation vector.

10 Figure 185 shows plasmid maps of sense and antisense constructs of TrPALb in pPZP221:35S² binary transformation vector.

Figure 186 shows a plasmid map of the cDNA encoding white clover PALf.

Figure 187 shows the full nucleotide sequence of white clover PALf cDNA (Sequence ID No: 333).

15 Figure 188 shows the deduced amino acid sequence of white clover PALf cDNA (Sequence ID No: 334).

Figure 189 shows plasmid maps of sense and antisense constructs of TrPALf in pDH51 transformation vector.

Figure 190 shows plasmid maps of sense and antisense constructs of TrPALf in
20 pPZP221:35S² binary transformation vector.

Figure 191 shows a plasmid map of the cDNA encoding white clover VRa.

Figure 192 shows the full nucleotide sequence of white clover VRa cDNA (Sequence ID No: 335).

Figure 193 shows the deduced amino acid sequence of white clover VRa cDNA (Sequence ID No: 336).

Figure 194 shows plasmid maps of sense and antisense constructs of TrVRa in pDH51 transformation vector.

- 5 Figure 195 shows plasmid maps of sense and antisense constructs of TrVRa in pPZP221:35S² binary transformation vector.

Figure 196 shows A, infiltration of Arabidopsis plants; B, selection of transgenic Arabidopsis plants on medium containing 75 μ g/ml gentamycin; C, young transgenic Arabidopsis plants; D, E, two representative results of real-time PCR
10 analysis of Arabidopsis transformed with chimeric genes involved in flavonoid biosynthesis.

Figure 197 shows the genetic map detailing the relation of perennial ryegrass genes involved in flavonoid biosynthesis.

EXAMPLE 1

- 15 **Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for CHI, CHI-like, CHS, CHS-like, CHR, CHR-like, DFR, DFR-like, LCR, LCR-like, F3'5'H, F3'5'H-like, F3H, F3H-like, F3'H, F3'H-like, PAL, PAL-like, VR and VR-like proteins from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*)**

20

cDNA libraries representing mRNAs from various organs and tissues of white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*) were prepared. The characteristics of the white clover and perennial ryegrass libraries, respectively, are described below (Tables 1 and 2).

TABLE 1**cDNA libraries from white clover (*Trifolium repens*)**

Library	Organ/Tissue
01wc	Whole seedling, light grown
02wc	Nodulated root 3, 5, 10, 14, 21 & 28 day old seedling
03wc	Nodules pinched off roots of 42 day old rhizobium inoculated plants
04wc	Cut leaf and stem collected after 0, 1, 4, 6 & 14 h after cutting
05wc	Inflorescences: <50% open, not fully open and fully open
06wc	Dark grown etiolated
07wc	Inflorescence – very early stages, stem elongation, < 15 petals, 15-20 petals
08wc	seed frozen at –80°C, imbibed in dark overnight at 10°C
09wc	Drought stressed plants
10wc	AMV infected leaf
11wc	WCMV infected leaf
12wc	Phosphorus starved plants
13wc	Vegetative stolon tip
14wc	stolon root initials
15wc	Senescing stolon
16wc	Senescing leaf

TABLE 2

5

cDNA libraries from perennial ryegrass (*Lolium perenne*)

Library	Organ/Tissue
01rg	Roots from 3-4 day old light-grown seedlings
02rg	Leaves from 3-4 day old light-grown seedlings
03rg	Etiolated 3-4 day old dark-grown seedlings
04rg	Whole etiolated seedlings (1-5 day old and 17 days old)
05rg	Senescing leaves from mature plants

Library	Organ/Tissue
06rg	Whole etiolated seedlings (1-5 day old and 17 days old)
07rg	Roots from mature plants grown in hydroponic culture
08rg	Senescent leaf tissue
09rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
10rg	Embryogenic suspension-cultured cells
11rg	Non-embryogenic suspension-cultured cells
12rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
13rg	Shoot apices including vegetative apical meristems
14rg	Immature inflorescences including different stages of inflorescence meristem and inflorescence development
15rg	Defatted pollen
16rg	Leaf blades and leaf sheaths (<i>rbcL</i> , <i>rbcS</i> , <i>cab</i> , <i>wir2A</i> subtracted)
17rg	Senescing leaves and tillers
18rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
19rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with half-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
20rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with double-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
21rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
22rg	Spikelets with open and maturing florets
23rg	Mature roots (specific subtraction with leaf tissue)

The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the

5 manufacturers' instructions. cDNAs may be generated using the SMART PCR

cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The

5 cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into *Escherichia coli* Epicurian coli XL10-Gold ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.

10 Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the

15 plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into *E. coli* DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).

Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared

20 from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert

25 DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analyzed using an Applied Biosystems ABI 3700 sequence analyser.

EXAMPLE 2

DNA sequence analyses

The cDNA clones encoding CHI, CHI-like, CHS, CHS-like, CHR, CHR-like, DFR, DFR-like, LCR, LCR-like, F3'5'H, F3'5'H-like, F3H, F3H-like, F3'H, F3'H-like, PAL, PAL-like, VR and VR-like proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul *et al.* (1993) *J. Mol. Biol.* 215:403-410) searches. The cDNA sequences obtained were analysed for similarity to all publicly available DNA sequences contained in the eBioinformatics nucleotide database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the SWISS-PROT protein sequence database using BLASTx algorithm (v 2.0.1) (Gish and States (1993) *Nature Genetics* 3:266-272) provided by the NCBI.

The cDNA sequences obtained and identified were then used to identify additional identical and/or overlapping cDNA sequences generated using the BLASTN algorithm. The identical and/or overlapping sequences were subjected to a multiple alignment using the CLUSTALw algorithm, and to generate a consensus contig sequence derived from this multiple sequence alignment. The consensus contig sequence was then used as a query for a search against the SWISS-PROT protein sequence database using the BLASTx algorithm to confirm the initial identification.

EXAMPLE 3

Identification and full-length sequencing of cDNAs encoding perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins

To fully characterise for the purposes of the generation of probes for hybridisation experiments and the generation of transformation vectors, a set of

cDNAs encoding perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins was identified and fully sequenced.

Full-length cDNAs were identified from our EST sequence database using
5 relevant published sequences (NCBI databank) as queries for BLAST searches. Full-length cDNAs were identified by alignment of the query and hit sequences using Sequencher (Gene Codes Corp., Ann Arbor, MI 48108, USA). The original plasmid was then used to transform chemically competent XL-1 cells (prepared in-house, CaCl₂ protocol). After colony PCR (using HotStarTaq, Qiagen) a minimum
10 of three PCR-positive colonies per transformation were picked for initial sequencing with M13F and M13R primers. The resulting sequences were aligned with the original EST sequence using Sequencher to confirm identity and one of the three clones was picked for full-length sequencing, usually the one with the best initial sequencing result.

15 Sequencing was completed by primer walking, i.e. oligonucleotide primers were designed to the initial sequence and used for further sequencing. In most cases the sequencing could be done from both 5' and 3' end. The sequences of the oligonucleotide primers are shown in Table 2. In some instances, however, an extended poly-A tail necessitated the sequencing of the cDNA to be completed
20 from the 5' end.

Contigs were then assembled in Sequencher. The contigs include the sequences of the SMART primers used to generate the initial cDNA library as well as pGEM-T Easy vector sequence up to the EcoRI cut site both at the 5' and 3' end.

25 Plasmid maps and the full cDNA sequences of perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins were obtained (Figures 110, 116, 121, 126, 131, 136, 141, 146, 151, 156, 161, 166, 171, 176, 181, 186 and 191).

TABLE 2**List of primers used for sequencing of the full-length cDNAs**

gene name	clone ID	sequencing primer	primer sequence (5'>3')
LpF3OH	08rg1YsF07	08rg1YsF07.f1	TTGAGAGCTTCGTCGACC
		08rg1YsF07.r1	AACTCCTCGTAGTACTCC
TrCHRe	11wc1IsD03	11wc1IsD03.f1	TTCAATTGGAGTACTTGG
		11wc1IsD03.r1	ACTCCTTGTTTCATATAACC
TrCHSa1	02wc2FsD07	02wc2FsD07.f1	ACATGGTGGTGGTTGAGG
		02wc2FsD07.f2	TGCTGCACTCATTGTTGG
		02wc2FsD07.f3	ACATTGATAAGGCATTGG
TrCHSa3	05wc1RsB06	05wc1RsB06.f1	AGGAGGCTGCAGTCAAGG
		05wc1RsB06.f2	TGCCTGAAATTGAGAAACC
		05wc1RsB06.f3	AAAGCTAGCCTTGAAGCC
TrCHSc	07wc1TsE12	07wc1TsE12.f1	TCGGACATAACTCATGTGG
		07wc1TsE12.f2	TTGGGTTGGAGAATAAGG
		07wc1TsE12.r1	TGGACATTTATTGGTTGC
		07wc1TsE12.r2	TATCATGTCTGGAAATGC
TrCHSd2	07wc1XsD03	07wc1XsD03.f1	TTTATGTGAGTACATGGC
		07wc1XsD03.f2	AGCAGCTGTGATTGTAGG
		07wc1XsD03.f3	TGAGAAAGCTCTTGTGAGG
TrCHSf	07wc1UsD07	07wc1UsD07.f1	AGATTGCATCAAAGAATGG
		07wc1UsD07.r1	GGTCCAAAAGCCAATCC
TrCHSh	13wc2IsG04	13wc2IsG04.f1	TAAGACGAGACATAGTGG
		13wc2IsG04.r1	TATTCATAAGCACATGC
TrDFRd	12wc1CsE09	12wc1CsE09.f1	TTACCTCGTCTGTCTCG
		12wc1CsE09.r1	AACACACACATGTCTACC
TrF3Ha	07wc1LsG03	07wc1LsG03.f1	TGAAGGATTGGAGAGAGC
		07wc1LsG03.r1	TACACAGTTGCATCTGG
TrPALa	04wc1UsB03	04wc1UsB03.f1	ATCGGAATCTGCTAGAGC
		04wc1UsB03.f2	TGTTGGTTCTGGTTTAGC
		04wc1UsB03.r1	TTCATATGCAATCCTTGC
		04wc1UsB03.r2	TCTTGGTTGTGTTGTTCC

TrPALb	05wc1PsH02	05wc1PsH02.f1	TGGGACTGATAGTTATGG
		05wc1PsH02.f2	TCTTGCTCTTGTTAATGG
		05wc1PsH02.r1	AGCACCATTCCTACTCTCC
		05wc1PsH02.r2	TTCTCTTCGCTACTTGGC
TrPALf	13wc2AsD12	13wc2AsD12.f1	ATAGTGGTGTGAGGGTGG
		13wc2AsD12.f2	TCTTGTTAATGGTACTGC
		13wc2AsD12.r1	ATTTATCGCACTCTTCGC
		13wc2AsD12.r2	AAAGTGGGAAGACATGAGC
TrVRa	11wc1NsA07	11wc1NsA07.f1	AAGAACAGTGGATGGAGC
		11wc1NsA07.r1	TCAACTCATCTACTGATAG

EXAMPLE 4

Development of transformation vectors containing chimeric genes with cDNA sequences from perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa

To alter the expression of the proteins involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa, through antisense and/or sense suppression technology and for over-expression of these key enzymes in transgenic plants, a set of sense and antisense transformation vectors was produced.

cDNA fragments were generated by high fidelity PCR using the original pGEM-T Easy plasmid cDNA as a template. The primers used (Table 3) contained recognition sites for appropriate restriction enzymes, for example EcoRI and XbaI, for directional and non-directional cloning into the target vector. After PCR amplification and restriction digest with the appropriate restriction enzyme (usually

XbaI), the cDNA fragments were cloned into the corresponding site in pDH51, a pUC18-based transformation vector containing a CaMV 35S expression cassette. The orientation of the constructs (sense or antisense) was checked by DNA sequencing through the multi-cloning site of the vector. Transformation vectors

5 containing chimeric genes using full-length open reading frame cDNAs encoding perennial ryegrass F3OH and white clover BANA, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins in sense and antisense orientations under the control of the CaMV 35S promoter were generated (Figures 113, 119, 124, 129, 134, 139, 144, 149, 154,

10 159, 164, 169, 174, 179, 184, 189 and 194).

TABLE 3**List of primers used to PCR-amplify the open reading frames**

gene name	clone ID	primer	primer sequence (5'→3')
LpF3OH	08rg1YsF07	08rg1YsF07f	GAATTCTAGAAGCAGAAAGTACGGACATCAGC
		08rg1YsF07r	GAATTCTAGAACCATATGGCGACACATCG
TrBANA	05wc2XsG02	05wc2XsG02f	GGATCCTCTAGAGCACTAGTGTGTATAAGTTTCTT GG
		05wc2XsG02r	GGATCCTCTAGACCCCCTTAGTCTTAAATACTCG
TrCH1a	06wc2AsF12	06wc2AsF12f	GAATTCTAGAGATCTGAAACAACATAGTCACC
		06wc2AsF12r	GAATTCTAGATCAATCTTGTGCTGCAATGC
TrCH1d	12wc1FsG04	12wc1FsG04f	GAATTCTAGAAAGTTCAACGAGATCAATGG
		12wc1FsG04r	GAATTCTAGATTCCGCTTGGTCTTTATTGC
TrCHRc	11wc1IsD03	11wc1IsD03f	GAATTCTAGAACATGGGTAGTGTGAAATTCC
		11wc1IsD03r	GAATTCTAGAAGATATTGAGTGAGCTTAAGG
TrCHSa1	02wc2FsD07	02wc2FsD07f	GACGTCGACATTACATACATAGCAGGAAC
		02wc2FsD07r	GACGTCGACAGTCTCTCATTTCTCATATAGC
TrCHSa3	05wc1RsB06	05wc1RsB06f	GAATTCTAGAAGATATGGTGAGTGTAGCTG
		05wc1RsB06r	GAATTCTAGAATCACACATCTTATATAGCC
TrCHSc	07wc1TsE12	07wc1TsE12f	GAATTCTAGAAGAAGAAATATGGGAGACGAAGG
		07wc1TsE12r	GAATTCTAGAAAGACTTCATGCACACAAGTTCC
TrCHSd2	07wc1XsD03	07wc1XsD03f	GAATTCTAGAATAACCTATCAGTACTCACC
		07wc1XsD03r	GAATTCTAGAATCTAGGCAATTTAAGTGGC

TrCHSf	07wc1UsD07	07wc1UsD07f	GAATTCTAGATGATTCATTGTTTGTTCATAAC
		07wc1UsD07r	GAATTCTAGAACATATTCATCTTCCTATCAC
TrCHSh	13wc2IsG04	13wc2IsG04f	GAATTCTAGATCCAAATTCTCGTACCTCACC
		13wc2IsG04r	GAATTCTAGATAGTTCACATCTCTCGGCAGG
TrDFRd	12wc1CsE09	12wc1CsE09f	GACGTCGACACAACAGTCTTCCACTTGAGC
		12wc1CsE09r	GACGTCGACTCTATACTCTGGTAACTATAGG
TrF3Ha	07wc1LsG03	07wc1LsG03f	GAATTCTAGAACCACACAACACACAAACACC
		07wc1LsG03r	GAATTCTAGAACCAAGCAGCTTAATACACG
TrPALa	04wc1UsB03	04wc1UsB03f	AGTACTGCAGAGATATGGAAGTAGTAGCAGCAGC
		04wc1UsB03r	AGTACTGCAGTAGCAAACCAGTTCCCAACTCC
TrPALb	05wc1PsH02	05wc1PsH02f	AGTACTGCAGATAATGGAGGGAATTACCAATGG
		05wc1PsH02r	AGTACTGCAGTGCTAATTAACATATTGGTAGAGG
TrPALf	13wc2AsD12	13wc2AsD12f	AGTACTGCAGATAATGGAGGGAATTACCAATGG
		13wc2AsD12r	AGTACTGCAGTGCTAATTAACATATTGGTAGAGG
TrVRa	11wc1NsA07	11wc1NsA07f	AGTACTGCAGATAAAGAGAGTCAAAAATGGC
		11wc1NsA07r	AGTACTGCAGAACACATACTTAGAGATAGCC

EXAMPLE 5

Development of binary transformation vectors containing chimeric genes with cDNA sequences from perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CH1c, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa

To alter the expression of the proteins involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CH1c, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa, through antisense and/or sense suppression technology and for over-expression of these key proteins in transgenic plants, a set of sense and antisense binary transformation vectors was produced.

cDNA fragments were generated by high fidelity PCR using the original pGEM-T Easy plasmid cDNA as a template. The primers used (Table 3) contained recognition sites for appropriate restriction enzymes, for example EcoRI and XbaI, for directional and non-directional cloning into the target vector. After PCR
5 amplification and restriction digest with the appropriate restriction enzyme (usually XbaI), the cDNA fragments were cloned into the corresponding site in a modified pPZP binary vector (Hajdukiewicz *et al.*, 1994). The pPZP221 vector was modified to contain the 35S² cassette from pKYLX71:35S² as follows. pKYLX71:35S² was cut with ClaI. The 5' overhang was filled in using Klenow and the blunt end was A-
10 tailed with Taq polymerase. After cutting with EcoRI, the 2kb fragment with an EcoRI-compatible and a 3'-A tail was gel-purified. pPZP221 was cut with HindIII and the resulting 5' overhang filled in and T-tailed with Taq polymerase. The remainder of the original pPZP221 multi-cloning site was removed by digestion with EcoRI, and the expression cassette cloned into the EcoRI site and the 3' T
15 overhang restoring the HindIII site. This binary vector contains between the left and right border the plant selectable marker gene *aaaC1* under the control of the 35S promoter and 35S terminator and the pKYLX71:35S²-derived expression cassette with a CaMV 35S promoter with a duplicated enhancer region and an *rbcS* terminator.

20 The orientation of the constructs (sense or antisense) was checked by restriction enzyme digest. Transformation vectors containing chimeric genes using full-length open reading frame cDNAs encoding perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins in sense and antisense
25 orientations under the control of the CaMV 35S² promoter were generated (Figures 114, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190 and 195).

EXAMPLE 6

Production and analysis of transgenic Arabidopsis plants carrying chimeric perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa genes involved in flavonoid biosynthesis

A set of transgenic Arabidopsis plants carrying chimeric perennial ryegrass and white clover genes involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, were produced.

pPZP221-based transformation vectors with *LpF3OH* and *TrBANa*, *TrCH1a*, *TrCH1d*, *TrCHRc*, *TrCHSa1*, *TrCHSa3*, *TrCHSc*, *TrCHSd2*, *TrCHSf*, *TrCHSh*, *TrDFRd*, *TrF3Ha*, *TrPALa*, *TrPALb*, *TrPALf* and *TrVRa* cDNAs comprising the full open reading frame sequences in sense and antisense orientations under the control of the CaMV 35S promoter with duplicated enhancer region (35S²) were generated as detailed in Example 6.

Agrobacterium-mediated gene transfer experiments were performed using these transformation vectors.

The production of transgenic Arabidopsis plants carrying the perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa cDNAs under the control of the CaMV 35S promoter with duplicated enhancer region (35S²) is described here in detail.

Preparation of Arabidopsis plants

Seedling punnets were filled with Debco seed raising mixture (Debco Pty. Ltd.) to form a mound. The mound was covered with two layers of anti-bird netting secured with rubber bands on each side. The soil was saturated with water and

enough seeds (*Arabidopsis thaliana* ecotype Columbia, Lehle Seeds #WT-02) sown to obtain approximately 15 plants per punnet. The seeds were then vernalised by placing the punnets at 4 °C. After 48 hours the punnets were transferred to a growth room at 22 °C under fluorescent light (constant illumination, 5 55 $\mu\text{molm}^{-2}\text{s}^{-1}$) and fed with Miracle-Gro (Scotts Australia Pty. Ltd.) once a week. Primary bolts were removed as soon as they appeared. After 4 – 6 days the secondary bolts were approximately 6 cm tall, and the plants were ready for vacuum infiltration.

Preparation of *Agrobacterium*

10 *Agrobacterium tumefaciens* strain AGL-1 were streaked on LB medium containing 50 $\mu\text{g/ml}$ rifampicin and 50 $\mu\text{g/ml}$ kanamycin and grown at 27 °C for 48 hours. A single colony was used to inoculate 5 ml of LB medium containing 50 $\mu\text{g/ml}$ rifampicin and 50 $\mu\text{g/ml}$ kanamycin and grown over night at 27 °C and 250 rpm on an orbital shaker. The overnight culture was used as an inoculum for 500 15 ml of LB medium containing 50 $\mu\text{g/ml}$ kanamycin only. Incubation was over night at 27 °C and 250 rpm on an orbital shaker in a 2 l Erlenmeyer flask.

The overnight cultures were centrifuged for 15 min at 5500 xg and the supernatant discarded. The cells were resuspended in 1 l of infiltration medium [5% (w/v) sucrose, 0.03% (v/v) Silwet-L77 (Vac-In-Stuff, Lehle Seeds #VIS-01)] 20 and immediately used for infiltration.

Vacuum infiltration

The *Agrobacterium* suspension was poured into a container (Décor Telfresh storer, #024) and the container placed inside the vacuum desiccator (Bel Art, #42020-0000). A punnet with *Arabidopsis* plants was inverted and dipped into 25 the *Agrobacterium* suspension and a gentle vacuum (250 mm Hg) was applied for 2 min. After infiltration, the plants were returned to the growth room where they were kept away from direct light overnight. The next day the plants were returned to full direct light and allowed to grow until the siliques were fully developed. The plants were then allowed to dry out, the seed collected from the siliques and either

stored at room temperature in a dry container or used for selection of transformants.

Selection of transformants

Prior to plating the seeds were sterilised as follows. Sufficient seeds for one
5 150 mm petri dish (approximately 40 mg or 2000 seeds) were placed in a 1.5 ml
microfuge tube. 500 μ l 70% ethanol were added for 2 min and replaced by 500 μ l
sterilisation solution (H_2O :4% chlorine:5% SDS, 15:8:1). After vigorous shaking,
the tube was left for 10 min after which time the sterilisation solution was replaced
with 500 μ l sterile water. The tube was shaken and spun for 5 sec to sediment the
10 seeds. The washing step was repeated 3 times and the seeds were left covered
with approximately 200 μ l sterile water.

The seeds were then evenly spread on 150 mm petri dishes containing
germination medium (4.61 g Murashige & Skoog salts, 10 g sucrose, 1 ml 1 M
KOH, 2 g Phytigel, 0.5 g MES and 1 ml 1000x Gamborg's B-5 vitamins per litre)
15 supplemented with 250 μ g/ml timetin and 75 μ g/ml gentamycin. After vernalisation
for 48 hours at 4 °C the plants were grown under continuous fluorescent light (55
 μ mol m⁻²s⁻¹) at 22 °C to the 6 – 8 leaf stage and transferred to soil.

Preparation of genomic DNA

3 – 4 leaves of Arabidopsis plants regenerated on selective medium were
20 harvested and freeze-dried. The tissue was homogenised on a Retsch MM300
mixer mill, then centrifuged for 10 min at 1700xg to collect cell debris. Genomic
DNA was isolated from the supernatant using Wizard Magnetic 96 DNA Plant
System kits (Promega) on a Biomek FX (Beckman Coulter). 5 μ l of the sample (50
 μ l) were then analysed on an agarose gel to check the yield and the quality of the
25 genomic DNA.

Analysis of DNA using real-time PCR

Genomic DNA was analysed for the presence of the transgene by real-time
PCR using SYBR Green chemistry. PCR primer pairs (Table 4) were designed

using MacVector (Accelrys). The forward primer was located within the 35S² promoter region and the reverse primer within the transgene to amplify products of approximately 150 - 250 bp as recommended. The positioning of the forward primer within the 35S² promoter region guaranteed that homologous genes in

5 Arabidopsis were not detected.

5 μ l of each genomic DNA sample was run in a 50 μ l PCR reaction including SYBR Green on an ABI (Applied Biosystems) together with samples containing DNA isolated from wild type Arabidopsis plants (negative control), samples containing buffer instead of DNA (buffer control) and samples containing

10 the plasmid used for transformation (positive plasmid control).

Plants were obtained after transformation with all chimeric constructs and selection on medium containing gentamycin. The selection process and two representative real-time PCR analyses are shown in Figure xx.

TABLE 4

15 **List of primers used for Real-time PCR analysis of Arabidopsis plants transformed with chimeric perennial ryegrass genes involved in flavonoid biosynthesis**

construct	primer 1 (forward)	primer 2 (reverse)
pPZP221LpF3OHsense	TTGGAGAGGACACGCTGAAATC	AGGAGAGGGTTGGACATCGC
pPZP221LpF3OHanti	CATTTTCATTTGGAGAGGACACGC	ACGAGGAGTTCTGGAAGATGGG
pPZP221TrBANasense	TTGGAGAGGACACGCTGAAATC	GCAACAAAACCAAGTGCCACC
pPZP221TrBANaanti	TCATTTGGAGAGGACACGCTG	GATGATTGCCCCAGCAAGG
pPZP221TrCHlasense	CATTTTCATTTGGAGAGGACACGC	CAAGGTCTCGACTTGATTGC
pPZP221TrCHlaanti	TCATTTGGAGAGGACACGCTG	AGATTACCTGCCTTGTGAACGAG
pPZP221TrCHldsense	TCATTTGGAGAGGACACGCTG	GACGGTAGGAGGGAATAGATTGTTC
pPZP221TrCHldanti	TCATTTGGAGAGGACACGCTG	CCAGGTATCCGAGTTATTCAACG
pPZP221TrCHRCsense	CCACTATCCTTCGCAAGACCC	TCCCATTCCAACCACAGGC
pPZP221TrCHRCanti	TCATTTGGAGAGGACACGCTG	CAAGCCAGGACTCAGTGACCTATG
pPZP221TrCHSa1sense	TCATTTGGAGAGGACACGCTG	CTGGTCAACACGATTGCTGG
pPZP221TrCHSa1anti	TCATTTGGAGAGGACACGCTG	AACCACAGGAGAAGGACTTGACTG

pPZP221TrCHSa3sense	CATTTTCATTTGGAGAGGACACGC	AACACGGTTTGGTGGATTTGC
pPZP221TrCHSa3anti	TCATTTGGAGAGGACACGCTG	ACAAGTTGGAGAAGGACTTGATTGG
pPZP221TrCHScsense	TTGGAGAGGACACGCTGAAATC	ACAAGTTGGTGAGGGAATGCC
pPZP221TrCHSchanti	TCATTTGGAGAGGACACGCTG	GGGATTGATACTTGCTTTTGGACC
pPZP221TrCHSd2sense	CCCACTATCCTTCGCAAGACC	AGTTGCAGTGCCGATTGCC
pPZP221TrCHSd2anti	CATTTTCATTTGGAGAGGACACGC	AAGATGGACTTGCCACAACAGG
pPZP221TrCHSfsense	CATTTTCATTTGGAGAGGACACGC	TCGTTGCCTTTCCTTGAGTAGG
pPZP221TrCHSfanti	TCATTTGGAGAGGACACGCTG	GATTGGCTTTTGGACCAGGG
pPZP221TrCHShsense	TCATTTGGAGAGGACACGCTG	CGGTCACCATTTTTTTGTTGGAGG
pPZP221TrCHShanti	TCATTTGGAGAGGACACGCTG	TGTTGTTTGGGTTTGGACCG
pPZP221TrDFRdsense	CATTTTCATTTGGAGAGGACACGC	ATTGAGATTTTGGACGGTGGC
pPZP221TrDFRdanti	CATTTTCATTTGGAGAGGACACGC	CGCAACCTGGATTGTTGAGAGC
pPZP221TrF3Hasense	TCATTTGGAGAGGACACGCTG	TCTTCCCTAACGAACTTGACTCG
pPZP221TrF3Haanti	TCATTTGGAGAGGACACGCTG	GAACAACAACCTAGGGACTTGAGG
pPZP221TrPALasense	ATGACGCACAATCCCACTATCC	TTGCCTCAGCAGCCACACC
pPZP221TrPALaanti	GGAGAGGACACGCTGAAATCAC	TGCCAAAAGAGGTTGAAAGTGC
pPZP221TrPALbsense	ATCCCACTATCCTTCGCAAGACCC	AATGACTCCCCATCAACGACTCCG
pPZP221TrPALbanti	TTGGAGAGGACACGCTGAAATC	GACAAATTGTTACAGCTATGTGCC
pPZP221TrPALfsense	ATCCCACTATCCTTCGCAAGACCC	CACCATACGCTTCACCTCATCC
pPZP221TrPALfanti	TCATTTGGAGAGGACACGCTG	TTGTTAGAGAGGAGTTAGGAACCGC
pPZP221TrVRasense	CCACTATCCTTCGCAAGACCC	GCTTACATCCCTCTTACGTTCTGG
pPZP221TrVRaanti	CCACTATCCTTCGCAAGACCC	AAAAGCTCGTGGACGCTGG

EXAMPLE 7

Genetic mapping of perennial ryegrass genes involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits

The cDNAs representing genes involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens;

- pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, were amplified by PCR from their respective plasmids, gel-purified and radio-labelled for use as probes to detect restriction fragment length polymorphisms (RFLPs). RFLPs were mapped in
- 5 the F_1 (first generation) population, $NA_6 \times AU_6$. This population was made by crossing an individual (NA_6) from a North African ecotype with an individual (AU_6) from the cultivar Aurora, which is derived from a Swiss ecotype. Genomic DNA of the 2 parents and 114 progeny was extracted using the 1 x CTAB method of Fulton et al. (1995).
- 10 Probes were screened for their ability to detect polymorphism using the DNA (10 μ g) of both parents and 5 F_1 progeny restricted with the enzymes *DraI*, *EcoRI*, *EcoRV* or *HindIII*. Hybridisations were carried out using the method of Sharp et al. (1988). Polymorphic probes were screened on a progeny set of 114 individuals restricted with the appropriate enzyme (Figure 115).
- 15 RFLP bands segregating within the population were scored and the data was entered into an Excel spreadsheet. Alleles showing the expected 1:1 ratio were mapped using MAPMAKER 3.0 (Lander et al. 1987). Alleles segregating from, and unique to, each parent, were mapped separately to give two different linkage maps. Markers were grouped into linkage groups at a LOD of 5.0 and
- 20 ordered within each linkage group using a LOD threshold of 2.0.
- Loci representing genes involved in flavonoid biosynthesis mapped to the linkage groups as indicated in Table 5 and in Figure 197. These gene locations can now be used as candidate genes for quantitative trait loci associated with flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light
- 25 absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits.

TABLE 5

Map locations of ryegrass genes involved in flavonoid biosynthesis across two genetic linkage maps of perennial ryegrass

Probe	Polymorphic	Mapped with	Locus	Linkage group	
				NA ₆	AU ₆
<i>LpDFRb</i>	Y	<i>Hind</i> III	<i>LpDFRb</i>	6	6

5

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Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as outlined herein.

15 It will also be understood that the term "comprises" (or its grammatical variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

CLAIMS

1. A substantially purified or isolated nucleic acid or nucleic acid fragment encoding a flavonoid biosynthetic enzyme selected from the group consisting of chalcone isomerase (CHI), chalcone synthase (CHS), chalcone reductase (CHR), dihydroflavonol 4-reductase (DFR), leucoanthocyanidin reductase (LCR), flavonoid 3', 5' hydrolase (F3'5'H), flavanone 3-hydroxylase (F3H), flavonoid 3'-hydroxylase (F3'H), phenylalanine ammonia-lyase (PAL) and vestitone reductase (VR) from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, or a functionally active fragment or variant thereof.

2. A nucleic acid or nucleic acid fragment according to Claim 1, wherein said clover species is white clover (*Trifolium repens*) and said ryegrass species is perennial ryegrass (*Lolium perenne*).

3. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a CHI or CHI-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 10, 12, 122 and 127 hereto (Sequence ID Nos: 1, 3 to 7, 8, 10 to 12, 13, 15 and 16, 17, 19 to 22, 307, and 309, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

4. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a CHS or CHS-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 13, 15, 16, 18, 19, 21, 22, 24, 25, 27, 28, 30, 31, 33, 34, 137, 142, 147, 152, 157 and 162 hereto (Sequence ID Nos: 23, 25 to 63, 64, 66 to 68, 69, 71 to 77, 78, 80 to 90, 91, 93 and 94, 95, 97 to 100, 101, 103 to 105, 106, 313, 315, 317, 319, 321, and 323, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

5. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a CHR or CHR-like protein and including nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 36, 38, 40, 41, 43 and 132 hereto (Sequence ID Nos: 108, 110, 112 to 116, 117, 119 to 134, and 5 311, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

6. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a DFR or DFR-like protein and including a nucleotide sequence selected 10 from the group consisting of (a) sequences shown in Figures 44, 46, 47, 49, 50, 52, 54, 55, 57, 59, 61, 62, 64, 101, 103, 104, 106, 117 and 167 hereto (Sequence ID Nos: 135, 137 to 146, 147, 149 to 152, 153, 155, 157 and 158, 159, 161, 163, 165 to 167, 168, 170 to 184, 286, 288 to 292, 293, 295 to 297, 305, and 325, respectively); (b) complements of the sequences recited in (a); (c) sequences 15 antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

7. A nucleic acid or nucleic acid fragment according to Claim 1, encoding an LCR or LCR-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 65 and 67 20 hereto (Sequence ID Nos: 185 and 187 to 193, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

8. A nucleic acid or nucleic acid fragment according to Claim 1, 25 encoding a F3'5'H or F3'5'H-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 68, 70 and 72 hereto (Sequence ID Nos: 194, 196, and 198 to 201, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants 30 of the sequences recited in (a), (b) and (c).

9. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a F3H or F3H-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 73, 75, 76, 78, 107, 109, 111 and 172 hereto (Sequence ID Nos: 202, 204 to 244, 245, 247, 298, 300
5 to 302, 303, and 327, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

10. A nucleic acid or nucleic acid fragment according to Claim 1,
10 encoding a F3'H or F3'H-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 80 and 82 hereto (Sequence ID Nos: 249, and 251 and 252, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences
15 recited in (a), (b) and (c).

11. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a PAL or PAL-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 83, 85, 86, 88, 89, 91, 93, 95, 97, 177, 182 and 187 hereto (Sequence ID Nos: 253, 255 to 257, 258,
20 260 to 267, 268, 270, 272, 274, 276 and 277, 329, 331, and 333, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

12. A nucleic acid or nucleic acid fragment according to Claim 1,
25 encoding a VR or VR-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 98, 100 and 192 hereto (Sequence ID Nos: 278, 280 to 285, and 335, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants
30 of the sequences recited in (a), (b) and (c).

13. A construct including a nucleic acid or nucleic acid fragment according to Claim 1.

14. A vector including a nucleic acid or nucleic acid fragment according to Claim 1.

5 15. A vector according to Claim 14, further including a promoter and a terminator, said promoter, nucleic acid or nucleic acid fragment and terminator being operatively linked.

16. A plant cell, plant, plant seed or other plant part, including a construct according to claim 13 or a vector according to Claim 14.

10 17. A plant, plant seed or other plant part derived from a plant cell or plant according to Claim 16.

15 18. A method of modifying flavonoid biosynthesis in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.

20 19. A method of modifying protein binding, metal chelation, anti-oxidation, and/or UV-light absorption in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.

20 20. A method of modifying pigment production in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.

25 21. A method of modifying plant defense to a biotic stress, said method including introducing into said plant an effective amount of a nucleic acid or nucleic

acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.

22. A method according to claim 21 wherein said biotic stress is selected from the group consisting of viruses, microorganisms, insects and fungal
5 pathogens.

23. A method of modifying forage quality of a plant by disrupting protein foam and/or conferring protection from rumen pasture bloat, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector
10 according to Claim 14.

24. Use of a nucleic acid or nucleic acid fragment according to Claim 1, and/or nucleotide sequence information thereof, and/or single nucleotide polymorphisms thereof as a molecular genetic marker.

25. A substantially purified or isolated polypeptide from a clover
15 (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of ASR and ASR-like, A22 and A22-like, CYS and CYS-like, LEA and LEA-like, DHN and DHN-like and PKABA and PKABA-like; and functionally active fragments and variants thereof.

26. A polypeptide according to Claim 25, wherein said clover species is
20 white clover (*Trifolium repens*) and said ryegrass species is perennial ryegrass (*Lolium perenne*).

27. A polypeptide according to Claim 25, wherein said polypeptide is CHI or CHI-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 2, 5, 8, 11, 123 and 128 hereto
25 (Sequence ID Nos: 2, 9, 14, 18, 308, and 310, respectively); and functionally active fragments and variants thereof.

28. A polypeptide according to Claim 25, wherein said polypeptide is CHS or CHS-like and includes an amino acid sequence selected from the group

consisting of sequences shown in Figures 14, 17, 20, 23, 26, 29, 32, 35, 138, 143, 148, 153, 158 and 163 hereto (Sequence ID Nos: 24, 65, 70, 79, 92, 96, 102, 107, 314, 316, 318, 320, 322, and 324, respectively); and functionally active fragments and variants thereof.

5 29. A polypeptide according to Claim 25, wherein said polypeptide is CHR or CHR-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 37, 39, 42 and 133 hereto (Sequence ID Nos: 109, 111, 118, and 312, respectively); and functionally active fragments and variants thereof.

10 30. A polypeptide according to Claim 25, wherein said polypeptide is DFR or DFR-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 45, 48, 51, 53, 56, 58, 60, 63, 102, 105, 118 and 168 hereto (Sequence ID Nos: 136, 148, 54, 156, 160, 162, 164, 169, 287, 294, 306, and 326, respectively); and functionally active fragments and
15 variants thereof.

31. A polypeptide according to Claim 25, wherein said polypeptide is LCR or LCR-like and includes an amino acid sequence shown in Figure 66 hereto (Sequence ID No: 186); and functionally active fragments and variants thereof.

32. A polypeptide according to Claim 25, wherein said polypeptide is
20 F3'5'H or F3'5'H-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 69 and 71 hereto (Sequence ID Nos: 195 and 197, respectively); and functionally active fragments and variants thereof.

33. A polypeptide according to Claim 25, wherein said polypeptide is
25 F3H or F3H-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 74, 77, 79, 108, 112 and 173 hereto (Sequence ID Nos: 203, 246, 248, 299, 304, and 328, respectively); and functionally active fragments and variants thereof.

34. A polypeptide according to Claim 25, wherein said polypeptide is F3'H or F3'H-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figure 81 hereto (Sequence ID No: 250); and functionally active fragments and variants thereof.
- 5 35. A polypeptide according to Claim 25, wherein said polypeptide is PAL or PAL-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 84, 87, 90, 92, 94, 96, 178, 183 and 188 hereto (Sequence ID Nos: 254, 259, 269, 271, 273, 275, 330, 332, and 334, respectively); and functionally active fragments and variants thereof.
- 10 36. A polypeptide according to Claim 25, wherein said polypeptide is VR or VR-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 99 and 193 hereto (Sequence ID Nos: 279 and 336, respectively); and functionally active fragments and variants thereof.

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TrCH1a : GCATTAAACANTGAAANTTGACCAGTCCCAACAAAGATCTGAAACACATAGCTCCCCATT : 60

TrCH1a : TTTTAACATTAAACTAAAAATATGTCGGCCATCACCGCAATCCAAGTCGAGAACCTTGAA : 120

TrCH1a : TTTCCGGCTGTGATTACTTCTCCGGCCACCGGTAAGTCATATTTTCTTGGTGGTGCAGGG : 180

TrCH1a : GAGAGAGGTTTGACTATTGAAGGAACTTCATCAAGTTCACTGCCATAGGAGTATATTTG : 240

TrCH1a : GAAGATGTAGCAGTGGCTTCACTTGCCACTAAATGGAAGGGCAAATCCTCTGAAGAGTTG : 300

TrCH1a : CTTGAGACCCTTGACTTCTACAGAGATATCATTTCAAGACCATTGAGAAGTTGATTCGA : 360

TrCH1a : GGATCGAAGATTAGGGAATTGAGTGGTCTGAGTACTCAAGGAAGGTTAATGAAAAGTGT : 420

TrCH1a : GTGGCACACTTAAAAATCTGTTGGGACTTATGGAGATGCAGAAGTTGAAGCTATGCAAAAA : 480

TrCH1a : TTTGTTGAAGCCTTCAAGCCTATTAATTTCCACCTGGTGCCTCTGTTTTTTACAGGCAA : 540

TrCH1a : TCACCTGATGGAATATTAGGGCTTAGTTTCTCTCAAGATGCAAGTATACCAGAAAAGGAA : 600

TrCH1a : GCTGCAGTAATAGAGAACAAGGGAGCTTCATCGGCG : 636

FIGURE 1

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TrCH1a : MSAITAIQVENLEFPVITSPATGKSYFLGGAGERGLTIEGNFIKFTAIGVYLEDVAVAS : 60

TrCH1a : LATKWKGKSSEELLETLDFYRDIISGPFKLRGSKIRELSGPEYSRKVNENCVAHLKSV : 120

TrCH1a : GTYGDAEVEAMQKFVEAFKPINFPPGASVFYRQSPDGILGLSFSQDASIPEKEAAVIENK : 180

TrCH1a : GASSA : 185

FIGURE 2

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		*	20	*	40	*	60		
TrCH1a1:	GCATTAAACAA	TTGAAA	-NAGT	-CNAAT	AAAAAAGATCTGAAACACATAGT	TNCCCCATT	:	57	
TrCH1a2:	-----	GNTTGC	CCCGTCCCAACAAAGATCTGAAACACATAGC	CCCCCATT	:	45			
TrCH1a3:	-----	-----	-----	GGATCTGAAACACATAG	TNCCCC	---	: 23		
TrCH1a4:	-----	-----	-----	CNGATCTGAAAAACNTAG	TACCCA	---	: 24		
TrCH1a5:	-----	GNTTAAANTT	GACCAGTCCNAACAAAGATCTGAAACACATAGC	CCCCCATT	:	51			
		*	80	*	100	*	120		
TrCH1a1:	TTTTAACATTAAACTAAAAATATGT	CGGCCATCACC	GCAATCCAAGTCGAGA	ACCTTGAA	:	117			
TrCH1a2:	TTTTAACATTAAACTAAAAATATGT	CGGCCATCACC	GCAATCCAAGTCGAGA	ACCTTGAA	:	105			
TrCH1a3:	TTTTAACATTAAACTAAAAATATGT	CGGCCATCACC	GCAATCCAAGTCGAGA	ACCTTGAA	:	83			
TrCH1a4:	TTTTAANATTAAACTAAAAATATGT	CGGCNATCACC	GCAATCCAAGTCGAGA	ACCTTGAA	:	84			
TrCH1a5:	TTTTAACATTAAACTAAAAATATGT	CGGCCATCACC	GCAATCCAAGTCGAGA	ACCTTGAC	:	111			
		*	140	*	160	*	180		
TrCH1a1:	TTTCCGGCTGTG	TTACTTCTCCGGCCACCGGTAAGTCATATTTTCTTGGTGGTGCAGGG	:	177					
TrCH1a2:	TTCCGGC	GTGATTACTTCTCCGG	CAACCGGTAAGTCATATTTTCTTGGTGGTGCAGGG	:	165				
TrCH1a3:	TTTCC	GCTGTGATTACTTCTCCGGCCACCGGTAAGTCATATTTTCTTGGTGGTGCAGGG	:	143					
TrCH1a4:	TTTCC	GCTGTGATTACTTCTCCGGCCACCGGTAAGTCATATTTTCTTGGTGGTGCAGGG	:	144					
TrCH1a5:	TTCCGGC	GTGATTACTTCTCCGG	CAACCGGTAAGTCATATTTTCTTGGTGGTGCAGGG	:	171				
		*	200	*	220	*	240		
TrCH1a1:	GAGAGAGGTTTGACTATTGAAGGAACTT	NTTCAANGCCCTG	ENATAGACCGTNTTNG	:	237				
TrCH1a2:	GAGAGAGGTTTGACTATTGAAGGAACTTCATCAAGTTCACTGCCATAGGAGTATATTTG	:	225						
TrCH1a3:	GAGAGAGGTTTGACTATTGAAGGAACTTCATCAAGTTCACTGCCATAGGAGTATATTTG	:	203						
TrCH1a4:	GAGAGAGGTTTGACTATTGAAGGAACTTCATCAAGTTCACTGCCATAGGAGTATATTTG	:	204						
TrCH1a5:	GAGAGAGGTTTGACTATTGAAGGAACTTCATCAAGTTCACTGCCATAGGAGTATATTTG	:	231						
		*	260	*	280	*	300		
TrCH1a1:	AAANA	-----	:	244					
TrCH1a2:	GAAGATGTAGCAGTGGCTTCACTTGCCACTAAATGGAAGGGCAAATCCTCTGAAGAGTTG	:	285						
TrCH1a3:	GAAGATGTAGCAGTGGCTTCACTTGCCACTAAATGGAAGGGCAAATCCTCTGAAGAGTTG	:	263						
TrCH1a4:	GAAGATGTAGCAGTGGCTTCACTTGCCACTAAATGGAAGGGCAAATCCTCTGAAGAGTTG	:	228						
TrCH1a5:	GAAGATGTAGCAGTGGCTTCACTTGCCACTAAATGGAAGGGCAAATCCTCTGAAGAGTTG	:	291						
		*	320	*	340	*	360		
TrCH1a1:	-----	:	-						
TrCH1a2:	CTTGAGACCCCTTGACTTCTACAGAGATATCATTTTCAAGGACCATTGAGAAGTTGATTTCGA	:	345						
TrCH1a3:	CTTGAGAC	CTTGACTTCTA	TAGAGATATCATTTTCAAGGACCCTTGAGAAGTTGATTTCGA	:	323				
TrCH1a4:	-----	:	-						
TrCH1a5:	CTTGAGACCCCTTGACTTCTACAGAGATATCATTTTCAAGGACCATTGAGAAGTTGATTTCGA	:	351						
		*	380	*	400	*	420		
TrCH1a1:	-----	:	-						
TrCH1a2:	GGATCGAAGATTAGGGAATTGAGTGGTCTGAGTACTCAAGGAAGGTTAATGAAAACCTGT	:	405						
TrCH1a3:	GGATCGAAGATTAGGGAATTGAGTGGTCTGAGTACTCAAGGAAGGTTAATGAAAACCTGC	:	383						
TrCH1a4:	-----	:	-						
TrCH1a5:	GGATCGAAGATTAGGGAATTGAGTGGTCTGAGTACTCAAGGAAGGTTAATGAAAACCTGT	:	411						

FIGURE 3

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	*	440	*	460	*	480		
TrCH1a1:	-----						:	-
TrCH1a2:	GTGGCACACTTAAATCTGTTGGGACTTACGGAGATGCAGAAGTTGAAGCTATGCAAAAA						:	465
TrCH1a3:	GTGGCCCACTTAAATCTGTTGGGACTTATGGAGATGCTGAAGCTGAAGCTATGCAAAAA						:	443
TrCH1a4:	-----						:	-
TrCH1a5:	GTGGCACACTTAAATCTGTTGGGACTTATGGAGATGCAGAAGTTGAAGCTATGCAAAAA						:	471

	*	500	*	520	*	540		
TrCH1a1:	-----						:	-
TrCH1a2:	TTTGTTGAAGCCTTCAAGCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTACAGGCAA						:	525
TrCH1a3:	TTTGTTGAAGCCTTCAAGCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTACAGGCAA						:	503
TrCH1a4:	-----						:	-
TrCH1a5:	TTTGTTGAAGCCTTCAAGCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTACAGGCAA						:	531

	*	560	*	580	*	600		
TrCH1a1:	-----						:	-
TrCH1a2:	TCACCTGATGGAATATTAGGGCTTAGTTTCTCTCAAGATGCAAGTATACCAGAAAAGGAA						:	585
TrCH1a3:	TCACCTGATGGAATATTAGGGCTTAGTTTCTCTCAAGATGCAAGTATACCAGAAAAGGAG						:	563
TrCH1a4:	-----						:	-
TrCH1a5:	TCACCTGATGGAATATTAGGGCTTAGTTTCTCTCAAGATGCAAGTATACCAGAAAAGN--						:	589

	*	620	*			
TrCH1a1:	-----			:	-	
TrCH1a2:	GCTGCAGTAATAGAGAACAANN-----			:	606	
TrCH1a3:	GCTGCAGTAATAGAGAACAAGGGAGCTTCATCGGCG			:	599	
TrCH1a4:	-----			:	-	
TrCH1a5:	-----			:	-	

FIGURE 3 (cont)

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TrCHIb : TTAAAATTGACACAGTCCCAACCTTAAANTTGACCNNGGTCCCAAACAAAGATCTGAAACA : 60

TrCHIb : ACATAGCCCCCATTTTAAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 120

TrCHIb : GTCGAGAACCTTGAATTCCTGGCGGTGATTACTTCTCCGGTCAACGGTAAGTCATATTTT : 180

TrCHIb : CTTGGTGGTGCAGGGGAGAGAGGTTNGACTATTGAAGGAACTTCATCAAGTTCACTGCC : 240

TrCHIb : ATAGGAGTATATTTGGAAGATGTAGCAGGGGCTTCACTTGCCACTAAATGGAAGGGCAGA : 300

TrCHIb : TCCTCTGAAGAGNGCTTGAGACCCTNGACTNC : 332

FIGURE 4

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TrCH1b : MSAITAIQVENLEFPVITSPVNGKSYFLGGAGERGXTIEGNFIKFTAIGVYLEDVAGAS : 60

TrCH1b : LATKWKGRSSEEXLRPXT : 78

FIGURE 5

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      *           20           *           40           *           60
TrCHib1: TTAAAATTGACCNAGTCCNAACCTTAAANTTGACCNGGTCCCAAACAAAGATCTGAAACA : 60
TrCHib2: -TTAAANTTGACACAGTCCCAACCTTAAANTTGACCNGGTCCCAAACAAAGATCTGAAACA : 59
TrCHib3: -----GCGTTAAANTTGACCCAGT-CCNAACAAAGATCTGAAAC- : 38

      *           80           *           100          *           120
TrCHib1: ACATAGCCCCCATTTTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 120
TrCHib2: ACATAGCCCCCATTTTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 119
TrCHib3: ACATAGCCCCCATTTTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 98

      *           140          *           160          *           180
TrCHib1: GTCGAGAACCTTGAATTCCCGGCGGTGATTACTTCTCCGGTCAACGGTAAGTCATATTTT : 180
TrCHib2: GTCGAGAACCTTGAATTCCCGGCGGTGATTACTTCTCCGGTCAACGGTAAGTCATATTTT : 179
TrCHib3: GTCGAGAACCTTGAATTCCCGGCGGTGATTACTTCTNCGGGAANGGGAAGGATATTTT : 158

      *           200          *           220          *           240
TrCHib1: CTTGGTGGTGCAGGGGAGAGAGGTTTGACTATTGAAGGAACTTCATCAAGTTCACTGCC : 240
TrCHib2: CTTGGTGGTGCAGGGGAGAGAGGTTTGACTATTGAAGGAACTTCATCAAGTTCACTGCC : 239
TrCHib3: CTTGGTGGTGCAGGNNAGANNNTNGN----- : 186

      *           260          *           280          *           300
TrCHib1: ATAGGAGTATATTTGGAAGATGTAGCAGGGGCTTCACTTGCCACTAAATGGAAGGGNAGA : 300
TrCHib2: ATAGGAGTATATTTGGAAGATGTAGCAGGGGCTTCACTTGCCACTAAATGGAAGGGCANA : 299
TrCHib3: ----- : -

      *           320          *
TrCHib1: TCCTCTGAAGAGNCNTTGANACCNTNGACTNN : 332
TrCHib2: TCCTCTGAAGAGCGCTTGAGACCCTTGACTTC : 331
TrCHib3: ----- : -

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FIGURE 6

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      *           20           *           40           *           60
TrCH1c : GTTAGNAGNAGNATNTCNCGGCACCCTTTGAAAAGTTGATTTCGAGGATCGAAGATTAGGGA : 60

      *           80           *           100          *           120
TrCH1c : ATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAAGTGCCTGGCACAACCTTAAATC : 120

      *           140          *           160          *           180
TrCH1c : TGTTGGGACTTATGGAGATGCAGAAGCTGAAGCTATGCAAAAATTTGTTGAAGCCTTCAA : 180

      *           200          *           220          *           240
TrCH1c : GCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTTACAGGCAATCACCTGATGGAATATT : 240

      *           260          *
TrCH1c : AGGGGTTAGTATTGCCAATTCATTTTTTTTAACT : 274
```

FIGURE 7

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TrCH1c : * 20 * 40 * 60
APFEKLIRGSKIRELSGPEYSRKVNENCVAHLKSVGTYGDAEAEAMQKFVEAFKPINFPP : 60

 * 80 *
TrCH1c : GASVFYRQSPDGILGVSIANSFFLTILIRVRFDG : 94

FIGURE 8

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      *           20           *           40           *           60
TrCHic1: GTTAGNAGNATNNTTTCNNGGCACCCTTTGAAAAGTTGATTTCGAGGATCGAAGATTAGGGA : 60
TrCHic2: -----GNATNTTTNGGACCCTTTGAAAAGTTGATTTCGAGGATCGAAGATTAGGGA : 50

      *           80           *           100          *           120
TrCHic1: ATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAAC TGCGTGGCACACTTAAAATC : 120
TrCHic2: ATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAAC TGCGTGGCACACTTAAAATC : 110

      *           140          *           160          *           180
TrCHic1: TGT TGGGACTTATGGAGATGCAGAAGCTGAAGCTATGCAAAAATTTGTTGAAGCCTTCAA : 180
TrCHic2: TGT TGGGACTTATGGAGATGCAGAAGCTGAAGCTATGCAAAAATTTGTTGAAGCCTTCAA : 170

      *           200          *           220          *           240
TrCHic1: GCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTTTACAGGCAATCACCTGATGGAATATT : 240
TrCHic2: GCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTTTACAGGCAATCACCTGATGGAATATT : 230

      *           260          *
TrCHic1: AGGGGTTAGTATTGCCAATTCATTTTTTTTAACT : 274
TrCHic2: AGGGGTTAGTATTGCCAATTCATTTTTTTTAACT : 264

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FIGURE 9

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TrCHId : TTNANTNNNNNTTNNCGGGCAATTACAACCTACACAACACCTTCTCCATTACCATCTATCTT : 60

TrCHId : CTACTAAGTTCAACGAGATCAATGGCACCTTCCTTCTGTCAACGCTTTGAATATCGAGAAC : 120

TrCHId : AATCTATTCCCTCCTACCGTCACACCACCGGGATCCACCAACAATTTCTTCCTCGGCGGT : 180

TrCHId : GCAGGAGAGCGGGGTCTTCAAATTCAAGACAAATTTGTCAAATTCACCGCTATTGGTGTT : 240

TrCHId : TATCTACAGGACATTGCTGTTTCCTTACCTCGCCACTAAATGGAAGGGTAAGACTGCTCAA : 300

TrCHId : GAGCTAACGGAACTGTTCCTTTCTTCAGGGACATCGTTACAGGTCCATTTGAGAAATTT : 360

TrCHId : ATGCAGGTGACAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTCAGAA : 420

TrCHId : AATTGTGTAGCTATTTGGAAGTCTCTTGGGATTTATACCGACGAAGAAGCCAAAGCAATT : 480

TrCHId : GAGAAGNNTGTTTCTGTCTTCAAAGANGAAACATTTCCACCAGGCTCCTCTATCCTTTTC : 540

TrCHId : ACAGNATTACCCAAAGGATTAGGATCACTAACGATAAGNTTCTCTAAAGATGGATCCATT : 600

TrCHId : CCAGAGACCGAGTCTGCAGTTATAGAGAATAAGCTACTCTCACAAGCTGTGCTNGAGTCG : 660

TrCHId : ATGATAGGGGCACACGGTGTCTCCCCTGCAGCAAAACAGAGTTTGGCCACCAGNTANC : 720

TrCHId : CGAGNTATTCAACGAGGNTGGCTGATGCCTAGCAACTTGATNATATCAACAAAACGAAAA : 780

TrCHId : TGAAAGNCCTTTTCTGCAATAAAGAACAAGCGGAAATTTTATTTT : 825

FIGURE 10

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TrCHId : MALPSVTALNIENNLFPPPTVTPPGSTNNFFLGGAGERGLQIQDKFVKFTAIGVYLQDIAV : 60

TrCHId : PYLATKWKGKTAQELTETVPFFRDIVTGPFKFMQVMTMILPLTGQQYSEKVSENCVAIWK : 120

TrCHId : SLGIYTDEEAKAIEKVSFVKETFPPGSSILFTLPKGLGSLTIXFSKDGSI PETESAVIEN : 180

TrCHId : KLLSQAVXESMIGAHGVSPAAKQSFGHQXXRXIQRXWLMPSNLXISTKRK : 230

FIGURE 11

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      *           20           *           40           *           60
TrCHId1: TTNANTNNNNNTNNCGGTTTNTNANAACCTACACAACACCTTCT-TTTTCCATTTATCTT : 59
TrCHId2: -----GCAATTACAACCTTNNCAACACCTTCTCC-TTA-CNTCTATCTT : 41
TrCHId3: -----TTAC-ACT-CACAACACCTTCTCCATTACCATCTATCTT : 37
TrCHId4: -----TGACATTATTACAATTACAACCTTAACAT : 28

      *           80           *           100          *           120
TrCHId1: CTACTAAGTTCAACGAGATCAATGGCACTTCCTTCTGTCTCCGCTTTGAATATCGAGAAC : 119
TrCHId2: CTACTAAGTTCAACGAGATCAATGGCACTTCCTTCTGTCTACCGCTTTGAATATCGAGAAC : 101
TrCHId3: CTACTAAGTTCAACGAGATCAATGGCACTTCCTTCTGTCTACCGCTTTGAATATCGAGAAC : 97
TrCHId4: TNACT-GCTAAAAAGAGATNAATGGCACTTCCTTCTGTCTACCGCTTTGGATATCGAGAAC : 87

      *           140          *           160          *           180
TrCHId1: AATCTATTCCCTCCTACCGTCAACCAACCGGATCCACCAACAATTTCTTCCTCGGCGGT : 179
TrCHId2: AATCTATTCCCTCCTACCGTCAACCAACCGGATCCACCAACAATTTCTTCCTCGGCGGT : 161
TrCHId3: AATCTATTCCCTCCTACCGTCAACCAACCGGATCCACCAACAATTTCTTCCTCGGCGGT : 157
TrCHId4: AATCTATTCCCTCCTACCGTCAACCAACCGGATCCACCAACAATTTCTTCCTCGGCGGT : 147

      *           200          *           220          *           240
TrCHId1: GCAGGAGAGCGGGGTCTTCAAATTCAAGACAAATTTGTCAAATTCACCGTATTGGTGTT : 239
TrCHId2: GCAGGAGAGCGGGGTCTTCAAATTCAAGACAAATTTGTCAAATTCACCGTATTGGTGTT : 221
TrCHId3: GCAGGAGAGCGGGGTCTTCAAATTCAAGACAAATTTGTCAAATTCACCGTATTGGTGTT : 217
TrCHId4: GCAGGAGAGCGGGGTCTTCAAATTCAAGACAAATTTGTCAAATTCACCGTATTGGTGTT : 207

      *           260          *           280          *           300
TrCHId1: TATCTACAGGACATTGCTGTTTCCTTACCTCGCCACTAAATGGAAGGGTAAGACTGCTCAA : 299
TrCHId2: TATCTACAGGACATTGCTGTTTCCTTACCTCGCCACTAAATGGAAGGGTAAGACTGCTCAA : 266
TrCHId3: TATCTACAGGACATTGCTGTTTCCTTACCTCGCCACTAAATGGAAGGGTAAGACTGCTCAA : 277
TrCHId4: TATCTACAGGACATTGCTGTTTCCTTACCTCGCCACTAAATGGAAGGGTAAGACTGCTCAA : 267

      *           320          *           340          *           360
TrCHId1: GAGCTAACGGAAACTGTTTCCTTTCTTCAGGGACATCGTTACAGGTCCATTTGAGAAATTT : 359
TrCHId2: ----- : -
TrCHId3: GAGCTAACGGAAACTGTTTCCTTTCTTCAGGGACATCGTTACAGGTCCATTTGAGAAATTT : 337
TrCHId4: GAGCTAACGGAAACTGTTTCCTTTCTTCAGGGACATCGTTACAGGTCCATTTGAGAAATTT : 327

      *           380          *           400          *           420
TrCHId1: ATGCAGGTGACAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTCAGAA : 419
TrCHId2: ----- : -
TrCHId3: ATGCAGGTGACAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTCAGAA : 397
TrCHId4: ATGCAGGTGACAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTCAGAA : 387

      *           440          *           460          *           480
TrCHId1: AATTGTGTAGCTATTGGAAGTCTCTTGGGATTTATACCGACGAAGAAGCCAAAGCAATT : 479
TrCHId2: ----- : -
TrCHId3: AATTGTGTAGCTATTGGAAGTCTCTTGGGATTTATACCGACGAAGAAGCCAAAGCAATT : 457
TrCHId4: AATTGTGTAGCTATTGGAAGTCTCTTGGGATTTATACCGACGAACAANCCAAANCAATT : 447

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FIGURE 12

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	* 500 * 520 * 540	
TrCHId1:	GAGAAGNNTGTTTCTGTCTTCAAAGANGAAACATTCCCACCAGGCTCCTCTATCCTTTTC	: 539
TrCHId2:	-----	: -
TrCHId3:	GAGAAGTTTCTTTCTGTCTTCAAAGATGAAACATTCCCACCAGGCTCCTCTATCCTTTTC	: 517
TrCHId4:	GANAANNNTGNTTCTGNTTNN -----	: 468
	* 560 * 580 * 600	
TrCHId1:	ACAGNATTACCCAAAGGATTANGATCACTAACGATAAGNTTCTCTAAAGATGGATCCATT	: 599
TrCHId2:	-----	: -
TrCHId3:	ACAGNATTACCCAAAGGATTAGGATCACTAACGATAAGTTTCTCTAAAGATGGATCCATT	: 577
TrCHId4:	-----	: -
	* 620 * 640 * 660	
TrCHId1:	CCAGAGACCGAGTCTGCAGTTATAGNGAATAAGCTACTCTCACAAGCTGTGCTNGAGTCC	: 659
TrCHId2:	-----	: -
TrCHId3:	CCAGAGACCGAGTCTGCAGTTATAGAGAATAAGCTACTCTCACAAGCTGTGCTNGAGTCC	: 637
TrCHId4:	-----	: -
	* 680 * 700 * 720	
TrCHId1:	ATGATAGGGGCANNCGGTGTCTNNCNTGCANCAAACATAGTTTTGNNCACCAGGNTANC	: 719
TrCHId2:	-----	: -
TrCHId3:	ATGATAGGGGCACCGGTGTCTCCCCTGCAGCAAAACAGAGTTTGCCACCAGGTTATC	: 696
TrCHId4:	-----	: -
	* 740 * 760 * 780	
TrCHId1:	CNAGNTATTCAACGAGGNTGGCTGATGCCTAGCANCTTGATNNNTNNAACAAAACNAAAA	: 779
TrCHId2:	-----	: -
TrCHId3:	CGAGTATTCAACGAGGTTGC-TGATG-CTAGCAAC-TGATTTATATCAACAAAACGAAAA	: 753
TrCHId4:	-----	: -
	* 800 * 820	
TrCHId1:	TGNANGNCCTTTTCTGCAATAAAGAACA -----	: 807
TrCHId2:	-----	: -
TrCHId3:	TGAAAGTCC-TTTCTGCAATAAAGAACAAGCGGAAATTTTATTTT	: 797
TrCHId4:	-----	: -

FIGURE 12 (cont)

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      *           20           *           40           *           60
TrCHSa: TATTNTNNGAAACCACTTGTGTTGAAGNCGTGAACCTTNGCTACCCCTCCATATNATACTAT : 60

      *           80           *           100          *           120
TrCHSa: NACCTCTTCTGAGACCCCTTCATCATAGAAANACAACACACNTCAGCNCTTTGCTNNTTCT : 120

      *           140          *           160          *           180
TrCHSa: ACAACAACCTATAACTANACATATTATTTTTATNTATTTAGTATATAAATTGAAATAAACT : 180

      *           200          *           220          *           240
TrCHSa: GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 240

      *           260          *           280          *           300
TrCHSa: GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTGAGCAG : 300

      *           320          *           340          *           360
TrCHSa: AGCACATATCCTGATTTCTACTTCAAAATCACAAACAGTGAGCACAAAGACTGAGCTCAAA : 360

      *           380          *           400          *           420
TrCHSa: GAGAAATTCCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTATCTAACA : 420

      *           440          *           460          *           480
TrCHSa: GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT : 480

      *           500          *           520          *           540
TrCHSa: AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAGGCT : 540

      *           560          *           580          *           600
TrCHSa: ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 600

      *           620          *           640          *           660
TrCHSa: GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 660

      *           680          *           700          *           720
TrCHSa: GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTGCTTCGTTTG : 720

      *           740          *           760          *           780
TrCHSa: GCAAAAGATTTGGCCGAGAACAACAAGGTGCTCGTGTGTTGGTTGTTTGTCTGAAGTA : 780

      *           800          *           820          *           840
TrCHSa: ACCGCAGTCACATTCCGCGGCCCCAGTGACACTCACTTGGACAGTCTTGTTGGACAAGCA : 840

      *           860          *           880          *           900
TrCHSa: CTATTTGGAGATGGAGCTGCTGCACTCATTGTTGGCTCAGACCCAGTACCAGAAATTGAG : 900

      *           920          *           940          *           960
TrCHSa: AAACCAATATTTGAGATGGTATGGACCGCACAGACAATTGCTCCAGACAGTGAAGGTGCC : 960

      *           980          *           1000         *           1020
TrCHSa: ATTGATGGTCACCTTCGTGAAGCTGGACTAACATTTTCATCTTCTTAAAGATGTTTCCTGGG : 1020

      *           1040         *           1060         *           1080
TrCHSa: ATTGTATCAAAGAACATTAATAAAGCATTGGTCGAGGCTTTCCAACCATTAGGAATTTCT : 1080

      *           1100         *           1120         *
TrCHSa: GATTACAACCTCAATCTTTTGGATTGCACACCCGGGTGGACCTGCAATTCT : 1130

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FIGURE 13

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TrCHSa : MVSVAEIRKAQRAEGPATILAIGTANPANRVEQSTYPDFYFKITNSEHKTELKEKFQRMCMC : 60

TrCHSa : DKSMIKSRYMYLTEEILKENPSLCEYMAPSLDARQDMVVVEVPRLGKEAAVKAIKEWGQP : 120

TrCHSa : KSKITHLIFCTTSGVDMPGADYQLTKLLGLRPYVKRYMMYQQGCFAGGTVLRLAKDLAEN : 180

TrCHSa : NKGARVLVVCSEVTAVTFRGPSDTHLDSL VGQALFGDGAAALIVGSDPVPEIEKPIFEMV : 240

TrCHSa : WTAQTIAPDSEGAIDGHLREAGLTFHLLKDVP GIVSKNINKALVEAFQPLGISDYN SIFW : 300

TrCHSa : IAHPGGPAI : 309

FIGURE 14

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	*	20	*	40	*	60	
TrCHSa1 :	TATTNTNNGAAACCACTTGTGTTGAAGNCGTGAACTTNGCTACCCCTCCATATNATACTAT						: 60
TrCHSa2 :	-----						: -
TrCHSa3 :	-----						: -
TrCHSa4 :	-----						: -
TrCHSa5 :	-----						: -
TrCHSa6 :	-----						: -
TrCHSa7 :	-----						: -
TrCHSa8 :	-----						: -
TrCHSa9 :	-----						: -
TrCHSa10 :	-----						: -
TrCHSa11 :	-----						: -
TrCHSa12 :	-----						: -
TrCHSa13 :	-----						: -
TrCHSa14 :	-----						: -
TrCHSa15 :	-----						: -
TrCHSa16 :	-----						: -
TrCHSa17 :	-----						: -
TrCHSa18 :	-----						: -
TrCHSa19 :	-----						: -
TrCHSa20 :	-----						: -
TrCHSa21 :	-----						: -
TrCHSa22 :	-----						: -
TrCHSa23 :	-----						: -
TrCHSa24 :	-----						: -
TrCHSa25 :	-----						: -
TrCHSa26 :	-----						: -
TrCHSa27 :	-----						: -
TrCHSa28 :	-----						: -
TrCHSa29 :	-----						: -
TrCHSa30 :	-----						: -
TrCHSa31 :	-----						: -
TrCHSa32 :	-----						: -
TrCHSa33 :	-----						: -
TrCHSa34 :	-----						: -
TrCHSa35 :	-----						: -
TrCHSa36 :	-----						: -
TrCHSa37 :	-----						: -
TrCHSa38 :	-----						: -
TrCHSa39 :	-----						: -

FIGURE 15

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	*	80	*	100	*	120	
TrCHSa1 :	NACCTCTTCTGAGACCCTTCATCATATATATATAACNCATCTCACCTCATACATATTTCC						: 120
TrCHSa2 :	-----GNANNACAACACACTTCNAC-CTTTGCT-TTTCT						: 32
TrCHSa3 :	-----CACNTTAGCNCTTTGCTTTTTCT						: 23
TrCHSa4 :	-----CACNTTAGC-CTTTGCT-TTTCT						: 21
TrCHSa5 :	-----GCANACACT						: 9
TrCHSa6 :	-----ACN						: 3
TrCHSa7 :	-----CC						: 2
TrCHSa8 :	-----CN						: 2
TrCHSa9 :	-----GC						: 2
TrCHSa10 :	-----						: -
TrCHSa11 :	-----						: -
TrCHSa12 :	-----						: -
TrCHSa13 :	-----						: -
TrCHSa14 :	-----						: -
TrCHSa15 :	-----						: -
TrCHSa16 :	-----						: -
TrCHSa17 :	-----						: -
TrCHSa18 :	-----						: -
TrCHSa19 :	-----						: -
TrCHSa20 :	-----						: -
TrCHSa21 :	-----						: -
TrCHSa22 :	-----						: -
TrCHSa23 :	-----						: -
TrCHSa24 :	-----						: -
TrCHSa25 :	-----						: -
TrCHSa26 :	-----						: -
TrCHSa27 :	-----						: -
TrCHSa28 :	-----						: -
TrCHSa29 :	-----						: -
TrCHSa30 :	-----						: -
TrCHSa31 :	-----						: -
TrCHSa32 :	-----						: -
TrCHSa33 :	-----						: -
TrCHSa34 :	-----						: -
TrCHSa35 :	-----						: -
TrCHSa36 :	-----						: -
TrCHSa37 :	-----						: -
TrCHSa38 :	-----						: -
TrCHSa39 :	-----						: -

FIGURE 15 (cont)

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      *           140           *           160           *           180
TrCHSa1 : ACAACAANCTATAACTTNNCGTCTTATNTANACCAATTGAGTNTCAAATTNACATACATA :180
TrCHSa2 : ACAACAACCTTCTATNTAAACCTTTTCTTAGT-TNA--AACTTACACTACTG--CTA--AA : 85
TrCHSa3 : ACNACNNCTTCTGTCTAAACCTTTTCTGAGTNTNACTTGCTATACATAGAAANNCTANNCT : 83
TrCHSa4 : AC-AC-TCTTGTGTCTAAACNTTTTCTGAGT-TNACTTGCTATACATAGAAA--CTA--CT : 74
TrCHSa5 : CTATCCCTTTCTTTTCTNTATAANNATACACTACTNGCAATAAACNACGCAATTNAATTACA : 69
TrCHSa6 : AAAACAAC-TAGGCATATT-ATATATATATA-TTAGTCTATA-ATTCAAACNAAA--CT : 57
TrCHSa7 : ANGGAAAACAACCTCCGNCATANTNTTATATATATANNGTCTATAATTGAAAGAAACT : 62
TrCHSa8 : ACAAAACACTCCCTATNCATATTTCTCTCTCTNGTCTATA-ATTCAAAG-AAA--CT : 57
TrCHSa9 : ACAAAACACTNCGCTANTATATATATATATNTATATATATAATTGAAAGAAACT : 62
TrCHSa10 : GCTACAANCTNTAACTTNNCGTCTTATNTNNAANNATTGAGTNTNNAATTNACATACATA : 60
TrCHSa11 : AAAACAAC-CCGCCATATT-ATATATATATA-TA-NGTCTATA-ATTCAAAG-AAA--CT : 52
TrCHSa12 : -CAACAACCN-TAACTT--CGTGTAT-TA-ACC-ATTGAGT-T-NAATT-ACATACATA : 50
TrCHSa13 : -CAACAACCTNTAACTTNNCGTCTTATNTNNAACNATTGAGTNTNNAATTNACATACATA : 59
TrCHSa14 : -GANTAA--CATCCGC-ATATATATAT-TATNTNTTAGT-TATAATTGAAAGAAACT : 58
TrCHSa15 : --ACAACCNATAACTT--CGTGTAT-TA-ACC-ATTGAGT-T-NAATT-ACATACATA : 50
TrCHSa16 : --AA--AAACAAC--NGCATATTAT-TAT-TATANNGTCTATAATTGAAAGAAACT : 58
TrCHSa17 : ---NNAACCTATAACTNCCGTTTATNTTAA--NCATTGAGTNTNNAATTNACATACATA : 57
TrCHSa18 : ----GGNTAAACAAC--NANAGTNC-TT-TTATNNTTNNTATNTAT--AATACATACATA : 56
TrCHSa19 : -----TAA--CAAAACACNCCG--NATATNT-TATNATNTT-GT-TATAATTGAAAGAAACT : 55
TrCHSa20 : -----TACA--TNCGCNATAT-TAT-T-TAT-TNTT-GT-TATAATTGAAAGAAACT : 53
TrCHSa21 : -----TAA--AAC--NCCG--A-TATNT-TANNNTT-T-NGTCTATAATTGAAAGAAACT : 52
TrCHSa22 : -----TAA--AAC--NCCG--A-TATNT-TANNNTT-T-NGTCTATAATTGAAAGAAACT : 49
TrCHSa23 : -----CCNATN-ACCTTC-T-TTATNNTTAC-TATAC-TACATACATAC-CA : 45
TrCHSa24 : -----AC--NNA--NACNTA-T-TTATNNTTAC-TATAC-TACATACATAC-CA : 47
TrCHSa25 : -----ACNCNCCG--TATNT-TTTAT-TATNTAGTCTATAATTGAAAGAAACT : 47
TrCHSa26 : -----AG--TANAC-TA-TCTT-T-A-TTACTTNTACT-CA-TAG-NGGACT : 40
TrCHSa27 : -----ACCTACTCTTC-TCTTAT-NGTT--N-A-ATT-CA-TATNG-CA : 37
TrCHSa28 : -----ACNACTTC-TCTTATCACTTNC--ANATACATACATACNCA : 42
TrCHSa29 : -----TCTNGTCTNTATTG-AAAGAAACT : 21
TrCHSa30 : -----GN : 2
TrCHSa31 : -----GT : 2
TrCHSa32 : ----- : -
TrCHSa33 : ----- : -
TrCHSa34 : ----- : -
TrCHSa35 : -----AAG : 3
TrCHSa36 : -----G : 1
TrCHSa37 : ----- : -
TrCHSa38 : ----- : -
TrCHSa39 : ----- : -

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FIGURE 15 (cont)

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      *           200           *           220           *           240
TrCHSa1 : GCGGAAGATACTTAATACAAGATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 240
TrCHSa2 : G--ATATA---TATCAAC--ATGGTTAGTGTGCTGAAATTCGCAAGGCTCAAAGGGCT : 137
TrCHSa3 : GCTAAAGANNNTATCAAGNATGGTTAGTGTGCTGAAATTCGCAAGGCTCAAAGGGCT : 143
TrCHSa4 : GCTAAAGA---TATCAAG--ATGGTTAGTGTGCTGAAATTCGCAAGGCTCAAAGGGCT : 128
TrCHSa5 : TAAAAATCTTACTATTAAGATATGGTGAGTGTATCTGAAATTCGTAAGGCTCAAAGGGCT : 129
TrCHSa6 : GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 116
TrCHSa7 : ACTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 122
TrCHSa8 : GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 116
TrCHSa9 : ACTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 122
TrCHSa10 : GCGGAAGATACTTAATACAAGATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 120
TrCHSa11 : GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 111
TrCHSa12 : GCGGAAGATACTTAATACAAGATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 110
TrCHSa13 : GCGGAAGNTACTTAATACAAGATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 119
TrCHSa14 : GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 117
TrCHSa15 : GCGGAAGATACTTAATACAAGATGGTTAGTGTCTGAAATTCGCAAGGCTCAGAGGGCT : 110
TrCHSa16 : ACTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 118
TrCHSa17 : GCGGAAGATACTTAATACAAGATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 117
TrCHSa18 : GCNAAAATATAGTATTAAGATATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 116
TrCHSa19 : GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 115
TrCHSa20 : GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 113
TrCHSa21 : GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 112
TrCHSa22 : NCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 109
TrCHSa23 : G--GACCAAGATATTAAGATATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 103
TrCHSa24 : GCAAAATCAAGTATTAAGATATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 107
TrCHSa25 : GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 107
TrCHSa26 : GCAAG-TATNAGTATTAAGATATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 98
TrCHSa27 : GC-AAACAAAGTATTAAGATATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 95
TrCHSa28 : GCNAAACAAAGTATTAAGATATGGTTAGTGTCTGAAATTCGCAAGGCTCAAAGGGCT : 102
TrCHSa29 : GCTA---AGA-TTTTAAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 77
TrCHSa30 : GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 61
TrCHSa31 : NCTAAA-NNN-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 58
TrCHSa32 : GATA-AGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 58
TrCHSa33 : --TAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 58
TrCHSa34 : GGNTCANA-----GGGCT : 13
TrCHSa35 : GCCC----- : 11
TrCHSa36 : GCCC----- : 9
TrCHSa37 : ---ATAAG----- : 5
TrCHSa38 : ---ATTA----- : 4
TrCHSa39 : ---GCT----- : 4

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FIGURE 15 (cont)

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          *           260           *           280           *           300
TrCHSa1 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAATCCAGCAAATCGTGTTCAG : 300
TrCHSa2 : GAAGGCCCTGCAACTATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 197
TrCHSa3 : GAAGGCCCTGCAACAATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 203
TrCHSa4 : GAAGGCCCTGCAACAATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 188
TrCHSa5 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 189
TrCHSa6 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 176
TrCHSa7 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 182
TrCHSa8 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 176
TrCHSa9 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 182
TrCHSa10 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 180
TrCHSa11 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 171
TrCHSa12 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAATCCAGCAAATCGTGTTCAG : 170
TrCHSa13 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAATCCAGCAAATCGTGTTCAG : 179
TrCHSa14 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 177
TrCHSa15 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAATCCAGCAAATCGTGTTCAG : 170
TrCHSa16 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 178
TrCHSa17 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAATCCAGCAAATCGTGTTCAG : 177
TrCHSa18 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 176
TrCHSa19 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 175
TrCHSa20 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 173
TrCHSa21 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 172
TrCHSa22 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 169
TrCHSa23 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 163
TrCHSa24 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 167
TrCHSa25 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 167
TrCHSa26 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 158
TrCHSa27 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 155
TrCHSa28 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 162
TrCHSa29 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 137
TrCHSa30 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 121
TrCHSa31 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 118
TrCHSa32 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 118
TrCHSa33 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 118
TrCHSa34 : GAAGGCCCTGCAACC-TTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTCAG : 71
TrCHSa35 : -----AATTTTGGCCATTGGCACTGCAAATCCAGCAAATCGTGTTCAG : 59
TrCHSa36 : -----ACCATTTTGGCCATTGGCACTGCAAATCCAGCAAATCGTGTTCAG : 57
TrCHSa37 : -----: -
TrCHSa38 : -----: -
TrCHSa39 : -----: -

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FIGURE 15 (cont)

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          *           320           *           340           *           360
TrCHSa1 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA : 360
TrCHSa2 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAAGTTGAGCTCAAA : 257
TrCHSa3 : AGCACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAAGTTGAGCTCAAA : 263
TrCHSa4 : AGCACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAAGTTGAGCTCAAA : 248
TrCHSa5 : AGCACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA : 249
TrCHSa6 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 236
TrCHSa7 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 242
TrCHSa8 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 236
TrCHSa9 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 242
TrCHSa10 : AGCACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA : 240
TrCHSa11 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 231
TrCHSa12 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA : 230
TrCHSa13 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA : 239
TrCHSa14 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 237
TrCHSa15 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA : 230
TrCHSa16 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 238
TrCHSa17 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA : 237
TrCHSa18 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAA : 236
TrCHSa19 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 235
TrCHSa20 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 233
TrCHSa21 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 232
TrCHSa22 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 229
TrCHSa23 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAA : 223
TrCHSa24 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAA : 227
TrCHSa25 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 227
TrCHSa26 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAA : 218
TrCHSa27 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAA : 215
TrCHSa28 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAA : 222
TrCHSa29 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 197
TrCHSa30 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 181
TrCHSa31 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 178
TrCHSa32 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 178
TrCHSa33 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 178
TrCHSa34 : AGCACATATCCTGATTTCTACTTCAAAATACAAACAGTGAGCACAAGACTGAGCTCAAA : 131
TrCHSa35 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA : 119
TrCHSa36 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA : 117
TrCHSa37 : -----GCTGAGCTTAAA : 17
TrCHSa38 : ----- : -
TrCHSa39 : ----- : -

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FIGURE 15 (cont)

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	*	380	*	400	*	420	
TrCHSa1 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 420
TrCHSa2 :	GAGAAATTCCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 317
TrCHSa3 :	GAGAAATTCCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 323
TrCHSa4 :	GAGAAATTCCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 308
TrCHSa5 :	GAGAAATTCCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 309
TrCHSa6 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 296
TrCHSa7 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 302
TrCHSa8 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 296
TrCHSa9 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 302
TrCHSa10 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 300
TrCHSa11 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 291
TrCHSa12 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 290
TrCHSa13 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 299
TrCHSa14 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 297
TrCHSa15 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 290
TrCHSa16 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 298
TrCHSa17 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 297
TrCHSa18 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 296
TrCHSa19 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 295
TrCHSa20 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 293
TrCHSa21 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 292
TrCHSa22 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 289
TrCHSa23 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 283
TrCHSa24 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 287
TrCHSa25 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 287
TrCHSa26 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 278
TrCHSa27 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 275
TrCHSa28 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 282
TrCHSa29 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 257
TrCHSa30 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 241
TrCHSa31 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 238
TrCHSa32 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 238
TrCHSa33 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 238
TrCHSa34 :	GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA						: 191
TrCHSa35 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 179
TrCHSa36 :	GAGAAATTTTCAGCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 177
TrCHSa37 :	GAGAAATTTTNNCGCATGTGTGATAAAATCTATGATCAAGAGCAGATACATGTATCTAACA						: 77
TrCHSa38 :	-----AGAGCAGATACATGTATCTAACA						: 27
TrCHSa39 :	-----						: -

FIGURE 15 (cont)

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	*	440	*	460	*	480	
TrCHSa1 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 480
TrCHSa2 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 377
TrCHSa3 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAGCACATGGCACCTTCATTGGATGCT						: 383
TrCHSa4 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAGCACATGGCACCTTCATTGGATGCT						: 368
TrCHSa5 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 369
TrCHSa6 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 356
TrCHSa7 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 362
TrCHSa8 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 356
TrCHSa9 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 362
TrCHSa10 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 360
TrCHSa11 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 351
TrCHSa12 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 350
TrCHSa13 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 359
TrCHSa14 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 357
TrCHSa15 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 350
TrCHSa16 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 358
TrCHSa17 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 357
TrCHSa18 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 356
TrCHSa19 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 355
TrCHSa20 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 353
TrCHSa21 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 352
TrCHSa22 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 349
TrCHSa23 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 343
TrCHSa24 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 347
TrCHSa25 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 347
TrCHSa26 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 338
TrCHSa27 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 335
TrCHSa28 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 342
TrCHSa29 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 317
TrCHSa30 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 301
TrCHSa31 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 298
TrCHSa32 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 298
TrCHSa33 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 298
TrCHSa34 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 251
TrCHSa35 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 239
TrCHSa36 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 237
TrCHSa37 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 137
TrCHSa38 :	GAAGAGATTTTGAAGAAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT						: 87
TrCHSa39 :	-----						:

FIGURE 15 (cont)

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          *           500           *           520           *           540
TrCHSa1 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 540
TrCHSa2 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 437
TrCHSa3 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 443
TrCHSa4 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 428
TrCHSa5 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 429
TrCHSa6 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 416
TrCHSa7 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 407
TrCHSa8 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 416
TrCHSa9 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 422
TrCHSa10 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 420
TrCHSa11 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 411
TrCHSa12 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 410
TrCHSa13 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 419
TrCHSa14 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 417
TrCHSa15 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 390
TrCHSa16 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 418
TrCHSa17 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 417
TrCHSa18 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 416
TrCHSa19 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 415
TrCHSa20 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 413
TrCHSa21 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 412
TrCHSa22 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 409
TrCHSa23 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 403
TrCHSa24 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 407
TrCHSa25 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 407
TrCHSa26 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 398
TrCHSa27 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 395
TrCHSa28 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 402
TrCHSa29 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 377
TrCHSa30 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 361
TrCHSa31 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 358
TrCHSa32 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 358
TrCHSa33 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 358
TrCHSa34 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 311
TrCHSa35 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 299
TrCHSa36 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 297
TrCHSa37 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 197
TrCHSa38 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT : 147
TrCHSa39 : ----- : -

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FIGURE 15 (cont)

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      *           560           *           580           *           600
TrCHSa1 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 600
TrCHSa2 : ATTAAGAATGGGGTCAACCAAATCTAAGATTACACATTGATCTTTTGCACCACAAGT : 497
TrCHSa3 : ATAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 503
TrCHSa4 : ATAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 488
TrCHSa5 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 489
TrCHSa6 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 476
TrCHSa7 : ----- : -
TrCHSa8 : ATTAAGAATGGGGTCAACCAAAGTCANAGATNACTNACTTAATCTTTTGCACCACAAGN : 476
TrCHSa9 : ATCAAAGAATGGGGTCAACCAAATCTAAGATTACACATTGATCTTTTGCACCACAAGT : 482
TrCHSa10 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 480
TrCHSa11 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 471
TrCHSa12 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 470
TrCHSa13 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 479
TrCHSa14 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 477
TrCHSa15 : ----- : -
TrCHSa16 : ATCAAAGAATGGGGTCAACCAAATCTAAGATTACACATTGATCTTTTGCACCACAAGT : 478
TrCHSa17 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 477
TrCHSa18 : ATTAAGAATGGGGCCANCCN----- : 437
TrCHSa19 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 475
TrCHSa20 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 473
TrCHSa21 : ATCAAAGAATGGGGTCAACCAAATCTAAGATTACACATTGATCTTTTGCACCACAAGT : 472
TrCHSa22 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 469
TrCHSa23 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 463
TrCHSa24 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 467
TrCHSa25 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 467
TrCHSa26 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 458
TrCHSa27 : ATTAAGAATGGGGTCAACCAAATCTAAGATTACACATTGATCTTTTGCACCACAAGT : 455
TrCHSa28 : ATTAAGAATGGGGTCAACCAAATCTAAGATTACACATTGATCTTTTGCACCACAAGT : 462
TrCHSa29 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 437
TrCHSa30 : ATTAANAATGGGGNCAACCAAAGCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 421
TrCHSa31 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 418
TrCHSa32 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 418
TrCHSa33 : ATTAAGAATGGGGTCAACCAAATCTAAGATTACACATTGATCTTTTGCACCACAAGT : 418
TrCHSa34 : ATTAAGAATGGGGTCAACCAAATCTAAGATTACACATTGATCTTTTGCACCACAAGT : 371
TrCHSa35 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 359
TrCHSa36 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 357
TrCHSa37 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 257
TrCHSa38 : ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT : 207
TrCHSa39 : ---TAAGAATGGGGCAACCAAATCTAAGATTACACATTGATCTTTTGCACCACAAGT : 61

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FIGURE 15 (cont)

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          *           620           *           640           *           660
TrCHSa1 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 660
TrCHSa2 : GGTGTAGACATGCCTGGTGCTGATTACCAAGCCACAAAACCTTTTAGGACTTCGTCCATAT : 557
TrCHSa3 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 563
TrCHSa4 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 548
TrCHSa5 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTGGGACTTCGTCCATAT : 549
TrCHSa6 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 536
TrCHSa7 : ----- : -
TrCHSa8 : GGNCCCN----- : 483
TrCHSa9 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGACTTCGTCCATAT : 542
TrCHSa10 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 540
TrCHSa11 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 531
TrCHSa12 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 530
TrCHSa13 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 539
TrCHSa14 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 537
TrCHSa15 : ----- : -
TrCHSa16 : GGTGTANACATGCCTGGTGCTGATTACCAACTGACAAAACCTNTTAGGACTTCGCCCATAT : 538
TrCHSa17 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 537
TrCHSa18 : ----- : -
TrCHSa19 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 535
TrCHSa20 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 533
TrCHSa21 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTGGGACTTCGTCCATAT : 532
TrCHSa22 : GGTGTTGACATGCCTGGAGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 529
TrCHSa23 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 523
TrCHSa24 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 527
TrCHSa25 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 527
TrCHSa26 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGTCCATAT : 518
TrCHSa27 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGTCCATAT : 515
TrCHSa28 : GGTGTANACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGTCCATAT : 522
TrCHSa29 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 497
TrCHSa30 : GGTGTTGACATGCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGNTTCGCCCATAT : 481
TrCHSa31 : GGTGTTGACATGCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGNTTCGCCCATAT : 478
TrCHSa32 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 478
TrCHSa33 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGCTTCGTCCATAT : 478
TrCHSa34 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGCTTCGTCCATAT : 431
TrCHSa35 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 419
TrCHSa36 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 417
TrCHSa37 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 317
TrCHSa38 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGTCCATAT : 267
TrCHSa39 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACCTCTTAGGTCTTCGCCCATAT : 121

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FIGURE 15 (cont)

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      *           680           *           700           *           720
TrCHSa1 : GTG-----: 663
TrCHSa2 : GTGAAGAGGTACATGATG-----: 575
TrCHSa3 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGC-----: 607
TrCHSa4 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTTCCTTCGTTT--: 606
TrCHSa5 : GTGAAGAGGTTCATGATGTACCAACAAGGTGCTTTTGCAGGAGGC-----: 594
TrCHSa6 : GTGAAGAGGTATATGATGTACCAACAAGGTGCTTTTGCAGGAGGCACGGTGCCTTCGTTTG: 596
TrCHSa7 : -----: -
TrCHSa8 : -----: -
TrCHSa9 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGC-----: 586
TrCHSa10: GTGAAGAGGTACATGATGTACCAACAAGGGTGCT-----: 574
TrCHSa11: GTGAAGAGGTATATGATGTACCAACAAGGTGCTTTTGCAGGAGGCACGGTGCCTTCGTTTG: 591
TrCHSa12: GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAG-----: 570
TrCHSa13: GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTTCCTTCGTTT--: 598
TrCHSa14: GTGAAGAGGTATATGATGTACCAACAAGGTGCTTTTGCAGGAGGCACGGTGCCTTCGTTTG: 597
TrCHSa15: -----: -
TrCHSa16: GTGAAGAGGTCCCTGCTGNNCCN-----: 561
TrCHSa17: GTGAAG-----: 543
TrCHSa18: -----: -
TrCHSa19: GTGAAGAGGTATATGATGTACCAACAAGGTGCTTTTGCAGGAGGCACGGTGCCTTCGTTTG: 595
TrCHSa20: GTGAAGAGGTATATGATGTACCAACAAGGTGCTTTTGCAGGAGGCACG-----: 581
TrCHSa21: GTGAAGAGGTTCATGATGTACCAACAAGGTGCTTTTGCAGGTGGGACGGTTCCTTCG-----: 588
TrCHSa22: GTGAAGAGGTATATGATGTACCAACAAGGTGCTTTTGCAGGAGGCACGGTGCCTTCGTTTG: 589
TrCHSa23: GTGAAGAGGTATATGATGTAT-----: 544
TrCHSa24: GTGAAGAGGTACATGATGTACCAACAAG-----: 555
TrCHSa25: GTGAAGAGGTATATGATGTACCAACAAGGTGCTTTTGCAGGAG-----: 570
TrCHSa26: GTGAAGAGGTACATGATGTACCAACAAG-----: 546
TrCHSa27: GTGAAGAGGTATATGATGTACCAACAAGGGTGCTTTTGCAGGTGGGACGGTGCCTTCGTTTG: 575
TrCHSa28: GTGAAGAGGTATATGATGTACCAACAAGGGTGCTTTTGCAGGTGGGACGGTGCCTTCGTTTG: 582
TrCHSa29: GTGAAGAGGTATATGATGTACCA-----: 521
TrCHSa30: GTGAAGAGGTATATGATGTACCA-----: 506
TrCHSa31: GTGAAGAGGTATATGATGTACCAACN-----: 504
TrCHSa32: GTGAAGAGGTATATGATGTACCAACAAGGTGCTTTTGCAGGAGGCACGGTGCCTTCGTTTG: 538
TrCHSa33: GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTTGCAGGTGGGACGGTTCCTTCGTTTG: 538
TrCHSa34: GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTTGCAGGTGGGACGGTTCCTTCGTTTG: 491
TrCHSa35: GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTTGCAGGTGGGACGGTTCCTTCGTTTG: 479
TrCHSa36: GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTTGCAGGTGGGACGGTTCCTTCGTTTG: 477
TrCHSa37: GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTTGCAGGTGGGACGGTTCCTTCGTTTG: 377
TrCHSa38: GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTTGCAGGTGGGACGGTTCCTTCGTTTG: 327
TrCHSa39: GTGAAGAGGTATATGATGTACCAACAAGGTGCTTTTGCAGGAGGCACGGTGCCTTCGTTTG: 181

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FIGURE 15 (cont)

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	*	740	*	760	*	780	
TrCHSa1 :	----		----		----		:-
TrCHSa2 :	----		----		----		:-
TrCHSa3 :	----		----		----		:-
TrCHSa4 :	----		----		----		:-
TrCHSa5 :	----		----		----		:-
TrCHSa6 :	GC	AAAAAGATT	TG	CCCGAGAACAACAAAGGTGCTCGTGTGCTAGTTGTTTGTCTGAAGTC			: 656
TrCHSa7 :	----		----		----		:-
TrCHSa8 :	----		----		----		:-
TrCHSa9 :	----		----		----		:-
TrCHSa10 :	----		----		----		:-
TrCHSa11 :	GC	AAAAAGATT	TG	----			: 604
TrCHSa12 :	----		----		----		:-
TrCHSa13 :	----		----		----		:-
TrCHSa14 :	GC	AAAAAGATT	TG	----			: 609
TrCHSa15 :	----		----		----		:-
TrCHSa16 :	----		----		----		:-
TrCHSa17 :	----		----		----		:-
TrCHSa18 :	----		----		----		:-
TrCHSa19 :	GC	AAAAAGATT	TG	----			: 607
TrCHSa20 :	----		----		----		:-
TrCHSa21 :	----		----		----		:-
TrCHSa22 :	GC	AAAAAGATT	TG	CCCGAGAACAAC			: 613
TrCHSa23 :	----		----		----		:-
TrCHSa24 :	----		----		----		:-
TrCHSa25 :	----		----		----		:-
TrCHSa26 :	----		----		----		:-
TrCHSa27 :	GC	AAAGG	----				: 582
TrCHSa28 :	GC	AAAGATT	TG	CCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGGTTGGTCTGAAGTC			: 642
TrCHSa29 :	----		----		----		:-
TrCHSa30 :	----		----		----		:-
TrCHSa31 :	----		----		----		:-
TrCHSa32 :	GC	AAAAAGATT	TG	CCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTCTGAAGTC			: 598
TrCHSa33 :	GC	TAAAGATT	TG	CCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTCTGAAGT			: 597
TrCHSa34 :	GC	TAAAGATT	TG	CCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTCTGAAGTA			: 551
TrCHSa35 :	GC	TAAAGATT	TG	CCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTCTGAAGTA			: 539
TrCHSa36 :	GC	TAAAGATT	TG	CCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTCTGAAGTA			: 537
TrCHSa37 :	GC	TAAAGATT	TG	CCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTCTGAAGTA			: 437
TrCHSa38 :	GC	TAAAGATT	TG	CCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTCTGAAGTC			: 387
TrCHSa39 :	GC	TAAAGATT	TG	CCCGAGAACAACAAAGGTGCTCGTGTGTTAGTTGTTTGTCTGAAGTA			: 241

FIGURE 15 (cont)

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	*	800	*	820	*	840	
TrCHSa1 :	-----						: -
TrCHSa2 :	-----						: -
TrCHSa3 :	-----						: -
TrCHSa4 :	-----						: -
TrCHSa5 :	-----						: -
TrCHSa6 :	ACCGCAGTCACATTTCGCGGCCCCAGTGATACTCACTTGGACAGTCTTGNTG						: 708
TrCHSa7 :	-----						: -
TrCHSa8 :	-----						: -
TrCHSa9 :	-----						: -
TrCHSa10 :	-----						: -
TrCHSa11 :	-----						: -
TrCHSa12 :	-----						: -
TrCHSa13 :	-----						: -
TrCHSa14 :	-----						: -
TrCHSa15 :	-----						: -
TrCHSa16 :	-----						: -
TrCHSa17 :	-----						: -
TrCHSa18 :	-----						: -
TrCHSa19 :	-----						: -
TrCHSa20 :	-----						: -
TrCHSa21 :	-----						: -
TrCHSa22 :	-----						: -
TrCHSa23 :	-----						: -
TrCHSa24 :	-----						: -
TrCHSa25 :	-----						: -
TrCHSa26 :	-----						: -
TrCHSa27 :	-----						: -
TrCHSa28 :	ACCGCAN						: 649
TrCHSa29 :	-----						: -
TrCHSa30 :	-----						: -
TrCHSa31 :	-----						: -
TrCHSa32 :	ACATGCAGTTACATTCCGTTGGCCCGAGTGACACTCACTTGGACAGTCTTGTTGGACAAGCA						: 658
TrCHSa33 :	-----						: -
TrCHSa34 :	ACATGCAGTCACATTCCGTTGGCCCGAGTGACACTCACTTG						: 590
TrCHSa35 :	ACCGCAGTCACATTCCGCGGCCCCAGTGACACTCAATTTGGACAGCTTGTTGGACAAGCA						: 599
TrCHSa36 :	ACCGCAGTCACATTCCGCGGCCCCAGTGACACTCAATTTGGACAGCTTGTTGGACAAGCA						: 597
TrCHSa37 :	ACCGCAGTCACATTCCGCGGCCCCAGTGACACTCAATTTGGACAGTCTTGTTGGACAAGCA						: 497
TrCHSa38 :	ACCGCAGTCACATTCCGTTGGCCCTAGTGACACTCAATTTGGACAGTCTTGTTGGACAAGCA						: 447
TrCHSa39 :	ACATGCAGTCACATTCCGCGGTTCCAAGTGACACTCACTTGGACAGTCTTGTTGGACAAGCA						: 301

FIGURE 15 (cont)

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	*	860	*	880	*	900	
TrCHSa1 :	-----		-----		-----		-
TrCHSa2 :	-----		-----		-----		-
TrCHSa3 :	-----		-----		-----		-
TrCHSa4 :	-----		-----		-----		-
TrCHSa5 :	-----		-----		-----		-
TrCHSa6 :	-----		-----		-----		-
TrCHSa7 :	-----		-----		-----		-
TrCHSa8 :	-----		-----		-----		-
TrCHSa9 :	-----		-----		-----		-
TrCHSa10 :	-----		-----		-----		-
TrCHSa11 :	-----		-----		-----		-
TrCHSa12 :	-----		-----		-----		-
TrCHSa13 :	-----		-----		-----		-
TrCHSa14 :	-----		-----		-----		-
TrCHSa15 :	-----		-----		-----		-
TrCHSa16 :	-----		-----		-----		-
TrCHSa17 :	-----		-----		-----		-
TrCHSa18 :	-----		-----		-----		-
TrCHSa19 :	-----		-----		-----		-
TrCHSa20 :	-----		-----		-----		-
TrCHSa21 :	-----		-----		-----		-
TrCHSa22 :	-----		-----		-----		-
TrCHSa23 :	-----		-----		-----		-
TrCHSa24 :	-----		-----		-----		-
TrCHSa25 :	-----		-----		-----		-
TrCHSa26 :	-----		-----		-----		-
TrCHSa27 :	-----		-----		-----		-
TrCHSa28 :	-----		-----		-----		-
TrCHSa29 :	-----		-----		-----		-
TrCHSa30 :	-----		-----		-----		-
TrCHSa31 :	-----		-----		-----		-
TrCHSa32 :	CTTTTGGAGATGGAGCTGCTGCACTTCATCGTTGGCTCAGACCAGTCCAGAAATTGAG						: 718
TrCHSa33 :	-----		-----		-----		-
TrCHSa34 :	-----		-----		-----		-
TrCHSa35 :	CTATTTGGAGATGGAGCTG-----						: 618
TrCHSa36 :	CTATTTGGAGATGGAGCTGCTG-----						: 619
TrCHSa37 :	CTATTTGGAGATGGAGCTGCTGCACTCATTGTTGGCTCAGACCCAGTACCAGAAATTGAG						: 557
TrCHSa38 :	CTATTTGGAGATGGAGCTGCTGCTCATTGTTGGCTCAGACCAGTACCAGAAATTGAG						: 507
TrCHSa39 :	CTATTTGGAGATGGAGCTGCTGCTCATTGTTGGCTCAGACCCGTACCAGAAATTGAG						: 361

FIGURE 15 (cont)

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	*	920	*	940	*	960	
TrCHSa1 :	-----		-----		-----		:
TrCHSa2 :	-----		-----		-----		:
TrCHSa3 :	-----		-----		-----		:
TrCHSa4 :	-----		-----		-----		:
TrCHSa5 :	-----		-----		-----		:
TrCHSa6 :	-----		-----		-----		:
TrCHSa7 :	-----		-----		-----		:
TrCHSa8 :	-----		-----		-----		:
TrCHSa9 :	-----		-----		-----		:
TrCHSa10 :	-----		-----		-----		:
TrCHSa11 :	-----		-----		-----		:
TrCHSa12 :	-----		-----		-----		:
TrCHSa13 :	-----		-----		-----		:
TrCHSa14 :	-----		-----		-----		:
TrCHSa15 :	-----		-----		-----		:
TrCHSa16 :	-----		-----		-----		:
TrCHSa17 :	-----		-----		-----		:
TrCHSa18 :	-----		-----		-----		:
TrCHSa19 :	-----		-----		-----		:
TrCHSa20 :	-----		-----		-----		:
TrCHSa21 :	-----		-----		-----		:
TrCHSa22 :	-----		-----		-----		:
TrCHSa23 :	-----		-----		-----		:
TrCHSa24 :	-----		-----		-----		:
TrCHSa25 :	-----		-----		-----		:
TrCHSa26 :	-----		-----		-----		:
TrCHSa27 :	-----		-----		-----		:
TrCHSa28 :	-----		-----		-----		:
TrCHSa29 :	-----		-----		-----		:
TrCHSa30 :	-----		-----		-----		:
TrCHSa31 :	-----		-----		-----		:
TrCHSa32 :	AAACCAATATTTGAGATGGTATGGACATGCACATACAATTGCTCCAGACAGTGAAGGTGCC						: 778
TrCHSa33 :	-----		-----		-----		:
TrCHSa34 :	-----		-----		-----		:
TrCHSa35 :	-----		-----		-----		:
TrCHSa36 :	-----		-----		-----		:
TrCHSa37 :	AN-----		-----		-----		: 559
TrCHSa38 :	AAGCCAATATTTGAGATGGTATGGACCGCACAGACAATTGCTCCAG-----						: 553
TrCHSa39 :	AAACCAATATTTGAGATGGTATGGACCGCACAGACAATTGCTCCAGACAGTGAAGGTGCC						: 421

FIGURE 15 (cont)

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	*	980	*	1000	*	1020	
TrCHSa1 :	-----		-----		-----		:
TrCHSa2 :	-----		-----		-----		:
TrCHSa3 :	-----		-----		-----		:
TrCHSa4 :	-----		-----		-----		:
TrCHSa5 :	-----		-----		-----		:
TrCHSa6 :	-----		-----		-----		:
TrCHSa7 :	-----		-----		-----		:
TrCHSa8 :	-----		-----		-----		:
TrCHSa9 :	-----		-----		-----		:
TrCHSa10 :	-----		-----		-----		:
TrCHSa11 :	-----		-----		-----		:
TrCHSa12 :	-----		-----		-----		:
TrCHSa13 :	-----		-----		-----		:
TrCHSa14 :	-----		-----		-----		:
TrCHSa15 :	-----		-----		-----		:
TrCHSa16 :	-----		-----		-----		:
TrCHSa17 :	-----		-----		-----		:
TrCHSa18 :	-----		-----		-----		:
TrCHSa19 :	-----		-----		-----		:
TrCHSa20 :	-----		-----		-----		:
TrCHSa21 :	-----		-----		-----		:
TrCHSa22 :	-----		-----		-----		:
TrCHSa23 :	-----		-----		-----		:
TrCHSa24 :	-----		-----		-----		:
TrCHSa25 :	-----		-----		-----		:
TrCHSa26 :	-----		-----		-----		:
TrCHSa27 :	-----		-----		-----		:
TrCHSa28 :	-----		-----		-----		:
TrCHSa29 :	-----		-----		-----		:
TrCHSa30 :	-----		-----		-----		:
TrCHSa31 :	-----		-----		-----		:
TrCHSa32 :	ATTG		-----		-----		: 782
TrCHSa33 :	-----		-----		-----		:
TrCHSa34 :	-----		-----		-----		:
TrCHSa35 :	-----		-----		-----		:
TrCHSa36 :	-----		-----		-----		:
TrCHSa37 :	-----		-----		-----		:
TrCHSa38 :	-----		-----		-----		:
TrCHSa39 :	ATTGATGGTCACCTTCGTGAAGCTGGACTAACATTTTCATCTTCTTAAAGATGTTCTCTGGG		-----		-----		: 481

FIGURE 15 (cont)

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	*	1040	*	1060	*	1080	
TrCHSa1 :	-----		-----		-----		:
TrCHSa2 :	-----		-----		-----		:
TrCHSa3 :	-----		-----		-----		:
TrCHSa4 :	-----		-----		-----		:
TrCHSa5 :	-----		-----		-----		:
TrCHSa6 :	-----		-----		-----		:
TrCHSa7 :	-----		-----		-----		:
TrCHSa8 :	-----		-----		-----		:
TrCHSa9 :	-----		-----		-----		:
TrCHSa10 :	-----		-----		-----		:
TrCHSa11 :	-----		-----		-----		:
TrCHSa12 :	-----		-----		-----		:
TrCHSa13 :	-----		-----		-----		:
TrCHSa14 :	-----		-----		-----		:
TrCHSa15 :	-----		-----		-----		:
TrCHSa16 :	-----		-----		-----		:
TrCHSa17 :	-----		-----		-----		:
TrCHSa18 :	-----		-----		-----		:
TrCHSa19 :	-----		-----		-----		:
TrCHSa20 :	-----		-----		-----		:
TrCHSa21 :	-----		-----		-----		:
TrCHSa22 :	-----		-----		-----		:
TrCHSa23 :	-----		-----		-----		:
TrCHSa24 :	-----		-----		-----		:
TrCHSa25 :	-----		-----		-----		:
TrCHSa26 :	-----		-----		-----		:
TrCHSa27 :	-----		-----		-----		:
TrCHSa28 :	-----		-----		-----		:
TrCHSa29 :	-----		-----		-----		:
TrCHSa30 :	-----		-----		-----		:
TrCHSa31 :	-----		-----		-----		:
TrCHSa32 :	-----		-----		-----		:
TrCHSa33 :	-----		-----		-----		:
TrCHSa34 :	-----		-----		-----		:
TrCHSa35 :	-----		-----		-----		:
TrCHSa36 :	-----		-----		-----		:
TrCHSa37 :	-----		-----		-----		:
TrCHSa38 :	-----		-----		-----		:
TrCHSa39 :	ATTGTATCAAAGAACATTAATAAAGCATTGGTCGAGGCTTTCCAACCATTAGGAATTCT						: 541

FIGURE 15 (cont)

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	*	1100	*	1120	*		
TrCHSa1	:	-----		-----	:	-	
TrCHSa2	:	-----		-----	:	-	
TrCHSa3	:	-----		-----	:	-	
TrCHSa4	:	-----		-----	:	-	
TrCHSa5	:	-----		-----	:	-	
TrCHSa6	:	-----		-----	:	-	
TrCHSa7	:	-----		-----	:	-	
TrCHSa8	:	-----		-----	:	-	
TrCHSa9	:	-----		-----	:	-	
TrCHSa10	:	-----		-----	:	-	
TrCHSa11	:	-----		-----	:	-	
TrCHSa12	:	-----		-----	:	-	
TrCHSa13	:	-----		-----	:	-	
TrCHSa14	:	-----		-----	:	-	
TrCHSa15	:	-----		-----	:	-	
TrCHSa16	:	-----		-----	:	-	
TrCHSa17	:	-----		-----	:	-	
TrCHSa18	:	-----		-----	:	-	
TrCHSa19	:	-----		-----	:	-	
TrCHSa20	:	-----		-----	:	-	
TrCHSa21	:	-----		-----	:	-	
TrCHSa22	:	-----		-----	:	-	
TrCHSa23	:	-----		-----	:	-	
TrCHSa24	:	-----		-----	:	-	
TrCHSa25	:	-----		-----	:	-	
TrCHSa26	:	-----		-----	:	-	
TrCHSa27	:	-----		-----	:	-	
TrCHSa28	:	-----		-----	:	-	
TrCHSa29	:	-----		-----	:	-	
TrCHSa30	:	-----		-----	:	-	
TrCHSa31	:	-----		-----	:	-	
TrCHSa32	:	-----		-----	:	-	
TrCHSa33	:	-----		-----	:	-	
TrCHSa34	:	-----		-----	:	-	
TrCHSa35	:	-----		-----	:	-	
TrCHSa36	:	-----		-----	:	-	
TrCHSa37	:	-----		-----	:	-	
TrCHSa38	:	-----		-----	:	-	
TrCHSa39	:	GATTACAAC TCAATCTTTTGGATTGCACACCCGGGTGGACCTGCAATTCT				:	591

FIGURE 15 (cont)

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      *           20           *           40           *           60
TrCHSb : TCTTCGNCNAGCTGGACNAACATTTNTGCTTCTTAAAGATGTTTCCTGAGATTGTCTCAAA : 60

      *           80           *           100          *           120
TrCHSb : GAACATTGATAAGGCATTGGTTGAGGCATTCCAACCATTAAACATCTCTGATTACAATTC : 120

      *           140          *           160          *           180
TrCHSb : AATCTTTTGGATTGCTCATCCAGGTGGTCTGCAATTCCTAGACCAAGTTGAGATAAAGTT : 180

      *           200          *           220          *           240
TrCHSb : GGGCTTAAACCTGAAAAAATGAAGGCCACCAGAGATGTACTTAGTGAATATGGTAACAT : 240

      *           260          *           280          *           300
TrCHSb : GTCAAGTGCATGTGTATTGTTTCATCTTAGATGAGATGCAAAGAAATCGGCTGAAAATGG : 300

      *           320          *           340          *           360
TrCHSb : ACTGAAAACACAGGAGAAGGACTTGACTGGGGTGTGTTGTTTGGATTGACCAGGACT : 360

      *           380          *           400          *           420
TrCHSb : TACCATTGAAACTGTTGTTCTACATAGTGTGGCTATATGAGAATGCGAGACTTGATTGTT : 420

      *           440          *           460          *           480
TrCHSb : TTGTATTGTATTGTATTGTATTGTATTACTTTTAATCTTGCTTGAATTTCCATTTAACAA : 480

      *           500          *           520          *           540
TrCHSb : TAAATATGGAGTTCAATAAGTACCATCAGTGTAAAATAATATATCGTTAATAGCTATTA : 540

      *           560          *           580          *           600
TrCHSb : TTTTAGTGTCTGTTTCTTTTACTAACTATATTTTATTTTAGTATTTGCTATTGATTG : 600

      *           620          *
TrCHSb : AAATAAATATTGTCCTCTTAAGTAAAAAAAAA : 634

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FIGURE 16

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TrCHSb : LRXAGXTFXLLKDVPEIVSKNIDKALVEAFQPLNISDYNISIFWIAHPGGPAILDQVEIKL : 60

TrCHSb : GLKPEKMKATRDVLSEYGNMSSACVLFILDEMOKKSAENGLKTTGEGLDWGVLFQFGPGGL : 120

TrCHSb : TIETVVLHSVAI : 132

FIGURE 17

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      *           20           *           40           *           60
TrCHSb1: TCTTCGNCNAGCTGGACNAACATTNTGCTTCTTAAAGATGTTCTCGAGATTGTCTCAAA : 60
TrCHSb2: ----- : -
TrCHSb3: ----- : -

      *           80           *           100          *           120
TrCHSb1: GAACATTGATAAGGCATTGGTTGAGGCATTCCAACCATTAACATCTCTGATTACAATTC : 120
TrCHSb2: ----- : -
TrCHSb3: ----- : -

      *           140          *           160           *           180
TrCHSb1: AATCTTTTGGATTGCTCATCCAGGTGGTCCTGCAATTCTAGACCAAGTTGAGATAAAGTT : 180
TrCHSb2: ----- : -
TrCHSb3: ----- : -

      *           200          *           220           *           240
TrCHSb1: GGGCTTAAACCTGAAAAAATGAAGGCCACCAGAGATGTACTTAGTGAATATGGTAACAT : 240
TrCHSb2: ----- : -
TrCHSb3: ----- : -

      *           260          *           280           *           300
TrCHSb1: GTCAAGTGCATGTGTATTGTTTCATCTTAGATGAGATGAGAAAGAAATCGGCTGAAAAATGG : 300
TrCHSb2: -----GAGATGCACAAAGAAATCGGCTTAAAAATGG : 29
TrCHSb3: -----GAGATGCCAAAGAAATCGGCTCAAAATGG : 29

      *           320          *           340           *           360
TrCHSb1: ACTTAAAACCACAGGAGAAGGACTTGACTGGGGTGTGTTGTTTGGATTGCGCCGGGACT : 360
TrCHSb2: ACTGAAAACCACAGGAGAAGGACTTGACTGGGGTGTGTTGTTTGGATTGCGACCAGGACT : 89
TrCHSb3: ACTGAAAACCACAGGAGAAGGACTTGACTGGGGTGTGTTGTTTGGATTGCGACCAGGACT : 89

      *           380          *           400           *           420
TrCHSb1: TACCATTGAAACTGTTGTTCTACATAGTGTGGCTATATGAGAATCGAGACTTGATTGTT : 420
TrCHSb2: TACCATTGAAACTGTTGTTCTACATAGTGTGGCTATATGAGAATGCGAGACTTGATTGTT : 149
TrCHSb3: TACCATTGAAACTGTTGTTCTACATAGTGTGGCTATATGAGAATGCGAGACTTGATTGTT : 149

      *           440          *           460           *           480
TrCHSb1: T--T--T--T--ATTGATTGTATTACTTTAATCTTGCTTGAAGTTCCATTTAANAA : 470
TrCHSb2: TTGTATTGTATTGTATTGTATTGTATTACTTTTAATCTTGCTTGAATTTCCATTTAACAA : 209
TrCHSb3: TTGTATTGTATTGTATTGTATTGTATTACTTTTAATCTTGCTTGAATTTCCATTTAACAA : 209

      *           500          *           520           *           540
TrCHSb1: TAAATATGGGNGTTCANTGGN----- : 491
TrCHSb2: TAAATATGGAGTTCAATAAGTACCATCAGTGTAAAATAATATATCGTTAATAGCTATTA : 269
TrCHSb3: TAAATATGGAGTTCAATAAGTACCATCAGTGTAAAATAATATATCGTTAATAGCTATTA : 269

      *           560          *           580           *           600
TrCHSb1: ----- : -
TrCHSb2: TTTTAGTGTCTGTTTCTTTTACTAAACTATATTTTATTTTAGTATTGCTATTGATTG : 329
TrCHSb3: TTTTAGTGTCTGTTTCTTTTACTAAACTATATTTTATTTTAGTATTGCTATTGATTG : 329

      *           620          *
TrCHSb1: ----- : -
TrCHSb2: AAATAAATATTGTCCTCTTAAGTGAIAAAAAAAAA : 363
TrCHSb3: AAATAAATATTGTCCTCTTAAGTGAIAAAAAAAAA : 363

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FIGURE 18

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      *           20           *           40           *           60
TrCHSc : GNTTCAATCTGTTGTGCATAAAATTNCTTTGCNATAGAAAACCATACACATTTGATCTTG : 60

      *           80           *           100          *           120
TrCHSc : CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 120

      *           140          *           160          *           180
TrCHSc : GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTC CCTCACCAACTTGTGATGCAAGAG : 180

      *           200          *           220          *           240
TrCHSc : TATTTAGTTGATGGTTATTTTAGGGACACTAATTGTGACAATCCTGAACCTTAAGCAGAAA : 240

      *           260          *           280          *           300
TrCHSc : CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 300

      *           320          *           340          *           360
TrCHSc : ATACTAAAGAAATATCCAGAACTTGTTGTCGAAGGCGCCTCAACTGTAAACAACGTTTA : 360

      *           380          *           400          *           420
TrCHSc : GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCAAGTTTGCCTAAAG : 420

      *           440          *           460          *           480
TrCHSc : AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT : 480

      *           500          *           520          *           540
TrCHSc : AGATTACCCGGTGGTGACCTATACTTGTCAAAAGGACTAGGACTAAACCCTAAAATTCAA : 540

      *           560          *           580          *           600
TrCHSc : AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA : 600

      *           620          *           640          *           660
TrCHSc : GACATAGCTGAGAACAACCCTGGAAGTAGAGTTTGTCTTGCTACTTCTGAAACTACAATT : 660

      *           680          *           700          *           720
TrCHSc : ATTGGATTCAAGCCACCAAGTGTGATAGACCTTATGATCTTGTGGTGTGGCACTCTTT : 720

      *           740          *           760          *           780
TrCHSc : GGAGATGGTGCTGGTGCTATGATAATTGGCTCAGACCCAATACTTGAAACTGAGACTCCA : 780

      *           800          *           820          *           840
TrCHSc : TTGTTTGAGCTTCATACTTCAGCTCAGGAGTTTATACCAGACACAGAGAAGAAAATAGAT : 840

      *           860          *           880          *
TrCHSc : GGGCGGCTGACGGAGGAGGGCATAAGTTTCACGCTAGCGAGGGAAGTCCCGCAGATA : 897

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FIGURE 19

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TrCHSc : MGDEGIVRGVTKQTTPGKATILALGKAFPHQLVMQEYLVLDGYFRDTNCDNPELKQKLARL : 60

TrCHSc : CKTTTVKTRYVVMNEEILKKYPELVVEGASTVKQRLEICNEAVTQMAIEASQVCLKNWGR : 120

TrCHSc : SLSDITHVVYVSSSEARLPGGDLVLSKGLGLNPKIQRTMLYFSGCSGGVAGLRVAKDIAE : 180

TrCHSc : NNPGSRVLLATSETTIIGFKPPSVDRPYDLVGVALFGDGAGAMIIGSDPILETETPLFEL : 240

TrCHSc : HTSAQEFIPDTEKKIDGRLTEEGISFTLARELPQI : 275

FIGURE 20

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      *           20           *           40           *           60
TrCHSc1: GNTTCAATCTGTTGTCATATAAATTNCTTTGTCNATAGAAAACNCTACACATTTGATCTTG : 60
TrCHSc2: ---TCAATCTGTTGTCGTCATTTTNTTNCNTTTGTCNATAGAAAACCATACACATTTGATCTTG : 57
TrCHSc3: -----TCTGTTGTCGTTTAACTTNCNTTTGTCNATAGAAAACCTACACATTTGATCTTG : 53
TrCHSc4: -----TCTGTTGTCGTTTAAATTACTTTGTCNNTAGAAAACNCTACACATTTGATCTTG : 53
TrCHSc5: -----TTAACATTTTNTTATTTGTCAGAAAATATACATTTGATCTAG : 40
TrCHSc6: -----GCANTAGAAAACCTACACATTTGATCTTG : 30
TrCHSc7: ----- : -

      *           80           *           100          *           120
TrCHSc1: CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 120
TrCHSc2: CTTTAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 117
TrCHSc3: CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 113
TrCHSc4: CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 113
TrCHSc5: CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 100
TrCHSc6: CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 90
TrCHSc7: ----- : -

      *           140          *           160          *           180
TrCHSc1: GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 180
TrCHSc2: GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 177
TrCHSc3: GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 173
TrCHSc4: GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 173
TrCHSc5: GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 160
TrCHSc6: GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 150
TrCHSc7: ----- : -

      *           200          *           220          *           240
TrCHSc1: TTTTAGTTGATGCTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 240
TrCHSc2: TTTTAGTTGATGCTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 237
TrCHSc3: TTTTAGTTGATGCTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 233
TrCHSc4: TTTTAGTTGATGCTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 233
TrCHSc5: TTTTAGTTGATGCTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 220
TrCHSc6: TTTTAGTTGATGCTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 210
TrCHSc7: ----- : -

      *           260          *           280          *           300
TrCHSc1: CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 300
TrCHSc2: CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 297
TrCHSc3: CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 293
TrCHSc4: CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 293
TrCHSc5: CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 280
TrCHSc6: CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 270
TrCHSc7: ----- : -

      *           320          *           340          *           360
TrCHSc1: ATACTAAAGAAATATCCAGAACTTGTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 360
TrCHSc2: ATACTAAAGAAATATCCAGAACTTGTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 357
TrCHSc3: ATACTAAAGAAATATCCAGAACTTGTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 353
TrCHSc4: ATACTAAAGAAATATCCAGAACTTGTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 353
TrCHSc5: ATACTAAAGAAATATCCAGAACTTGTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 340
TrCHSc6: ATACTAAAGAAATATCCAGAACTTGTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 330
TrCHSc7: -----NTCCNGAACTTACTGTGGAAGGCGCCTCAACTGTAAAACAACGTTTA : 47

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FIGURE 21

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		*	380	*	400	*	420	
TrCHSc1:	GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG							: 420
TrCHSc2:	GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG							: 417
TrCHSc3:	GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG							: 413
TrCHSc4:	GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG							: 413
TrCHSc5:	GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG							: 400
TrCHSc6:	GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG							: 390
TrCHSc7:	GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG							: 107
		*	440	*	460	*	480	
TrCHSc1:	AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT							: 480
TrCHSc2:	AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT							: 477
TrCHSc3:	AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT							: 473
TrCHSc4:	AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT							: 473
TrCHSc5:	AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT							: 460
TrCHSc6:	AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT							: 450
TrCHSc7:	AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT							: 167
		*	500	*	520	*	540	
TrCHSc1:	AGATTACCCGGTGGTGACCTATACTTGTCAAAGGACTAGGACTAAACCCCTAAAATTCAA							: 540
TrCHSc2:	AGATTACCCGGTGGTGACCTATACTTGTCAAAGGACTAGGACTAAACCCCTAAAATTCAA							: 537
TrCHSc3:	AGATTACCCGGTGGTGACCTATACTTGTCAAAGGACTAGGACTAAACCCCTAAAATTCAA							: 533
TrCHSc4:	AGATTACCCGGTGGTGACCTATACTTGTCAAAGGACTAGGACTAAACCCCTAAAATTCAA							: 533
TrCHSc5:	AGATTACCCGGTGGTGACCTATACTTGTCAAAGGACTAGGACTAAACCCCTAAAATTCAA							: 520
TrCHSc6:	AGATTACCCGGTGGTGACCTATACTTGTCAAAGGACTAGGACTAAACCCCTAAAATTCAA							: 510
TrCHSc7:	AGATTACCCGGTGGTGACCTATACTTGTCAAAGGACTAGGACTAAACCCCTAAAATTCAA							: 227
		*	560	*	580	*	600	
TrCHSc1:	AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCG-----							: 577
TrCHSc2:	AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA							: 597
TrCHSc3:	AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA							: 581
TrCHSc4:	AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA							: 588
TrCHSc5:	AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA							: 563
TrCHSc6:	AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA							: 570
TrCHSc7:	AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA							: 287
		*	620	*	640	*	660	
TrCHSc1:	-----							: -
TrCHSc2:	GA-----							: 599
TrCHSc3:	-----							: -
TrCHSc4:	-----							: -
TrCHSc5:	-----							: -
TrCHSc6:	GACATAGCTGAGAACAACCCCTGGAAGTAGAGTT-----							: 603
TrCHSc7:	GACATAGCTGAGAACAACCCCTGGAAGTAGAGTTTTTGCTTGCTACTTCTGAAACTACAATT							: 347
		*	680	*	700	*	720	
TrCHSc1:	-----							: -
TrCHSc2:	-----							: -
TrCHSc3:	-----							: -
TrCHSc4:	-----							: -
TrCHSc5:	-----							: -
TrCHSc6:	-----							: -
TrCHSc7:	ATTGGATTCAAGCCACCAAGTGTGATAGACCTTATGATCTTGTGGTGTGGCACTCTTT							: 407

FIGURE 21 (cont)

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      *      740      *      760      *      780
TrCHSc1: ----- : -
TrCHSc2: ----- : -
TrCHSc3: ----- : -
TrCHSc4: ----- : -
TrCHSc5: ----- : -
TrCHSc6: ----- : -
TrCHSc7: GGAGATGGTGCTGGTGCTATGATAATTGGCTCAGACCCAATACTTGAAACTGAGACTCCA : 467

      *      800      *      820      *      840
TrCHSc1: ----- : -
TrCHSc2: ----- : -
TrCHSc3: ----- : -
TrCHSc4: ----- : -
TrCHSc5: ----- : -
TrCHSc6: ----- : -
TrCHSc7: TTGTTTGAGCTTCATACTTCAGCTCAGGAGTTTATACCAGACACAGAGAAGAAAATAGAT : 527

      *      860      *      880      *
TrCHSc1: ----- : -
TrCHSc2: ----- : -
TrCHSc3: ----- : -
TrCHSc4: ----- : -
TrCHSc5: ----- : -
TrCHSc6: ----- : -
TrCHSc7: GGCGGCTGACGGAGGAGGGCATAAGTTTCACGCTAGCGAGGGAAGTCCCGCAGATA : 584
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FIGURE 21 (cont)

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      *           20           *           40           *           60
TrCHSd : GTAGCAACACACACTTTGATTTCTTTTGTAGTCCTTGCTACGTGGCNTTACCAAAAAACG : 60

      *           80           *           100          *           120
TrCHSd : TTGCTAAGTCATCAACCATTCCAATTCTTAATATAACCTATCAGTACTCACCATCTTTT : 120

      *           140          *           160          *           180
TrCHSd : CTTCTCCCTGCTAACTTTTATACTTAGAGAAGATGGTGAAAGTTAATGAGATCCGCCAGG : 180

      *           200          *           220          *           240
TrCHSd : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT : 240

      *           260          *           280          *           300
TrCHSd : GTGTTGATCAGAGTACATACCCCGACTACTACTTCCGCATCACAAACAGTGAGCACAGA : 300

      *           320          *           340          *           360
TrCHSd : CAGAGCTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA : 360

      *           380          *           400          *           420
TrCHSd : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT : 420

      *           440          *           460          *           480
TrCHSd : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG : 480

      *           500          *           520          *           540
TrCHSd : CAACAAAGGCAATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACCCACCTCATCTTTT : 540

      *           560          *           580          *           600
TrCHSd : GCACCACAAGTGGTGTGGACATGCCCCGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC : 600

      *           620          *           640          *           660
TrCHSd : TTCGTCCGCATGTGAAGCGTTACATGATGTACCAACAAGGTTGTTTTGCTGGTGGCACGG : 660

      *           680          *           700          *           720
TrCHSd : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAGGTGCCCCGTGTATTGGTGGTTT : 720

      *
TrCHSd : GTTCAGAGATAACTG : 735

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FIGURE 22

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TrCHSd : MVKVNEIRQAQRAEGPATVLAIGTATPPNCVDQSTYPDYYFRITNSEHKTELKEKFQRM C : 60

TrCHSd : DKSMIKKRYMHLTEEILKENPSLCEYMAPSLDARQDMVVVEVPRLGKEAATKAIKEWGQP : 120

TrCHSd : KSKITHLIFCTTSGVDMFGADYQLTKLLGLRPHVKRYMMYQQGCFAGGTVLRRLAKDLAEN : 180

TrCHSd : NKGARVLVVCSEIT : 194

FIGURE 23

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      *           20           *           40           *           60
TrCHSd1 : GTAGCAACACACACTTTGATTTCTTTTTGAGTCCTTGCTACGTGGCNTTACCAAAAAACG : 60
TrCHSd2 : GTAGCAACACACACTTTGATTTCTTTTTGAGTCCTTGCTACGTGGCNTTACCAAAAAACG : 60
TrCHSd3 : GTAGCAACACACACTTTGATTTCTTTTTGAGTCCTTGCTACGTGGCNTTACCAAAAAACG : 60
TrCHSd4 : -----NNNCACNCACACTTTTTTCNATCCCTGCTACGTGGCNTTACCAAAAAACG : 50
TrCHSd5 : -----: -
TrCHSd6 : -----: -
TrCHSd7 : -----: -
TrCHSd8 : -----: -
TrCHSd9 : -----: -
TrCHSd10: -----: -
TrCHSd11: -----: -

      *           80           *           100          *           120
TrCHSd1 : TTGCTAATCATCAACCATTCCAATTCCTTAATATAACCTATCAGTACTTACCATCTTTT :120
TrCHSd2 : TTGCTAAGTCATCAACCATTCCAATTCCTTAATATAACCTATCAGTACTCACCATCTTTT :120
TrCHSd3 : TTGCTAAGTNATCAACCATTCCAATTCCTTAATATAACCTATCAGTACTCACCATCTTTT :120
TrCHSd4 : TTGCTAAGTCNTCAACCATTCCAATTCCTTAATATAACCTATCAGTACTCACCATCTTTT :110
TrCHSd5 : -----ATCCTCT : 10
TrCHSd6 : -----TATGCTNT : 10
TrCHSd7 : -----TCNAT : 6
TrCHSd8 : -----: -
TrCHSd9 : -----: -
TrCHSd10: -----: -
TrCHSd11: -----: -

      *           140          *           160          *           180
TrCHSd1 : CTTCTCCCTGCTAACTTTTAACTAGAGAAGATGGTGAAAGTTAATGAGATCCGCCAGG :180
TrCHSd2 : CTTCTCCCTGCTAACTTTTAACTAGAGAAGATGGTGAAAGTTAATGAGATCCGCCAGG :180
TrCHSd3 : CTTCTCCCTGCTAACTTTTAACTAGAGAAGATGGTGAAAGTTAATGAGATCCGCCAGG :180
TrCHSd4 : CTTCTCCCTGCTAACTTTTAACTAGAGAAGATGGTGAAAGTTAATGAGATCCGCCAGG :170
TrCHSd5 : ATTTACTTTCTTTTACTTAAAGAAATGGTAAAGTTAATGAGATCCGCCAGG : 70
TrCHSd6 : ATTTACTTTCTTTTACTTAAAGAAATGGTAAAGTTAATGAGATCCGCCAGG : 70
TrCHSd7 : ATTTACTTTCTTTTACTTAAAGAAATGGTAAAGTTAATGAGATCCGCCAGG : 66
TrCHSd8 : -----GCNNATACTTTANAATNAGAGAAGATGGTGAAAGTTAATGAGATCCGCCAGG : 53
TrCHSd9 : -----TNNNTTTANAATNAGAGAAGATGGTGAAAGTTAATGAGATCCGCCAGG : 48
TrCHSd10: -----TTCTTTTAAAGAAATGGTAAAGTTAATGAGATCCGCCAGG : 45
TrCHSd11: -----: -

      *           200          *           220          *           240
TrCHSd1 : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT :240
TrCHSd2 : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT :240
TrCHSd3 : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT :240
TrCHSd4 : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT :230
TrCHSd5 : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT :130
TrCHSd6 : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT :130
TrCHSd7 : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT :126
TrCHSd8 : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT :113
TrCHSd9 : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT :108
TrCHSd10: CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT :105
TrCHSd11: -----TAAACT : 7

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FIGURE 24

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          *           260           *           280           *           300
TrCHSd1 : GTGTCGATCAGAGTACATACCCG GACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :300
TrCHSd2 : GTGTCGATCAGAGTACATACCCG GACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :300
TrCHSd3 : GTGTCGATCAGAGTACATACCCG GACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :300
TrCHSd4 : GTGTTGATCAGAGTACATACCCG GACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :290
TrCHSd5 : GTGTTGATCAGAGTACATACCCCG GACTACTACTTCCGAATCACAAACAGCGAACACAAGA :190
TrCHSd6 : GTGTTGATCAGAGTACATACCCCG GACTACTACTTCCGAATCACAAACAGCGAACACAAGA :190
TrCHSd7 : GTGTTGATCAGAGTACATACCCCG GACTACTACTTCCGAATCACAAACAGCGAACACAAGA :186
TrCHSd8 : GTGTTGATCAGAGTACATACCCG GACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :173
TrCHSd9 : GTGTTGATCAGAGTACATACCCG GACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :168
TrCHSd10: GTGTTGATCAGAGTACATACCCCG GACTACTACTTCCGAATCACAAACAGCGAACACAAGA :165
TrCHSd11: GTGTTGATCAGAGTACATACCCCG GACTACTACTTCCGAATCACAAACAGCGAACACAAGA : 67

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          *           320           *           340           *           360
TrCHSd1 : CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :360
TrCHSd2 : CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :360
TrCHSd3 : CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :360
TrCHSd4 : CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :350
TrCHSd5 : CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :250
TrCHSd6 : CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :250
TrCHSd7 : CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :246
TrCHSd8 : CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :233
TrCHSd9 : CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :228
TrCHSd10: CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :225
TrCHSd11: CAGAGCTCAAAGAAAAAATTCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :127

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          *           380           *           400           *           420
TrCHSd1 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :420
TrCHSd2 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :420
TrCHSd3 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :420
TrCHSd4 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :410
TrCHSd5 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :310
TrCHSd6 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :310
TrCHSd7 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :306
TrCHSd8 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :293
TrCHSd9 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :288
TrCHSd10: TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :285
TrCHSd11: TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :187

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          *           440           *           460           *           480
TrCHSd1 : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :480
TrCHSd2 : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :480
TrCHSd3 : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :480
TrCHSd4 : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :470
TrCHSd5 : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :370
TrCHSd6 : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :370
TrCHSd7 : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :366
TrCHSd8 : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :353
TrCHSd9 : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :348
TrCHSd10: CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :345
TrCHSd11: CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :247

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FIGURE 24 (cont)

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      *           500           *           520           *           540
TrCHSd1 : CAACAAAGGCAATTAAAGGAATGGGGTCAACCTAAGTCCAAGATTACCCACCTCATCTTTT : 540
TrCHSd2 : CAACAAAGGCTATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT : 540
TrCHSd3 : CAACAAAGGCTATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT : 540
TrCHSd4 : TAACAAAGGCAATTAAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT : 530
TrCHSd5 : CAACAAAGGCTATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT : 430
TrCHSd6 : CAACAAAGGCTATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT : 430
TrCHSd7 : CAACAAAGGCTATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT : 426
TrCHSd8 : CAACAAAGGCAATTAAAGGAATGGGGTCAACCTAAGTCCAAGATTACCCACCTCATCTTTT : 413
TrCHSd9 : CAACAAAGGCAATTAAAGGAATGGGGTCAACCTAAGTCCAAGATTACCCACCTCATCTTTT : 408
TrCHSd10 : CAACAAAGGCAATTAAAGGAATGGGGTCAACCTAAGTCCAAGATTACCCACCTCATCTTTT : 405
TrCHSd11 : CCN----- : 250

      *           560           *           580           *           600
TrCHSd1 : GCACCACAGTGGTGTGACATGCCCGGTGCCCG----- : 574
TrCHSd2 : GCACCACAAGTGGTGTGGACATGCCCGGCCGACTATCAGCTTACAAAGCTTTTAG----- : 597
TrCHSd3 : GCACCACAAGTGGTGTGGACATGCCCGGCCGACTATCAGCTTACAAAGCTTTTAGGCC : 600
TrCHSd4 : GCACCACAGTGGTGTGGACATGCCCGGTGCCGACTATCAGCTTACAAAGCTTTT----- : 585
TrCHSd5 : GCACCACAAGTGGTGTGGACATGCCCGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC : 490
TrCHSd6 : GCACCACAAGTGGTGTGGACATGCCCGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC : 490
TrCHSd7 : GCACCACAAGTGGTGTGGACATGCCCGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC : 486
TrCHSd8 : GCACCACAGTGGTGTGACATGCCCGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC : 473
TrCHSd9 : GCACCACAGTGGTGTGACATGCCCGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC : 468
TrCHSd10 : GCACCACAGTGGTGTGGACATGCCCGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC : 465
TrCHSd11 : ----- : -

      *           620           *           640           *           660
TrCHSd1 : ----- : -
TrCHSd2 : ----- : -
TrCHSd3 : TTCGTCCGCATGTGAW----- : 616
TrCHSd4 : ----- : -
TrCHSd5 : TTCGTCCGCATGTGAAGCGTTATATGATGTACCAACAAGGTTGTTTTGCTGGTGGCACGG : 550
TrCHSd6 : TTCGTCCGCATGTGAAGCGTTATATGATGTACCAACAAGGTTGTTTTGCTGGTGGCACGG : 550
TrCHSd7 : TTCGTCCGCATGTGAAGCGTTATATGATGTACCAACAAGGTTGTTTTGCTGGTGGCACGG : 546
TrCHSd8 : TTCGTCCATATGTGAAGCGTTACATGATGTATCAACAAGGTTGTTTTGCTGGTGGCACGG : 533
TrCHSd9 : TTCGTCCATATGTGAAGCGTTACATGATGTATCAACAAGGTTGTTTTGCTGGTGGCACGG : 528
TrCHSd10 : TTCGTCCATATGTGAAGCGTTACATGATGTATCAACAAGGTTGTTTTGCTGGTGGCACGG : 525
TrCHSd11 : ----- : -

      *           680           *           700           *           720
TrCHSd1 : ----- : -
TrCHSd2 : ----- : -
TrCHSd3 : ----- : -
TrCHSd4 : ----- : -
TrCHSd5 : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAGGTGCCCG----- : 596
TrCHSd6 : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAGGTGCCCGTGTATTGGTGGTTT : 610
TrCHSd7 : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAGGTGCCCGTGTATTGGTGGTTT : 606
TrCHSd8 : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAN----- : 571
TrCHSd9 : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAANGTGCCCGTGTGTTGGTGGGTT : 588
TrCHSd10 : TACTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAGGTGCCCGTGTGTTGGTGGTTT : 585
TrCHSd11 : ----- : -

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FIGURE 24 (cont)

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*

TrCHSd1	:	-----	:	-
TrCHSd2	:	-----	:	-
TrCHSd3	:	-----	:	-
TrCHSd4	:	-----	:	-
TrCHSd5	:	-----	:	-
TrCHSd6	:	G TTCAGAG -----	:	618
TrCHSd7	:	GTT -----	:	609
TrCHSd8	:	-----	:	-
TrCHSd9	:	G TTCANAGATAACTG	:	603
TrCHSd10	:	GTT -----	:	588
TrCHSd11	:	-----	:	-

FIGURE 24 (cont)

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      *           20           *           40           *           60
TrCHSe : GNAGCAACACACACTTTGATTTCTTTTGAATCCCTGCTACGTGGCNCACCAAAAAACGT : 60

      *           80           *           100          *           120
TrCHSe : TGCTAAGTCATCAACCATTCCAATTCCTTAATATAACCTATCAGTACTCACCATCTTTTC : 120

      *           140          *           160          *           180
TrCHSe : TTCCTCCCTGCTAACTTTAGACTCAGTAGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 180

      *           200          *           220          *           240
TrCHSe : CACAGAGAGCTGAAGGCCCTGCCACCGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT : 240

      *           260          *           280          *           300
TrCHSe : GTGTTGATCAGAGTACATACCCGGACTACTACTTCCGCATCACAAACAGTGAGCACAAGA : 300

      *           320          *           340          *           360
TrCHSe : CAGAGCTCAAAGAAAAATTCCAGCGCACGTGTAAGATATTTATCTTATACTCCATGCATG : 360

      *           380          *           400          *           420
TrCHSe : TCTTTTTCTGCTGACTGCCGTGTTTATATATTGTTTTGTTTTGTTTCCTTAAATTTGTTAT : 420

      *           440          *           460          *           480
TrCHSe : GTCACTCTCACATGTACAAAACACTTAAGACTAAACTGCATATCATTTTTTTCAGGGACA : 480

      *           500          *           520          *           540
TrCHSe : AATCTATGATTAAGAAGAGATACATGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAA : 540

      *           560          *           580
TrCHSe : GTTTATGTGAGNACATGGCACCTTCTTGGGATGCAAGACAAGT : 583

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FIGURE 25

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TrCHSe : MVNVNEIRQAQRAEGPATVLAIGTATPPNCVDQSTYPDYYFRITNSEHKTELKEKFQRTTR : 60

TrCHSe : DKSMIKKRYMHLTEEILKENPSLCEXMAPSWDARQ : 95

FIGURE 26

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      *           20           *           40           *           60
TrCHSe1: GNAGCAACACACACTTTGATTTCCTTTTGAATCCCTGCTACGTGGCTTACCAAAAAACGT : 60
TrCHSe2: -----ATCCCTGCTGCGTGGCNCACC-AAAAACGT : 29

      *           80           *           100          *           120
TrCHSe1: TGCTAAGTCATCAACCATTCCAATTCCCTTAATATAACCTATCAGTACTCACCATTTTTTC : 120
TrCHSe2: TGCTAAGT-NTGAACC-TTCC-ATTCCTTAATATAACCTATCAGTACTCACCATCTTTTC : 86

      *           140          *           160          *           180
TrCHSe1: TTCCTCCCTGCTAACTTTAGACTCAG-AGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 179
TrCHSe2: TTCCTCCCTGCTAACTTTAGACTCAGTAGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 146

      *           200          *           220          *           240
TrCHSe1: CACAGAGAGCTGAAGGCCCTGCCACCGTGTGGCAATCGGCACTGCAACTCCTCCAAACT : 239
TrCHSe2: CACAGAGAGCTGAAGGCCCTG----- : 167

      *           260          *           280          *           300
TrCHSe1: GTGTTGATCAGAGTACATACCCGGACTACTTCCGCATCACAAACAGTGAGCACAAGA : 299
TrCHSe2: ----- : -

      *           320          *           340          *           360
TrCHSe1: CAGAGCTCAAAGAAAAATTCCAGCGCACGTGTAAGATATTTATCTTATACTCCATGCATG : 359
TrCHSe2: ----- : -

      *           380          *           400          *           420
TrCHSe1: TCTTTTCTGCTGACTGCCGTGTTTATATATTGTTTTGTTTTGTTCTTAAATTGTTAT : 419
TrCHSe2: ----- : -

      *           440          *           460          *           480
TrCHSe1: GTCACTCTCACATGTACAAAACACTTAAGACTAAACTGCATATCATTTTTTTCAGGGACA : 479
TrCHSe2: ----- : -

      *           500          *           520          *           540
TrCHSe1: AATCTATGATTAAAGAAGAGATACATGCATTGACAGAAGAGATTTGAAGGAGAATCCAA : 539
TrCHSe2: ----- : -

      *           560          *           580
TrCHSe1 : GTTTATGTGAGNACATGGCACCTTCTTGGGATGCAAGACAAGT : 582
TrCHSe2 : ----- : -

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FIGURE 27

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      *           20           *           40           *           60
TrCHSf : GCNTAAGCCTTGATTNNTGTTTGTTCCTAACACAAGAACTAGTGTTGCTTGAATCTTA : 60

      *           80           *           100          *           120
TrCHSf : AGAAAAAATGCCTCAAGGTGATTGAATGGAAGTTCCTCGGTGAATGGAGCACGTGCTAG : 120

      *           140          *           160          *           180
TrCHSf : ACGTGCTCCTACTCAGGGAAAGGCAACGATACTTGCAATTAGGAAAGGCTTTCCCGCCCA : 180

      *           200          *           220          *           240
TrCHSf : AGTCCTCCCTCAAGAGTGCTTGGTGGAAGGATTCATTCGCGGACACTAAGTGTGACGATAC : 240

      *           260          *           280          *           300
TrCHSf : TTATATTAAGGAGAAAATTGGAGCGTCTTTGCAAAAACACAACGTGTAACAAGATACAC : 300

      *           320          *           340          *           360
TrCHSf : AGTAATGTCAAAGGAGATCTTAGACAACATCCAGAGCTAGCCATAGATGGAACACCAAC : 360

      *           380          *           400          *           420
TrCHSf : AATAAGGCAAAAGCTTGAAATAGCAAATCCAGCAGTAGTTGAAATGGCAACAAGAGCAAG : 420

      *   *           440          *           460          *           480
TrCHSf : CAAAGATTGCATCAAAGAATGGGGAAGGTCACCTCAAGATATCACACACATAGTCTATGT : 480

      *           500          *           520          *           540
TrCHSf : TTCCTCGAGCGAAATTTCGTCTACCCGGTGGTGACCTTTATCTTGCAAATGAACTCGGCTT : 540

      *           560          *           580          *           600
TrCHSf : AAACAGCGATGTTAATCGCGTAATGCTCTATTCTCGGTTGCTACGGCGGTGTCACTGG : 600

      *
TrCHSf : CTTACGTGTCGCC : 613

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FIGURE 28

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TrCHSf : MPQGD^{*}LN²⁰GSSSVNGARARRAPTQ^{*}GKATILALGKA⁴⁰FPAQVLPQECLVEGFIRD^{*}TKCDDTYI⁶⁰ : 60

TrCHSf : KEKLERLCKNTTVKTRYTVMSKEILDNYPELAIDGTP^{*}TIRQKLEIANPAVVEMAT⁸⁰TRASKD¹⁰⁰ : 120

TrCHSf : CIKEWGRSPQDITHIVYVSSEIRLP^{*}GGDLYLANELGLNSDVNRV¹⁴⁰MLYFLG¹⁶⁰CYGGVTGLR¹⁸⁰ : 180

TrCHSf : VA : 182

FIGURE 29

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	* 20 * 40 * 60	
TrCHSf1:	GCNTAAGCCTTGATTNNTGTTTTCCTAACACAAGAAGTCTGTTTGCTTGAATCTTA	: 60
TrCHSf2:	---TAAGCCTTGATTNNTGTTTTCCTAACACAAGAAGTCTGTTTGCTTGAATCTTA	: 57
TrCHSf3:	-----TTGATTGTTTGTTCCTAACACAAGAAGTCTGTTTGCTTGAATCTTA	: 51
TrCHSf4:	-----GTTTGTTCCTAACACAAGAAGTCTGTTTGCTTGAATCTTA	: 42

	* 80 * 100 * 120	
TrCHSf1:	AGAAAAATGCCTCAAGGTGATTTGAATGGAAGTTCTCGGTGAATGGAGCACGTGCTAG	: 120
TrCHSf2:	AGAAAAATGCCTCAAGGTGATTTGAATGGAAGTTCTCGGTGAATGGAGCACGTGCTAG	: 117
TrCHSf3:	AGAAAAATGCCTCAAGGTGATTTGAATGGAAGTTCTCGGTGAATGGAGCACGTGCTAG	: 111
TrCHSf4:	AGAAAAATGCCTCAAGGTGATTTGAATGGAAGTTCTCGGTGAATGGAGCACGTGCTAG	: 102

	* 140 * 160 * 180	
TrCHSf1:	ACGTGCTCCTACTCAGGGAAAGGCAACGATACTTGCATTAGGAAAGGCTTTCCCGCCCA	: 180
TrCHSf2:	ACGTGCTCCTACTCAGGGAAAGGCAACGATACTTGCATTAGGAAAGGCTTTCCCGCCCA	: 177
TrCHSf3:	ACGTGCTCCTACTCAGGGAAAGGCAACGATACTTGCATTAGGAAAGGCTTTCCCGCCCA	: 171
TrCHSf4:	ACGTGCTCCTACTCAGGGAAAGGCAACGATACTTGCATTAGGAAAGGCTTTCCCGCCCA	: 162

	* 200 * 220 * 240	
TrCHSf1:	AGTCCTCCCTCAAGAGTGCTTGGTGGAAGGATTCATTGCGGACACTAAGTGTGACGATAC	: 240
TrCHSf2:	GTCTCTCCCTCAAGAGTGCTTGGTGGAAGGATTCATTGCGGACACTAAGTGTGACGATAC	: 237
TrCHSf3:	GTCTCTCCCTCAAGAGTGCTTGGTGGAAGGATTCATTGCGGACACTAAGTGTGACGATAC	: 231
TrCHSf4:	AGTCCTCCCTCAAGAGTGCTTGGTGGAAGGATTCATTGCGGACACTAAGTGTGACGATAC	: 222

	* 260 * 280 * 300	
TrCHSf1:	TTATATTAAGGAGAAATTGGAGCGTCTTTGCAAAAACACAAGTGTAAAAACAAGATACAC	: 300
TrCHSf2:	TTATATTAAGGAGAAATTGGAGCGTCTTTGCAAAAACACAAGTGTAAAAACAAGATACAC	: 297
TrCHSf3:	TTATATTAAGGAGAAATTGGAGCGTCTTTGCAAAAACACAAGTGTAAAAACAAGATACAC	: 291
TrCHSf4:	TTATATTAAGGAGAAATTGGAGCGTCTTTGCAAAAACACAAGTGTAAAAACAAGATACAC	: 282

	* 320 * 340 * 360	
TrCHSf1:	AGTAATGTCAAAGGAGATCTTAGACAACATATCCAGAGCTAGCCATAGATGGAACACCAAC	: 360
TrCHSf2:	AGTAATGTCAAAGGAGATCTTAGACAACATATCCAGAGCTAGCCATAGATGGAACACCAAC	: 357
TrCHSf3:	AGTAATGTCAAAGGAGATCTTAGACAACATATCCAGAGCTAGCCATAGATGGAACACCAAC	: 351
TrCHSf4:	AGTAATGTCAAAGGAGATCTTAGACAACATATCCAGAGCTAGCCATAGATGGAACACCAAC	: 342

	* 380 * 400 * 420	
TrCHSf1:	AATAAGGCAAAAGCTTGAAATAGCAAATCCAGCAGTAGTTGAAATGGCAACAAGAGCAAG	: 420
TrCHSf2:	AATAAGGCAAAAGCTTGAAATAGCAAATCCAGCAGTAGTTGAAATGGCAACAAGAGCAAG	: 417
TrCHSf3:	AATAAGGCAAAAGCTTGAAATAGCAAATCCAGCAGTAGTTGAAATGGCAACAAGAGCAAG	: 411
TrCHSf4:	AATAAGGCAAAAGCTTGAAATAGCAAATCCAGCAGTAGTTGAAATGGCAACAAGAGCAAG	: 402

	* 440 * 460 * 480	
TrCHSf1:	CAAAGATTGCATCAAAGAATGGGGAAGGTCACCTCAAGATATCACACACATAGTCTATGT	: 480
TrCHSf2:	CAAAGATTGCATCAAAGAATGGGGAAGGTCACCTCAAGATATCACACACATAGTCTATGT	: 477
TrCHSf3:	CAAAGATTGCATCAAAGAATGGGGAAGGTCACCTCAAGATATCACACACATAGTCTATGT	: 471
TrCHSf4:	CAAAGATTGCATCAAAGAATGGGGAAGGTCACCTCAAGATATCACACACATAGTCTATGT	: 462

FIGURE 30

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      *           500           *           520           *           540
TrCHSf1: TTCCTCGAGCGAAATTTCGTCTACCCGGTGGTGACCTTTATCTTGCAAATGAACTCGGCTT : 540
TrCHSf2: TTCCTCGAGCGAAATTTCGTCTACCCGGTGGTGACCTTTATCTTGCAAATGAACTCGGCTT : 537
TrCHSf3: TTCCTCGAGCGAAATTTCGTCTACCCGGTGGTGACCTTTATCTTGCAAATGAACTCGGCTT : 531
TrCHSf4: TTCCTCGAGCGAAATTTCGTCTACCCGGTGGTGACCTTTATCTTGCAAATGAACTCGGCTT : 522

      *           560           *           580           *           600
TrCHSf1: AAACAGCGATGTTAATCGCGTAATGCTCTATTTTCCTCGGTTGCTACGGCGGTGCTACTGC : 600
TrCHSf2: AAACAGCGATGTTAATCGCGTAATGCTCTATTT----- : 570
TrCHSf3: AAACAGCGATGTTAATCGCGTAATGCTCTATTTTCCTCGGTTGCT----- : 575
TrCHSf4: AAACAGCGATGTTAATCGCGTAATGCTCTATTTTCCTCGGTTGCTACGGCGG----- : 573

      *
TrCHSf1 : CTTACGTGTCGCC : 613
TrCHSf2 : ----- : -
TrCHSf3 : ----- : -
TrCHSf4 : ----- : -

```

FIGURE 30 (cont)

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TrCHSg : GTATACCAAGGTTGTTTTGCTGGTGGCACGGTACTTCGTTTGGCTAAAGACTTGGCTGAA : 60

TrCHSg : AACAAACAAGGTGCCCCGTGTGTTGGTGGTTTGTTCAGAGATAACTGCAGTTACTTTCCGT : 120

TrCHSg : GGACCCAGTGACACTCACCTTGATAGCCTTGTGGGGCAAGCATTGTTTGGAGATGGTGCA : 180

TrCHSg : GCAGCTGTGATTGTTGGTTCAGACCCTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG : 240

TrCHSg : GTATGGACCGCACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC : 300

TrCHSg : GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTTCCCTAGCCTTGTCTCAAATAACATT : 360

TrCHSg : GAGAAAGCGCTTGTTGATGCCTTTCAACCTTTGAATATTTCTGACTACAATTCCATCTTT : 420

TrCHSg : TGGATTGCACACCCAGGCGGACCAGCAATTCTTGACCAAGTTGAAGCTAAGTTAGGCTTA : 480

TrCHSg : AAGCCAGAGAAAATGCAAGCCACTCGACATGTACTTAGCGAATATGGTAACATGTCAAGT : 540

TrCHSg : GCGTGTGTGTTATTTATCTTGATGAGATGAGGAGGAAGTCAAAAGAAGACGGACTTGCC : 600

TrCHSg : ACAACAG : 607

FIGURE 31

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TrCHSg : VYQGCFAGGTVLRLAKDLAENNKGARVLVVCSEITAVTFRGPSDTHLDSL VGQALFGDGA : 60

TrCHSg : AAVIVGSDPLPEVEKPLFELVWTAQTIAPDSEGAIDGHLREAGLTFHLLKDVPSLVSNNI : 120

TrCHSg : EKALVDAFQPLNISDYN SIFWIAHPGGPAILDQVEAKLGLKPEKMQATRHVLSEYGNMSS : 180

TrCHSg : ACVLFILDEMRRKSKEDGLATT : 202

FIGURE 32

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	* 20 * 40 * 60	
TrCHSg1:	GTATACCAAGGTTGTTTTGCTGGTGGCACGGTACTTCGTTTGGCTAAAGACTTGGCTGAA	: 60
TrCHSg2:	-----CCAAGGTTGTTTTGCTGGTGGCACGGTACTTCGTTTGGCTAAAGACTTGGCTGAA	: 55
TrCHSg3:	-----GGTTGTTTTGCTGGTGGCACGGTACTTCGTTTGGCTAAAGACTTGGCTGAA	: 51
	* 80 * 100 * 120	
TrCHSg1:	AACAACAAAGGTGCCCCGTGTGTTGGTGGTTTGTTCAGAGATAACTGCAGTTACTTTCCGT	: 120
TrCHSg2:	AACAACAAAGGTGCCCCGTGTGTTGGTGGTTTGTTCAGAGATAACTGCAGTTACTTTCCGT	: 115
TrCHSg3:	AACNACAAAGGTGCCCCGTGTGTTGGTGGTTTGTTCAGAGATAACTGCAGTTACTTTCCGT	: 111
	* 140 * 160 * 180	
TrCHSg1:	GGACCCAGTGACACTCACTTGTATAGCCTTGTGGGGCAAGCATTGTTTGGAGATGGTGCA	: 180
TrCHSg2:	GGACCCAGTGACACTCACCTTGTATAGCCTTGTGGGGCAAGCATTGTTTGGAGATGGTGCA	: 175
TrCHSg3:	GGACCCAGTGACACTCACCTTGTATAGCCTTGTGGGGCAAGCATTGTTTGGAGATGGTGCA	: 171
	* 200 * 220 * 240	
TrCHSg1:	GCAGCTGTGATTGTTGGTTTCAGACCCCTTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG	: 240
TrCHSg2:	GCAGCTGTGATTGTTGGTTTCAGACCCCTTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG	: 235
TrCHSg3:	GCAGCTGTGATTGTTGGTTTCAGACCCCTTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG	: 231
	* 260 * 280 * 300	
TrCHSg1:	GTATGGACCGCACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC	: 300
TrCHSg2:	GTATGGACCGCACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC	: 295
TrCHSg3:	GTATGGACCGCACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC	: 291
	* 320 * 340 * 360	
TrCHSg1:	GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTTCCCTAGCCTTGTCTCAAATAACATT	: 360
TrCHSg2:	GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTTCCCTAGCCTTGTCTCAAATAACATT	: 355
TrCHSg3:	GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTTCCCTAGCCTTGTCTCAAATAACATT	: 351
	* 380 * 400 * 420	
TrCHSg1:	GAGAAAGCGCTTGTGTTGATGCCTTTCAACCTTTGAATATTTCTGACTACAATTCCATCTTT	: 420
TrCHSg2:	GAGAAAGCGCTTGTGTTGATGCCTTTCAACCTTTGAATATTTCTGACTACAATTCCATCTTT	: 415
TrCHSg3:	GAGAAAGCGCTTGTGTTGATGCCTTTCAACCTTTGAATATTTCTGACTACAATTCCATCTTT	: 411
	* 440 * 460 * 480	
TrCHSg1:	TGGATTGCACACCCAGGCGGACCAGCAATTCTTGACCAAGTTGAAGCTAAGTTAGGCTTA	: 480
TrCHSg2:	TGGATTGCACACCCAGGCGGACCAGCAATTCTTGACCAAGTTGAAGCTAAGTTAGGCTTA	: 475
TrCHSg3:	TGGATTGCACACCCAGGCGGACCAGCAATTCTTGACCAAGTTGAAGCTAAGTTAGGCTTA	: 471
	* 500 * 520 * 540	
TrCHSg1:	AAGCCAGAGAAAATGCAATCCCACTCGACATGTACTTAGCGAATATGGTAACATGTCAAGT	: 540
TrCHSg2:	AAGCCAGAGAAAATGCAAGCCACTCGACATGTACTTAGCGAATATGGTAACATGTCAAGT	: 535
TrCHSg3:	AAGCCAGAGAAAATGCAAGCCACTCGACATGTACTTAGCGAATATGGTAACATGTCAAGT	: 531

FIGURE 33

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          *          560          *          580          *          600
TrCHSg1: GCGTGTGTGTTATTTATCTTGGATGAGATGAGGAGGAAGTCAAAAGAAGACGGACTTGCC : 600
TrCHSg2: GCGTGTGTGTTATTTATCTTGGATGAGATGAGGAGGAAGTCAAAAGAAGACGGACTTGC : 591
TrCHSg3: GCGTGTGTGTTATTTATCTTGGATGAGATGAGGAGGAAGTCAAAAGAAGACGGACTTGC : 590
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TrCHSg1 : ACAACAG : 607
TrCHSg2 : ----- : -
TrCHSg3 : ----- : -
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FIGURE 33 (cont)

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TrCHSh : AATNACACCNTNANACCTTCCAATTCTCGTACCTCACCAATCTCATTTTTATTATATATC : 60
 * 20 * 40 * 60

TrCHSh : TTGGTACATCTTTTGTTACCTCCAACAAAAAATGGTGACCGTAGAAGAGATTTCGTAACG : 120
 * 80 * 100 * 120

TrCHSh : CCCAACGTTCAAATGGCCCTGCCACTATCTTAGCTTTTGGCACAGCCACTCCTTCTAACT : 180
 * 140 * 160 * 180

TrCHSh : GTGTCACCTCAAGCTGATTATCCTGATTACTACTTTCGTATCACCAACAGCGAACATATGA : 240
 * 200 * 220 * 240

TrCHSh : CTGATCTTAAGGAAAAATTCAAGCGGATGTGTGATAGATCAATGATAAAGAAACGTTACA : 300
 * 260 * 280 * 300

TrCHSh : TGCACCTAACAGAAGACTTTCTGAAGGAGAATCCAAATATGTGTGAATACATGGCACCAT : 360
 * 320 * 340 * 360

TrCHSh : CACTAGATGTAAGACGAGACATAGTGGTTGTTGAAGNACCAAAGCTAGGTAAAGAANCAC : 420
 * 380 * 400 * 420

TrCHSh : CAAAAAAGCCATATGNGAATGGGGACAACCAAAATCNAAAATCACACATGCTTGGGTTTC : 480
 * 440 * 460 * 480

TrCHSh : TGACCACTTCCGGTGNTGACATGCCCCGGGG : 510
 * 500 *

FIGURE 34

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TrCHSh : MVTVEEIRNAQRSNGPATILAFGTATPSNCVTQADYPDYFRITNSEHMTDLKEKFKRMC : 60

TrCHSh : DRSMIKKRYMHLTEDFLKENPNMCEYMAPSLDVRRDIVVVEPKLGKEPKKAIXEWGQPK : 120

TrCHSh : XKITHAWFLTTSGDMPG : 137

FIGURE 35

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TrCHRa : GACAAATGCNTGTGGTTGGAATGGGATCCGCACCTGATTTTACATGTAAGAAAGACACAA : 60

TrCHRa : AAGATGCAATCGTTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGCTT : 120

TrCHRa : ATGGCTCANAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCANTTGAACCTGGTCTTGCTCA : 180

TrCHRa : CTANAGAAGAGCTNTTGTACTTCTAACTTTGGGNNACTGAAAATCATNCTAACCTTG : 240

FIGURE 36

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TrCHRa : QMXVVGMSAPDFTCKKDTKDAIVEAIKQGYRHFDTAAAYGSXQALGEGGLKEAXELGLVT : 60

TrCHRa : XEEXFVTSKLWXTENHXNL : 79

FIGURE 37

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TrCHRB : GTGTAGCAGAGTNAGAAAAAGAGAGAAAAAAAACATGGCAGGAAAGAAAATCCCAGAAG : 60

TrCHRB : TGTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 120

TrCHRB : GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGCC : 180

TrCHRB : ATTTGATTCTGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAG : 240

TrCHRB : CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTTCATCACTTCAAAGCCATGGA : 300

TrCHRB : ATACTGATGCAGATTATGAACTTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 360

TrCHRB : GGACGGAGTATGTGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTG : 420

TrCHRB : AAAACCCTGTTGTTTTTACCAAAGAAGATTTACTTCCCTTTGATATAGAAGGGACATGGA : 480

TrCHRB : AAGCTATGGAAGAATGTTATAAGTTAGGCTTAGCAAAGTCTATTGGTATATGCAATTATG : 540

TrCHRB : GTACCAAAAACTCACCAAACTCTTGGAACAGCCACCATTACCCCTGCAGTCAATCAGG : 600

TrCHRB : TGGA : 604

FIGURE 38

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TrCHRB : * 20 * 40 * 60
MAGKKIPEVLLNSGHKMPVIGMGTSVDNRPSNDVLASIFVDAIEVGYRHFDSASVYGTEE : 60

 * 80 * 100 * 120
TrCHRB : AIGIALAKALEKGLIKSRDEVFITSKPWN TDADYELIVPALKTTLKKGTEYVDLYLIHW : 120

 * 140 * 160 * 180
TrCHRB : PVRLRHDLENPVVFTKEDLLPFDIEGTWKAMEECYKLGLAKSIGICNYGTTKLTLETA : 180

TrCHRB : TITPAVNQV : 189

FIGURE 39

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```

      *           20           *           40           *           60
TrCHRB1: CTGTAGCAGNATTAGANAAANATATAAAAAAAAAAACATGGCAGGAAAGAAAATCCCAGAAG : 60
TrCHRB2: --GTAGCAGNCTTAGNANAAGCNNGAAAAAAAAAACATGGCAGGAAAGAAAATCCCAGAAG : 58
TrCHRB3: -----AGTNNGAAAAAGAGAGAAAAAAAAAACNTGGCAGGAAAGAAAATCCCAGAAG : 51
TrCHRB4: -----AGTNNGAAAAAGAGAGAAAAAAAAAACNTGGCAGGAAAGAAAATCCCAGAAG : 51
TrCHRB5: -----ACATGGCAGGAAAGAAAATCCCAGAAG : 27

      *           80           *           100          *           120
TrCHRB1: TGTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 120
TrCHRB2: TGTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 118
TrCHRB3: TGTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 111
TrCHRB4: TGTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 111
TrCHRB5: TGTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 87

      *           140          *           160           *           180
TrCHRB1: GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGCC : 180
TrCHRB2: GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGCC : 178
TrCHRB3: GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGCC : 171
TrCHRB4: GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGCC : 171
TrCHRB5: GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGTC : 147

      *           200          *           220           *           240
TrCHRB1: ATTTTCGATTCTGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAAG : 240
TrCHRB2: ATTTTCGATTCTGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAAG : 238
TrCHRB3: ATTTTCGATTCTGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAAG : 231
TrCHRB4: ATTTTCGATTCTGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAAG : 231
TrCHRB5: ATTTTCGATTCTGCTTCTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAAG : 207

      *           260          *           280           *           300
TrCHRB1: CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTCATCACTTCAAGCATGGA : 300
TrCHRB2: CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTCATCACTTCAAGCCATGGA : 298
TrCHRB3: CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTCATCACTTCAAGCCATGGA : 291
TrCHRB4: CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTCATCACTTCAAGCCATGGA : 291
TrCHRB5: CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTCATCACTTCAAGCCATGGA : 267

      *           320          *           340           *           360
TrCHRB1: ATACTGATGCAGATTATGAACCTATTGTTNCAAN----- : 334
TrCHRB2: ATACTGATGCAGATTATGAACCTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 358
TrCHRB3: ATACTGATGCAGATTATGAACCTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 351
TrCHRB4: ATACTGATGCAGATTATGAACCTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 351
TrCHRB5: ATACTGATGCAGATTATGATCTTATTGNTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 327

      *           380          *           400           *           420
TrCHRB1: ----- : -
TrCHRB2: GGACGGAGTATGTGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTG : 418
TrCHRB3: GGACGGAGTATGTGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTG : 411
TrCHRB4: GGACGGAGTATGTGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTG : 411
TrCHRB5: GGACGGA----- : 334

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FIGURE 40

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	*	440	*	460	*	480	
TrCHRB1:	-----						:
TrCHRB2:	AAAACCCTGTTGTTTTCACCAAAGAAGATTTACTTCCCTTTGATATAGAAGGGACATGGA						: 478
TrCHRB3:	AAAACCCTGTTGTTTTCACCAAAGAAGATTTACTTCCCTTTGATATAGAAGGGACATGGA						: 471
TrCHRB4:	AAAACCCTGTTGTTTTCACCAAAGAAGATTTACTTCCCTTTGATATAGAAGGGACATGGA						: 471
TrCHRB5:	-----						:

	*	500	*	520	*	540	
TrCHRB1:	-----						:
TrCHRB2:	AAGCTATGGAAGAATGTTATAAGTTAGGCTTAGCAAAGTCTATTGGTATATGCAATTATG						: 538
TrCHRB3:	AAGCTATGGAAGAATGTTATAAGTTAGGCTTAGCAAAGTCTATTGGTATATGCAATTATG						: 531
TrCHRB4:	AAGCTATGGAAGAATGTTATAAGTTAGGCTTAGCAAAGTCTATTGGTATATGCAATTATG						: 531
TrCHRB5:	-----						:

	*	560	*	580	*	600	
TrCHRB1:	-----						:
TrCHRB2:	GTACCAAAAACTCACCAAACCTCTTGGAACAGCCACCATTACCCCTGCAGTCAATCAGG						: 598
TrCHRB3:	GTACCAAAAACTCACCAAACCTCTTGGAACAGCCACCATTACCCCTGCAGTC-----						: 584
TrCHRB4:	GTACCAAAAACTCAC-----						: 547
TrCHRB5:	-----						:

TrCHRB1:	----	:	-
TrCHRB2:	TGGA	:	602
TrCHRB3:	----	:	-
TrCHRB4:	----	:	-
TrCHRB5:	----	:	-

FIGURE 40 (cont)

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```

      *           20           *           40           *           60
TrCHRC : TAAGAATGAANCAATTTTATCTNANAAAAGGNNCANGCAAGTNAGTTNNATTCAAACATA : 60

      *           80           *           100          *           120
TrCHRC : GNCTTAAAGTGTGTAACATATTTCTTAACTTAAANNNTTTTNACCCNACAAAAAAAACAA : 120

      *           140          *           160          *           180
TrCHRC : AGACAATAACATGGGTAGTGTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA : 180

      *           200          *           220          *           240
TrCHRC : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTACATGTAAGAAAGATAC : 240

      *           260          *           280          *           300
TrCHRC : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC : 300

      *           320          *           340          *           360
TrCHRC : TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAAC TTGGCCTTGT : 360

      *           380          *           400          *           420
TrCHRC : CACTAGAGAAGAGCTTTTTGTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT : 420

      *           440          *           460          *           480
TrCHRC : TGTGTGTTCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA : 480

      *           500          *           520          *           540
TrCHRC : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTTCATTTCCAATTGATGTGGC : 540

      *           560          *           580          *           600
TrCHRC : AGATCTCTTGCCATTTGATGTGAAGGTTGTTGGGAATCCATGGAAGAAGGCTTGAAACT : 600

      *           620          *           640          *           660
TrCHRC : TGGACTCACTAAAGCTATTGGTGT TAGTAACTTCTCTGTCAAGAACTTCAAATCTTGT : 660

      *           680          *
TrCHRC : CTCAGTTGCCACCGTTCTTCCTGCGGTCAATCAG : 694

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FIGURE 41

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TrChRc : MGSVEIPTKVL^{*}TNTSSQVKMPVVG^{*}MGSAPDFTCKKDKDAII^{*}EAIKQGYRHFDTAAAYGS^{*} : 60

TrChRC : EQALGEGLEKAEI^{*}ELGLVTREELFVTSKLWVTENHPHLVVPALQKSLKTLQLEYLDLYLIH^{*} : 120

TrChRc : WPLSSQPGKFSFPIDVADLLPFDVKGWVWESMEEGLKLGLTKAIGVSNFSVKKLQNLVSVA : 180

TrCHRC : TVLPAVNQ : 188

FIGURE 42

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      *           20           *           40           *           60
TrCHRC1 : TAAGAATGAANCAATTTTATCTTAATAAAAAGGTCNCANGCAAGTTAGTTNCTATTAAACATA : 60
TrCHRC2 : -----TCTNNNAAAAGGNNCANGCAAGTNAGTTNNTANTTTNAACTA : 41
TrCHRC3 : -----GNAATTCAAACATA : 13
TrCHRC4 : -----ATTCAAACATA : 11
TrCHRC5 : -----TTCAAACATA : 10
TrCHRC6 : -----TTCNAAACATA : 10
TrCHRC7 : -----AACATA : 6
TrCHRC8 : -----ACA : 3
TrCHRC9 : -----CA : 2
TrCHRC10 : -----CA : 2
TrCHRC11 : -----CA : 2
TrCHRC12 : -----CA : 2
TrCHRC13 : ----- : -
TrCHRC14 : ----- : -
TrCHRC15 : ----- : -
TrCHRC16 : ----- : -

      *           80           *           100          *           120
TrCHRC1 : GNCTTAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTGACCCACACAAAAAAAACAA : 120
TrCHRC2 : GNCTTAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTGACCCACACAAAAAAAACAA : 101
TrCHRC3 : GNCTTAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCACACAAAAAAAACAA : 73
TrCHRC4 : GNCTTAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCNACAAAAAAAACAA : 71
TrCHRC5 : GCCTCCAGTGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCACNATAAAAAACAA : 70
TrCHRC6 : GNCTTAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTGACCCACACAAAAAAAACAA : 70
TrCHRC7 : GNCTTAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTGACCCACACAAAAAAAACAA : 66
TrCHRC8 : TNCTTAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCNACAAAAAAAACAA : 63
TrCHRC9 : TAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCNACAAAAAAAACAA : 62
TrCHRC10 : TAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCNACAAAAAAAACAA : 62
TrCHRC11 : TAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCNACAAAAAAAACAA : 62
TrCHRC12 : TAAAGTGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCNACAAAAAAAACAA : 62
TrCHRC13 : -----CGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCNACAAAAAAAACAA : 52
TrCHRC14 : -----CGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCNACAAAAAAAACAA : 52
TrCHRC15 : -----GTGTGTAACATATTCCTTAACCTTAAACNATTTTNACCCNACAAAAAAAACAA : 52
TrCHRC16 : -----NTTCTTAAACNATTTTNACCCNACAAAAAAAACAA : 38

      *           140          *           160          *           180
TrCHRC1 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 180
TrCHRC2 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 161
TrCHRC3 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 133
TrCHRC4 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 131
TrCHRC5 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 130
TrCHRC6 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 130
TrCHRC7 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 126
TrCHRC8 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 123
TrCHRC9 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 122
TrCHRC10 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 122
TrCHRC11 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 122
TrCHRC12 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 122
TrCHRC13 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 112
TrCHRC14 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 112
TrCHRC15 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 112
TrCHRC16 : AGACAATAACATGGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 98

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FIGURE 43

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		*	200	*	220	*	240	
TrCHRC1 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :240
TrCHRC2 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :221
TrCHRC3 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :193
TrCHRC4 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :191
TrCHRC5 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :190
TrCHRC6 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :190
TrCHRC7 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :186
TrCHRC8 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :183
TrCHRC9 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :182
TrCHRC10 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :182
TrCHRC11 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :182
TrCHRC12 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :182
TrCHRC13 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :172
TrCHRC14 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :172
TrCHRC15 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :172
TrCHRC16 :	AGT	GAAA	ATGC	CTGT	GGTT	TGGA	ATGG	GATCAGCTCCTGATTTACATGTAAGAAAGATAC :158
		*	260	*	280	*	300	
TrCHRC1 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :300
TrCHRC2 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :281
TrCHRC3 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :253
TrCHRC4 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :251
TrCHRC5 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :250
TrCHRC6 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :250
TrCHRC7 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :246
TrCHRC8 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :243
TrCHRC9 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :242
TrCHRC10 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :242
TrCHRC11 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :242
TrCHRC12 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :242
TrCHRC13 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :232
TrCHRC14 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :232
TrCHRC15 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :232
TrCHRC16 :	AAA	AGAT	GCAAT	CATT	GAA	GCCAT	CAAACA	AGGTTATAGACACTTTGATACTGCTGCTGC :218
		*	320	*	340	*	360	
TrCHRC1 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :360
TrCHRC2 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :341
TrCHRC3 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :313
TrCHRC4 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :311
TrCHRC5 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :293
TrCHRC6 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :310
TrCHRC7 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :306
TrCHRC8 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :303
TrCHRC9 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :302
TrCHRC10 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :302
TrCHRC11 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :302
TrCHRC12 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :302
TrCHRC13 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :292
TrCHRC14 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :292
TrCHRC15 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :292
TrCHRC16 :	TTAT	GGCT	CAGA	ACA	AAGCTCTT	GGTGA	AGGTTT	TGAAAGAAGCAATTGAACCTTGGCTTGT :278

FIGURE 43 (cont)

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		*	380	*	400	*	420	
TrCHRC1 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACT						: 420
TrCHRC2 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACT						: 401
TrCHRC3 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 373
TrCHRC4 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 371
TrCHRC5 :								: -
TrCHRC6 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 370
TrCHRC7 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 366
TrCHRC8 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACT						: 363
TrCHRC9 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 362
TrCHRC10 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 362
TrCHRC11 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACT						: 362
TrCHRC12 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 362
TrCHRC13 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 352
TrCHRC14 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 352
TrCHRC15 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 352
TrCHRC16 :	CACTAGAGAAGAGCTTTTGTGTTGCTTCTAAACTTTGGGTC	CACTGAAAATCATCCTCACCT						: 338
		*	440	*	460	*	480	
TrCHRC1 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 480
TrCHRC2 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 461
TrCHRC3 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 433
TrCHRC4 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 431
TrCHRC5 :								: -
TrCHRC6 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 430
TrCHRC7 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 426
TrCHRC8 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 423
TrCHRC9 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 422
TrCHRC10 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 422
TrCHRC11 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 422
TrCHRC12 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 422
TrCHRC13 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 412
TrCHRC14 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 412
TrCHRC15 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 412
TrCHRC16 :	TGTTGTTCCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA							: 398
		*	500	*	520	*	540	
TrCHRC1 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 540
TrCHRC2 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 521
TrCHRC3 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 493
TrCHRC4 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 491
TrCHRC5 :								: -
TrCHRC6 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 490
TrCHRC7 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 486
TrCHRC8 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 483
TrCHRC9 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 482
TrCHRC10 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 482
TrCHRC11 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 482
TrCHRC12 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 482
TrCHRC13 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 472
TrCHRC14 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 472
TrCHRC15 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 472
TrCHRC16 :	TTTGATCCATTGGCCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC							: 458

FIGURE 43 (cont)

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          *           560           *           580           *           600
TrCHRC1 : AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGG-----: 576
TrCHRC2 : AG-----: 524
TrCHRC3 : AGATCTCTTGCCATTTGATGTGAGGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 553
TrCHRC4 : AGATCTCTTGCCATTTGATGTGAGGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 551
TrCHRC5 : -----: -
TrCHRC6 : AATCTCTTGCCATTTGATGTGAANGGTGTGTTGGGAATCCATGGAAGAANGCTTNAAACT: 550
TrCHRC7 : AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 546
TrCHRC8 : AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 543
TrCHRC9 : AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 542
TrCHRC10: AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 542
TrCHRC11: AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 542
TrCHRC12: AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 542
TrCHRC13: AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGAATCCATGGAAGAANGCTTGAAACT: 532
TrCHRC14: AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 532
TrCHRC15: AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 532
TrCHRC16: AGATCTCTTGCCATTTGATGTGAAGGGTGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT: 518

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          *           620           *           640           *           660
TrCHRC1 : -----: -
TrCHRC2 : -----: -
TrCHRC3 : TGGACTCACTAAAGCTATTGGTGT-----: 577
TrCHRC4 : TGGACTCACTAAAGCTATTGGTGTAGTAACCTCTCTGTCAAGAAN-----: 597
TrCHRC5 : -----: -
TrCHRC6 : TGGACTCACTAAAGCTATTGGTGTGCAANNAACCTCTCTNTCAANAACTTCAAAATCTTNT: 610
TrCHRC7 : TGGACTCACTAAAGCTATTGGTGT-----: 570
TrCHRC8 : TGGACTCACTAAAGCTATTGGTGTAGTAACCTCTCTGTCAAGAACTTCAAAATCTTGT: 603
TrCHRC9 : TGGACTCACTAAAGCTATTGGTGTAGTAAN-----: 573
TrCHRC10: TGGACTCACTAAAGCTATTGGTGTAGTAACCTCTCTGTCT-----: 583
TrCHRC11: TGGACTCACTAAAGCTATTGGTGTAGTAACCTCTCTGTCAAGAACTTCAAAAT-----: 597
TrCHRC12: TGGACTCACTAAAGCTATTGGTGTAGTAACCTCTCTGTCAAGAACTTCAAAAT-----: 597
TrCHRC13: TGGACTCCTAAAGCTATTGGTGTAGTAANNACTTCTTGTNAN-----: 574
TrCHRC14: TGGACTCACTAAAGCTATTGGTGTAGTAACCTCTCTGTCAAGAAN-----: 578
TrCHRC15: TGGACTCACTAAAGCTATTGGTGTAGTAACCTCTCTGTCAAGAACTTCAAAATCTTGT: 592
TrCHRC16: TGGACTCACTAAAGCTATTGGTGTAGTAACCTCTCTGTCAAGAACTTCAAAATCTTGT: 578

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          *           680           *
TrCHRC1 : -----: -
TrCHRC2 : -----: -
TrCHRC3 : -----: -
TrCHRC4 : -----: -
TrCHRC5 : -----: -
TrCHRC6 : CTCAAATTGCCACCGTTCTTCTGCGG-----: 636
TrCHRC7 : -----: -
TrCHRC8 : CTCAGTTGCCACCGTTCT-----: 621
TrCHRC9 : -----: -
TrCHRC10: -----: -
TrCHRC11: -----: -
TrCHRC12: -----: -
TrCHRC13: -----: -
TrCHRC14: -----: -
TrCHRC15 : CTCAGTTG-----: 600
TrCHRC16 : CTCAGTTGCCACCGTTCTTCCTGCGGTCAATCAG: 612

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FIGURE 43 (cont)

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      *           20           *           40           *           60
TrDFRa : GCACACNTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 60

      *           80           *           100          *           120
TrDFRa : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACG : 120

      *           140          *           160           *           180
TrDFRa : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 180

      *           200          *           220           *           240
TrDFRa : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTTCGAAATGGATCTTCTTAACAG : 240

      *           260          *           280           *           300
TrDFRa : CGACTCTATTGCGGCCGCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCCTAA : 300

      *           320          *           340           *           360
TrDFRa : CATCATTGGTGAAGTCAAAGACCCCGAGAAGCAAATTTTGGAACCGGCAATTCAAGGAAC : 360

      *           380          *           400           *           420
TrDFRa : GGTAAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC : 420

      *           440          *           460           *           480
TrDFRa : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGAGAAGATTG : 480

      *           500          *           520           *           540
TrDFRa : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAATTATCTACCCCATTGCAAAGACACT : 540

      *           560          *           580           *           600
TrDFRa : AGCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTTGATGTTGTTATGATTAA : 600

      *
TrDFRa : CCCTGGTACT : 610

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FIGURE 44

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TrDFRa : MSKTVCTXGASGAIGSWVVRLLLERGYIVHATIQDLEDENETKHLEAMEGAKGHLKFFEM : 60

TrDFRa : DLLNSDSIAAAVKGCGAGVIHLACPNIIGEVKDPEKQILEPAIQGTNVNVLKVAKEAGVERV : 120

TrDFRa : VATSSISAIIPSPNWPADKIKGEDCWTDLDYCKEKKLYPIAKTLAEKAGWEFAKETGFD : 180

TrDFRa : VVMINPGT : 188

FIGURE 45

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      *           20           *           40           *           60
TrDFRa1 : GCACACCTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 60
TrDFRa2 : GCNCACNTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 60
TrDFRa3 : GCACACNTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGGACAGT : 60
TrDFRa4 : GCACACNTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 60
TrDFRa5 : --GCCNCTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 58
TrDFRa6 : --CCNCTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 58
TrDFRa7 : -----CNTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGGACAGT : 55
TrDFRa8 : -----CNTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 55
TrDFRa9 : -----TTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 54
TrDFRa10 : -----TTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 5

      *           80           *           100          *           120
TrDFRa1 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACC : 120
TrDFRa2 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACC : 120
TrDFRa3 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACC : 120
TrDFRa4 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACC : 120
TrDFRa5 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACC : 118
TrDFRa6 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACC : 118
TrDFRa7 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACC : 115
TrDFRa8 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACC : 115
TrDFRa9 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACC : 114
TrDFRa10 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTTCGCCTCCTCCTCGAACC : 65

      *           140          *           160          *           180
TrDFRa1 : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTTT : 180
TrDFRa2 : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTTT : 180
TrDFRa3 : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTTT : 180
TrDFRa4 : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTTT : 180
TrDFRa5 : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTTT : 178
TrDFRa6 : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTTT : 178
TrDFRa7 : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTTT : 175
TrDFRa8 : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTTT : 175
TrDFRa9 : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTTT : 174
TrDFRa10 : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTTT : 125

      *           200          *           220          *           240
TrDFRa1 : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 240
TrDFRa2 : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 240
TrDFRa3 : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 240
TrDFRa4 : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 240
TrDFRa5 : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 238
TrDFRa6 : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 238
TrDFRa7 : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 235
TrDFRa8 : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 235
TrDFRa9 : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 234
TrDFRa10 : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 185

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FIGURE 46

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      *           260           *           280           *           300
TrDFRa1 : CGACTCTATTGCGGNCGCCGTGAAAGGTTGNGCCGGAGTTATACATNTTGNCTGTCTCTAC : 300
TrDFRa2 : TGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATNTTGCATGTCTCTAA : 300
TrDFRa3 : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCTCTAA : 300
TrDFRa4 : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCTCTAA : 298
TrDFRa5 : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCTCTAG : 298
TrDFRa6 : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCTCTAG : 295
TrDFRa7 : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCTCTAA : 295
TrDFRa8 : TGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCTCTAA : 294
TrDFRa9 : CGACTCTATTGCGGNCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCTCTAA : 232
TrDFRa10: NGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATN-----

      *           320           *           340           *           360
TrDFRa1 : CCGCCTTGGGGANGAGNNNGCACCCNN----- : 327
TrDFRa2 : CATCATTTGCTGAANGNAAANACCCNGANAAACGNGATTTTGNAAACCCGNN----- : 349
TrDFRa3 : CATCATTTGGTGAAGTCAAAGACCCCCGAGAAGCAAATTTTGGAAACCGGCAATTCAAGGAAC : 360
TrDFRa4 : CATCATTTGGTGAAGTCAAAGACCCCCGAGAAGCAAATTTTGGAAACCGGCAATTCAAGGAAC : 360
TrDFRa5 : CATCATTTGGTGAAGTCAAAGACCCCCGAGAAGCAAATTTTGGAAACCGGCAATTCAAGGAAC : 358
TrDFRa6 : CATCATTTGGTGAAGTCAAAGACCCCCGAGAAGCAAATTTTGGAAACCGGCAATTCAAGGAAC : 358
TrDFRa7 : CATCATTTGGTGAAGTCAAAGACCCCCGAGAAGCAAATTTTGGAAACCGGCAATTCAAGGAAC : 355
TrDFRa8 : CATCATTTGGTGAAGTCAAAGACCCCCGAGAAGCAAATTTTGGAAACCGGCAATTCAAGGAAC : 355
TrDFRa9 : CATCATTTGGGGAAGCNAAAGNACCCNATAAGNAN----- : 328
TrDFRa10: ----- : -

      *           380           *           400           *           420
TrDFRa1 : ----- : -
TrDFRa2 : ----- : -
TrDFRa3 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC : 420
TrDFRa4 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC : 420
TrDFRa5 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC : 418
TrDFRa6 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC : 418
TrDFRa7 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC : 415
TrDFRa8 : GGTTAAGGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC : 415
TrDFRa9 : ----- : -
TrDFRa10: ----- : -

      *           440           *           460           *           480
TrDFRa1 : ----- : -
TrDFRa2 : ----- : -
TrDFRa3 : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGGAGAAGATTG : 480
TrDFRa4 : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGGAGAAGATTG : 480
TrDFRa5 : GATCTCTGGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGGAGAAGATTG : 478
TrDFRa6 : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGGAGAAGATTG : 478
TrDFRa7 : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGGAGAAGATTG : 475
TrDFRa8 : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGGAGAAGATTG : 475
TrDFRa9 : ----- : -
TrDFRa10: ----- : -

```

FIGURE 46 (cont)

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```

          *           500           *           520           *           540
TrDFRa1 : ----- : -
TrDFRa2 : ----- : -
TrDFRa3 : NTGGACAGACCTTGATTATTGCAANGAAAAGAAGTTATACTACCCCATTGCAAAGACATT : 540
TrDFRa4 : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACACT : 540
TrDFRa5 : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACACT : 538
TrDFRa6 : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACACT : 538
TrDFRa7 : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACATT : 535
TrDFRa8 : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACACT : 535
TrDFRa9 : ----- : -
TrDFRa10: ----- : -

```

```

          *           560           *           580           *           600
TrDFRa1 : ----- : -
TrDFRa2 : ----- : -
TrDFRa3 : AATCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTGATGTTGTT----- : 592
TrDFRa4 : AGCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTGATGTTGTTAT----- : 594
TrDFRa5 : AGCAGAAAAAGCTGGTTGGGAATTTGCTAAGAGACCGGTTTTGCT----- : 583
TrDFRa6 : AGCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTGATGTTGTTATGATTAA : 598
TrDFRa7 : AATCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGAC----- : 571
TrDFRa8 : AGCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTGATGTTGTT----- : 586
TrDFRa9 : ----- : -
TrDFRa10: ----- : -

```

```

          *
TrDFRa1 : ----- : -
TrDFRa2 : ----- : -
TrDFRa3 : ----- : -
TrDFRa4 : ----- : -
TrDFRa5 : ----- : -
TrDFRa6 : CCCTGGTACT : 608
TrDFRa7 : ----- : -
TrDFRa8 : ----- : -
TrDFRa9 : ----- : -
TrDFRa10: ----- : -

```

FIGURE 46 (cont)

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TrDFRb : ATAAAACCAANCTNCAAAACTGATTGGAACCTCAGAAAAATAGAAGAAAAGAGATGCCTGA : 60
 * 20 * 40 * 60

TrDFRb : GTTTTGTGTACAGGGGGCACTGGCTTCATAGCAGCCTACCTAGTGAAAAGCCTTATTAGA : 120
 * 80 * 100 * 120

TrDFRb : AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTA : 180
 * 140 * 160 * 180

TrDFRb : TCTAACTGAACTAAGTGAAGACAAAGAGAGATTGAAGATTTTAAAAGCAGATCTATTGGT : 240
 * 200 * 220 * 240

TrDFRb : GGAAGGGAGTTTTGATGAGGCAGTGAGTGGTGTGATGGTGTGTTTCATACAGCTTCCCC : 300
 * 260 * 280 * 300

TrDFRb : TGTTCCTGTTCCACATGATGACAACATTCAGGTTACTTTGATTGATCCATGTATAAAAGG : 360
 * 320 * 340 * 360

TrDFRb : AACACAAAATGTGCTTAACTCATGCATCAAAGCAAAGGTGAAACGTGTGGTGTAAACATC : 420
 * 380 * 400 * 420

TrDFRb : TTCATGCTCTTCCATAAGATAACCGTGACGATGTGCAACAAATTTCTCCTCTTAATGAATC : 480
 * 440 * 460 * 480

TrDFRb : TCATTGGAGTGATTCTGAATACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 540
 * 500 * 520 * 540

TrDFRb : TTTAGGAGAAAAAGAAGCATGGAGGATTGCAAAGGAAAGTGGAATTGATCTAGTTGTAGT : 600
 * 560 * 580 * 600

TrDFRb : TAACCCCTCTTTTGTGGTGGTC : 623
 * 620

FIGURE 47

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TrDFRb : MPEFCVTGGTGFIAAYLVKALLEKGHTVVRTTVRNPDDLEKVGYLTELSEDKERLKILKAD : 60

TrDFRb : LLVEGSFDEAVSGVDGVFHTASPVLPVPHDDNIQVTLIDPCIKGTQNVNLNSCIKAKVKRVV : 120

TrDFRb : LTSSCSSIRYRDDVQQISPLNESHWS DSEYCKRYNLWYAYAKTLGEKEAWRIAKESGIDL : 180

TrDFRb : VVVNPSFVGG : 190

FIGURE 48

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	*	20	*	40	*	60	
TrDFRb1:	ATAAAACCAANCTNCAAAACTGATTGGAACCTAGAAAAATAGAAGAAAAGAGATGCCTGA						: 60
TrDFRb2:	-----GNACTCCTNNAAAAATAGAAGAAAAGAGATGCCTGA						: 35
TrDFRb3:	-----GAAAAGAGATGCCTGA						: 16
TrDFRb4:	-----GAGATGCCTGA						: 11

	*	80	*	100	*	120	
TrDFRb1:	GTTTTGTGTTACAGGGGGCACTGGCTTCATAGCAGCCTACCTAGTGAAAGCCTTATTAGA						: 120
TrDFRb2:	GTTTTGTGTTACAGGGGGCACTGGCTTCATAGCAGCCTACCTAGTGAAAGCCTTATTAGA						: 95
TrDFRb3:	GTTTTGTGTTACAGGGGGCACTGGCTTCATAGCAGCTTACCTAGTGAAAGCCTTATTAGA						: 76
TrDFRb4:	GTTTTGTGTTACAGGGGGCACTGGCTTCATAGCAGCTTACCTAGTGAAAGCCTTATTAGA						: 71

	*	140	*	160	*	180	
TrDFRb1:	AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTA						: 180
TrDFRb2:	AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTA						: 155
TrDFRb3:	AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTA						: 136
TrDFRb4:	AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTA						: 131

	*	200	*	220	*	240	
TrDFRb1:	TCTAACTGAACTAAGTGAAGACAAAGAGAGATTGAAGATTTTAAAAGCAGATCTATTGGT						: 240
TrDFRb2:	TCTAACTGAACTAAGTGAAGACAAAGAGAGATTGAAGATTTTAAAAGCAGATCTATTGGT						: 215
TrDFRb3:	TCTAACTGAACTAAGTGAAGACAAAGAGAGATTGAAGATTTTAAAAGCAGATCTATTGGT						: 196
TrDFRb4:	TCTAACTGAACTAAGTGAAGACAAAGAGAGATTGAAGATTTTAAAAGCAGATCTATTGGT						: 191

	*	260	*	280	*	300	
TrDFRb1:	GGAAGGGAGTTTTTGATGAGGCAGTGAGTGGTGTGTTGATGGTGTGTTTCATACAGCTTCCCC						: 300
TrDFRb2:	GGAAGGGAGTTTTTGATGAGGCAGTGAGTGGTGTGTTGATGGTGTGTTTCATACAGCTTCCCC						: 275
TrDFRb3:	GGAAGGGAGTTTTTGATGAGGCAGTGAGTGGTGTGTTGATGGTGTGTTTCATACAGCTTCCCC						: 256
TrDFRb4:	GGAAGGGAGTTTTTGATGAGGCAGTGAGTGGTGTGTTGATGGTGTGTTTCATACAGCTTCCCC						: 251

	*	320	*	340	*	360	
TrDFRb1:	TGTTCTTGTTCCACATGATGACAAATTTCAGGTTACTTTGATTGATCCATGTATAAAAGG						: 360
TrDFRb2:	TGTTCTTGTTCCACATGATGACAAATTTCAGGTTACTTTGATTGATCCATGTATAAAAGG						: 335
TrDFRb3:	TGTTCTTGTTCCACATGATGACAAATTTCAGGTTACTTTGATTGATCCATGTATAAAAGG						: 316
TrDFRb4:	TGTTCTTGTTCCACATGATGACAAATTTCAGGTTACTTTGATTGATCCATGTATAAAAGG						: 311

	*	380	*	400	*	420	
TrDFRb1:	AACACAAAATGTGCTTAACCTCATGCATCAAAGCAAAGGTGAAACGTGTGGTGTTAACATC						: 420
TrDFRb2:	AACACAAAATGTGCTTAACCTCATGCATCAAAGCAAAGGTGAAACGTGTGGTGTTAACATC						: 395
TrDFRb3:	AACACAAAATGTGCTTAACCTCATGCATCAAAGCAAAGGTGAAACGTGTGGTGTTAACATC						: 376
TrDFRb4:	AACACAAAATGTGCTTAACCTCATGCATCAAAGCAAAGGTGAAACGTGTGGTGTTAACATC						: 371

	*	440	*	460	*	480	
TrDFRb1:	TTCATGCTCTTCCATAAGATACCGTGACGATGTGCAACAAATTTCTCCTCTTAATGAATC						: 480
TrDFRb2:	TTCATGCTCTTCCATAAGATACCGTGACGATGTGCAACAAATTTCTCCTCTTAATGAATC						: 455
TrDFRb3:	TTCATGCTCTTCCATAAGATACCGTGACGATGTGCAACAAATTTCTCCTCTTAATGAATC						: 436
TrDFRb4:	TTCATGCTCTTCCATAAGATACCGTGACGATGTGCAACAAATTTCTCCTCTTAATGAATC						: 431

FIGURE 49

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```

          *           500           *           520           *           540
TrDFRb1: TCATTGGAGTGATTCTGAATACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 540
TrDFRb2: TCATTGGAGTGATTCTGAAT TACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 515
TrDFRb3: TCATTGGAGTGATTCTGAATACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 496
TrDFRb4: TCATTGGAGTGATTCTGAATACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 491

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          *           560           *           580           *           600
TrDFRb1: ATTAGGAGAAAAAGAAGCATGGAGGATTGC----- : 570
TrDFRb2: TTTAGGAGAAAAAGAAGCATGGAGGATTGCAAAGGAAAGTGGGATT AATCTAGTTGT--- : 572
TrDFRb3: TTTAGGAGAAAAAGAAGCATGGAGGATTGCAAAGGAAAGTGG AATTGATCTAGTTGTAGT : 556
TrDFRb4: TTTAGGAGAAAAAGAAGCATGGAGGATTGCAAAGGAAAGTGAATTGATCTAGTTGTAGT : 551

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          *           620
TrDFRb1 : ----- : -
TrDFRb2 : ----- : -
TrDFRb3 : TAACCCCTCTTTTGT----- : 572
TrDFRb4 : TAACCCCTCTTTTGTGGTGGTC : 574

```

FIGURE 49 (cont)

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```

      *           20           *           40           *           60
TrDFRc : GNGAAGANCTAGTTTGCCTAACCCGGANCAACGGTTTCATCGGAACATGGCTAGTTAAAA : 60

      *           80           *           100          *           120
TrDFRc : CCCTACTCCAAAAACACTACAAAATTCAGCCACAATCTTCCCAAT'TCCAACGCATCTC : 120

      *           140          *           160          *           180
TrDFRc : ATCTCTTCACACTCCACCCGGAAGCTCAATCCCGGATCACAATTTTCCCTGTCGATATCC : 180

      *           200          *           220          *           240
TrDFRc : TCGACTCCACCGCCGCTTCTCTCCGCTATCAATAACTGCTCAGGTGTCTTTCATGCCGCTT : 240

      *           260          *           280          *           300
TrDFRc : CTCCATGTACCCCTCGAAGATCCAAGTATCCGCAAAAAGAGCTTCTAGAACCTGCTGTAC : 300

      *           320          *           340          *           360
TrDFRc : AAGGAACCCCTAAATGTTCTAGAAAGCATCCAGCGCGCAGGTACCAAACCCTAATTGGCCGG : 360

      *           380          *           400          *           420
TrDFRc : AGAAAAAGGCGATCGATGAGGCGTCGTGGACGGATGTTGAGTACTGTAAATTGAGAGGGA : 420

      *           440          *           460          *           480
TrDFRc : AGTGGTATCTGGTGTGCGAAAACGGAGGCGGAGAAGGCGGCTTGGGATTTTCGAGAGAAAA : 480

      *           500          *           520          *           540
TrDFRc : ATGGTGGTGTGATGTGGGGGCGGNTCATCCGGGGACTTGTTTGGGAGAGTTGATACAGA : 540

      *           560          *           580          *           600
TrDFRc : AGGAGTTGAATGCGAGTTCAGCGGNTTTACAGAGGTTGATGATGGGGAGTGAGGATACTC : 600

      *           620          *           640
TrDFRc : AAGAGTGNATATGGNNGGGGGGCTGMNNATGNTAAAGATGN : 641

```

FIGURE 50

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TrDFRc : * 20 * 40 * 60
EXLVCVTRXNGFIGTWLVKTLLQKHYKIHATIFPNSNASHLFTLHPEAQSRITIFPVDIL : 60

TrDFRc : * 80 * 100 * 120
DSTAVFSAINNC SGVFHAASPCTLEDPTDPQKELLEPAVQGT LNVLEASSAQVPNPNWPE : 120

TrDFRc : * 140 * 160 * 180
KKAIDEASWTDVEYCKLRGKWYLVSKTEAEKAAWDFREKNGGVDVGAXHPGTCLGELIQK : 180

TrDFRc : * 200
ELNASSALQRLMMGSED TQEXYWXGG : 206

FIGURE 51

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TrDFRd : GCNTTGATCAGCGTATNAACACACANGTCTTCCCTTGAGCTCTGTTTCTCCACATGTCTGA : 60
 TrDFRd : AGCTAGTTTGCGTCACCGGCGGCAGCGGATGCATCGGTTTCATGGCTAGTCCATCTCCTTC : 120
 TrDFRd : TCCTCCGCGGCTACACTGTTTCAGCCACCGTCCAAAATCTCAATGATGAGAACGAAACGA : 180
 TrDFRd : AGCATCTAGAAGCTCTCGAAGGAGCACAACTAATCTCCGTCTCTTCCAGATCGATCTCC : 240
 TrDFRd : TTAACACGACACAATCCTCGCTGCTGTCCGCGGTTGCGTCGGAATTTTCCACCTCGCTT : 300
 TrDFRd : CACCTTGCACTGTAGACAAAGTTCATGATCCTCAGAAGGAGCTTTTGGATCCTGCAATTA : 360
 TrDFRd : AAGGGACTTTGAATGTGCTTACTGCAGCTAAGGAAGTAGGGGTGAAGCGTGTGGTTGTTA : 420
 TrDFRd : CCTCGTCTGTCTCGGCGATTACTCCTAGTCTGATTGGCCTTCTGATGTTGTTAAAAGAG : 480
 TrDFRd : AGGATTGTTGGACTGATGTTGAATATTGCAAGAAAAAAGAGTTGGGGTATCCGTTGTCCA : 540
 TrDFRd : AAACATTGGCTGAAAAAGCTGCGTGGGATTTTNCNAAAGAAAATGGTTTGGATGTTGTTG : 600
 TrDFRd : NGGTGAATCCCGNACTGNGATGGGTCTGTTTTTCCACCACGGCATAATGCAAGCATGC : 660
 TrDFRd : TCATGCCTTGGGAACTTTTTTGAAGGCTGGNNCTGAAACATTTGAAGACTATTTTATGG : 720
 TrDFRd : GATTGGCCNNCTTTAAAGATGTNGCATTGGCNCATNNTTTGGGGTATGAGAACAAANANN : 780
 TrDFRd : CTTTGGGANACATNGGNGGGTTGAACTATCNCCTTACGG : 822

FIGURE 52

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TrDFRd : MSKLVCVTGGSGCIGSWLVHLLLLRGYTVHATVQNLNDENETKHLEALEGAQTNLRLFQI : 60

TrDFRd : DLLNYDTILAAVRGCVGIFHLASPCTVDKVHDPQKELLDPAIKGTLNVLTAAKEVGVKRV : 120

TrDFRd : VVTSSVSAITPSPDWPSDVVKREDCWTDVEYCKKKELGYPLSKTLAEKAAWDFXKENGLD : 180

TrDFRd : VVXVNPXTXMGPFVPPRHNASMLMPWETFLKAXXETFEDYFMGLAXFKDXALXHXLYEN : 240

TrDFRd : KXXLGXXXGLKLXXLT : 256

FIGURE 53

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	* 20 * 40 * 60	
TrDFRd1:	GCN ¹ TTGATCAGCGTATNAACACACANGTCTTCCCTTGAGCTCTGTTTCTCC ² NCATGTCTGA	: 60
TrDFRd2:	-----NACANN ¹ TCTTCCCTTGAGCTCTGTTTCTCCACATGTCTGA	: 39
	* 80 * 100 * 120	
TrDFRd1:	AGCTAGTTTGCCTCACCGGCGGCAGCGGATGCATCGGTTTCATGGCTAGTCCATCTCCTTC	: 120
TrDFRd2:	AGCTAGTTTGCCTCACCGGCGGN ² CGCGGATGCATCGGTTTCATGGCTAGTCCATCTCCTTC	: 99
	* 140 * 160 * 180	
TrDFRd1:	TCCTCCGCGGCTACACTGTTTCACGCCACCGTCCAAAATCTCAATGATGAGAACGAAACGA	: 180
TrDFRd2:	TCCTCCGCGGCTACACTGTTTCACGCCACCGTCCAAAATCTCAATGATGAGAACGAAACGA	: 159
	* 200 * 220 * 240	
TrDFRd1:	AGCATCTAGAAGCTCTCGAAGGAGCACAAACTAATCTCCGTCTCTTCCAGATCGATCTCC	: 240
TrDFRd2:	AGCATCTAGAAGCTCTCGAAGGAGCACAAACTAATCTCCGTCTCTTCCAGATCGATCTCC	: 219
	* 260 * 280 * 300	
TrDFRd1:	TTAACTACGACACAATCCTCGCTGCTGTCCGCGGTTGCGTCGGAATTTTCCACCTCGCTT	: 300
TrDFRd2:	TTAACTACGACACAATCCTCGCTGCTGTCCGCGGTTGCGTCGGAATTTTCCACCTCGCTT	: 279
	* 320 * 340 * 360	
TrDFRd1:	CACCTTGCACTGTAGACAAAGTTCATGATCCTCAGAAGGAGCTTTTGGATCCTGCAATTA	: 360
TrDFRd2:	CACCTTGCACTGTAGACAAAGTTCATGATCCTCAGAAGGAGCTTTTGGATCCTGCAATTA	: 339
	* 380 * 400 * 420	
TrDFRd1:	AAGGGACTTTGAATGTGCTTACTGCAGCTAAGGAAGTAGGGGTGAAGCGTGTGGTTGTTA	: 420
TrDFRd2:	AAGGGACTTTGAATGTGCTTACTGCAGCTAAGGAAGTAGGGGTGAAGCGTGTGGTTGTTA	: 399
	* 440 * 460 * 480	
TrDFRd1:	CCTCGTCTGTCTCGGCGATTACTCCTAGTCTGATTGGCCTTCTGATGTTGTTAAAAGAG	: 480
TrDFRd2:	CCTCGTCTGTCTCGGCGATTACTCCTAGTCTGATTGGCCTTCTGATGTTGTTAAAAGAG	: 459
	* 500 * 520 * 540	
TrDFRd1:	AGGATTGTTGGACTGATGTTGAATATTGCAAGAAAAAGAGTTG ¹ GGTATCCGTT-----	: 535
TrDFRd2:	AGGATTGTTGGACTGATGTTGAATATTGCAAGAAAAAGAGTTGGGGTATCCGTTGTCCA	: 519
	* 560 * 580 * 600	
TrDFRd1:	-----	: -
TrDFRd2:	AAACATTGGCTGAAAAAGCTGCGTGGGATTTTTNCAAGAAAATGGTTTGGATGTTGTTG	: 579
	* 620 * 640 * 660	
TrDFRd1:	-----	: -
TrDFRd2:	NGGTGAATCCCGNACTGNGATGGGTCTGTTTTTCCACCACGGCATAATGCAAGCATGC	: 639

FIGURE 54

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```

      *           680           *           700           *           720
TrDFRd1 : -----
TrDFRd2 : TCATGCCTTGGGAAACTTTTTTGAAGGCTGGNNCTGAAACATTTGAAGACTATTTTATGG : 699

      *           740           *           760           *           780
TrDFRd1 : -----
TrDFRd2 : GATTGGCCNNCTTTAAAGATGTNGCATTGGCNCATNNTTTGGGGTATGAGAACAAANANN : 759

      *           800           *           820
TrDFRd1 : -----
TrDFRd2 : CTTTGGGANACATNGGNGGGTTGAAACTATCNNTCCTTACGG : 801
```

FIGURE 54 (cont)

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```

      *           20           *           40           *           60
TrDFRe : GTCAC TTATGAAATGGAACACAAAGGTGGAGACAAAGTATGTGTGACAGGGGCATCAGGC : 60

      *           80           *           100          *           120
TrDFRe : TTTT TAGCATCTTGGCTTATTAAGAACTTCTTTTGTCTGGCTATCAAGTCATTGGAACA : 120

      *           140          *           160          *           180
TrDFRe : GTTAGAGATTTAGGGAAGAAGAAGAAAGTTGAACATTTATGGAAATTGGAAGGAGCAACA : 180

      *           200          *           220          *           240
TrDFRe : GAAAGACTAGAACTAATCCAAGCTGATTTAATGGAAGAAAATAGTTTCGACAAAGCGATC : 240

      *           260          *           280          *           300
TrDFRe : ATGGGATGCAAAGGTGTCTTCCACATTGCCTCTCCAGTACTCAATCATATATCAGATAAT : 300

      *           320          *           340          *           360
TrDFRe : CCTAAGGCGGAAATCTTGGAACCGGCAGTCCAAGGTACGCTAAATGTGTTGCGTTCTTGT : 360

      *           380          *           400          *           420
TrDFRe : AAGAGGAACCCCGATCTTGTTTCGAGTGGTGCTAGCCTCATCATCTTCGGCTGTTAGAGTA : 420

      *           440          *           460          *           480
TrDFRe : AGAGCTGATTTTGTATCCAAGCATACCAATTGATGAATCATCTTGGAGCTCCTTGGAATTG : 480

      *           500          *           520          *           540
TrDFRe : TCGAGAAACTCAAGGCATGGTACCCAATGTCAAAGACAATGGCAGAAAAAGCAGCTTGG : 540

      *           560          *           580
TrDFRe : GAATATAGCAAAGAGAATGGAATAGACTTAGTGACTATTTTC : 582

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FIGURE 55

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TrDFRe : MEHKGGDKVCVTGASGFLASWLIKLLLSGYQVIGTVRDLGKKKKVEHLWKLEGATERLE : 60

TrDFRe : LIQADLMEENSFDKAIMGCKGVFHIA SPVLNHISDNPKAEILEPAVQGT LNVLRSCRNP : 120

TrDFRe : DLVRVVLASSSSAVRVRADFDPSIPIDESSWSSLELCEKLKAWYPMSKTMAEKA AWEYSK : 180

TrDFRe : ENGIDLVTIF : 190

FIGURE 56

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TrDFRf : TNCNNGCTNCNTNCGGGCAGAGANTTTCCTGACCTATNTGTTACTNAAGAATATTTCTA : 60

TrDFRf : TATATATATTTGTGTTTCAAGAACCCAAAAAATAGAATAGTGATGGAAAGGAGTTGCAAG : 120

TrDFRf : GTTTGTGTCACCGGTGGTGTGTTATATTGGTTCTCTTTTAGTCAAAAAGCTTTTGAA : 180

TrDFRf : AAGGGTTACACCGTTCATGCTACTCTTAGAACTTGAAGGACGAATCCAAAGTAGATTTT : 240

TrDFRf : TTGAGAGGCTTTCCACATGCAGATACTAGACTTATGTTATTTGAAGCTGATATATACAAA : 300

TrDFRf : TCAGATGAATTTTGGCCCGCAATTCAAGGTTGTGAGTTTGTGTTTTCACCTTGCTACTCCT : 360

TrDFRf : TTTCAACATCAAAGTATCTCAGTTTAAGAGCATAGAGGAAGCTGCAATAGCAGGGGTA : 420

TrDFRf : AAAAGCATAGCTGAAAATTGCATAAAATCAGGAACAGTGAGAAAATTGATATACACTGGA : 480

TrDFRf : ACTGTAATTGCTTCTTCTCTGAAAGATGATGGAAGTGGCTACAAAGACTTCATTGAT : 540

TrDFRf : GAAACTTGTTGGACACCTCTCCATCTTCCTCT : 572

FIGURE 57

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TrDFRf : MERSCKVCVTGGAGYIGSLLVKKLLEKGYTVHATLRNLKDESKVDFLRGFPHADTRLMLF : 60

TrDFRf : EADIYKSDEFWPAIQGCEVFVHFLATPFQHQTD SQFKSIEEAAIAGVK SIAENCIKSGTVR : 120

TrDFRf : KLIYTGTVIASSSLKDDGSGYKDFIDETCWTPLHLP : 156

FIGURE 58

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```

      *           20           *           40           *           60
TrDFRg : GCCNTTGCCTACTACTAAACTATATATTATTATTATTATTATATGATGATACATAGTGACA : 60

      *           80           *           100          *           120
TrDFRg : TTAATAATTGGAAGGGAGAATAAATAGTTGAAAAACACACAGTTGGAGTGTTTTTGTGTGT : 120

      *           140          *           160          *           180
TrDFRg : TAAAGAAGCTNGAAAAATGGAGGAAGCNACAAAGATGGTGAAAAAGAGTGGACAAATTGTT : 180

      *           200          *           220          *           240
TrDFRg : CCTACTGCCAAATACTGTGTTACAGGAGCAACAGGCTATATTGGTTCATGGCTTGTTGAA : 240

      *           260          *           280          *           300
TrDFRg : GCTCTTCTTCAAAGAGGTTGCACTGTTTCATGCTACTGTTAGAGATCCTGAAAAATCGTTA : 300

      *           320          *           340          *           360
TrDFRg : CACCTCCTGTGCGTTGTGGAAGGTAGTGACCAATTGAGAATTTTCCGTGCGGATTTGCAA : 360

      *           380          *           400          *           420
TrDFRg : GAAGAAGGAAGTTTCGATGATGCCGTAAAAGGATGTATTGGTGTGTTCCATGTTGCAGCT : 420

      *           440          *           460          *           480
TrDFRg : TCAATGCAATTCAATATTAGTGACAAAGAAAACACTGAGGACTTTGTTGAAGCAAATATA : 480

      *           500          *           520          *           540
TrDFRg : ATTGACCCTGCAATCAAAGGAACCATAAATCTTCTCAAATCATGCTTGAAATCAAATTCA : 540

      *           560          *           580          *           600
TrDFRg : GTGAAAAGGGTTGTTTTACATCTTCCATAAGTACTATTACTGCTAAAGACAACGACGGA : 600

      *           620          *           640          *           660
TrDFRg : AAATGGAAACCTATTGTTGATGAATCTTGCCAAACAAAACTGAGATTCTGTGGAATACA : 660

      *           680          *           700          *
TrDFRg : CAACCAAGTGGATGGGTTTATGCACTTTCAAAGCTTCATGCAGAAGAAGCGGCT : 714

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FIGURE 59

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TrDFRg : MVKKSGQIVPTAKYCVTGATGYIGSWLVEALLQRGCTVHATVRDPEKSLHLLSLWKGSDQ : 60

TrDFRg : LRIFRADLQEEGSFDDAVKGCIGVFHVAASMQFNISDKENTEDFVEANIIDPAIKGTINL : 120

TrDFRg : LKSLKSNVSRVFTSSISTITAKDNDGKWKPIVDESCQTKTEILWNTQPSGWVYALSK : 180

TrDFRg : LHAEAEA : 187

FIGURE 60

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	* 20 * 40 * 60	
TrDFRg1:	GCCNTTGCCTACTACTAAACTATATATTATTATTATTATATGATGATACATACTGACA	: 60
TrDFRg2:	-----	: -
TrDFRg3:	-----	: -
	* 80 * 100 * 120	
TrDFRg1:	TTAATAATTGGAAGGGAGAAATAAATAGTTGAAAAACACACAGTTGGAGTGTTTTGTGTTGT	: 120
TrDFRg2:	-----	: -
TrDFRg3:	-----	: -
	* 140 * 160 * 180	
TrDFRg1:	TAAAGAAGCTTAAAAATGGAGGAAACACAAAGATGGTGAAAAATAGTGACAAATTTGTT	: 180
TrDFRg2:	---AGAAGCTNGAAAATGGAGGAAGCNACAAAGATGGTGAAAAAGAGTGACAAATTTGTT	: 57
TrDFRg3:	-----CTNGAAAATGGAGGAAGCNACAAAGATGGTGAAAAAGAGTGACAAATTTGTT	: 52
	* 200 * 220 * 240	
TrDFRg1:	CCTAAGCCAAATACTGTGTACAGGAGCAACAGGCTATATTGGTTCATGGCTTGTGAA	: 240
TrDFRg2:	CCTACTGCCAAATACTGTGTACAGGAGCAACAGGCTATATTGGTTCATGGCTTGTGAA	: 117
TrDFRg3:	CCTACTGCCAAATACTGTGTACAGGAGCAACAGGCTATATTGGTTCATGGCTTGTGAA	: 112
	* 260 * 280 * 300	
TrDFRg1:	GCTCTTCTTCAAAGAGGTTGCACTGTTTCATGCTACTGTTAGAGATCCTG-----	: 289
TrDFRg2:	GCTCTTCTTCAAAGAGGTTGCACTGTTTCATGCTACTGTTAGAGATCCTGAAAAATCGTTA	: 177
TrDFRg3:	GCTCTTCTTCAAAGAGGTTGCACTGTTTCATGCTACTGTTAGAGATCCTGAAAAATCGTTA	: 172
	* 320 * 340 * 360	
TrDFRg1:	-----	: -
TrDFRg2:	CACCTCCTGTCGTTGTGGAAGGTTAGTGACCAATTGAGAATTTTCCGTGCGGATTTGCAA	: 237
TrDFRg3:	CACCTCCTGTCGTTGTGGAAGGTTAGTGACCAATTGAGAATTTTCCGTGCGGATTTGCAA	: 232
	* 380 * 400 * 420	
TrDFRg1:	-----	: -
TrDFRg2:	GAAGAAGGAAGTTTCGATGATGCCGTAAAAGGATGTATTGGTGTGTTCCATGTTGCAGCT	: 297
TrDFRg3:	GAAGAAGGAAGTTTCGATGATGCCGTAAAAGGATGTATTGGTGTGTTCCATGTTGCAGCT	: 292
	* 440 * 460 * 480	
TrDFRg1:	-----	: -
TrDFRg2:	TCAATGCAATTCAATATTAGTGACAAAGAAAACACTGAGGACTTTGTTGAAGCAAATATA	: 357
TrDFRg3:	TCAATGCAATTCAATATTAGTGACAAAGAAAACACTGAGGACTTTGTTGAAGCAAATATA	: 352
	* 500 * 520 * 540	
TrDFRg1:	-----	: -
TrDFRg2:	ATTGACCCTGCAATCAAAGGAACCATAAATCTTCTCAAATCATGCTTGAAATCAAATTCA	: 417
TrDFRg3:	ATTGACCCTGCAATCAAAGGAACCATAAATCTTCTCAAATCATGCTTGAAATCAAATTCA	: 412

FIGURE 61

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      *           560           *           580           *           600
TrDFRg1: ----- : -
TrDFRg2: GTGAAAAGGGTTGTTTTACATCTTCCATAAGTACTATTACTGCTAAAGACAACGACGGA : 477
TrDFRg3: GTGAAAAGGGTTGTTTTACATCTTCCATAAGTACTATTACTGCTAAAGACAACGACGGA : 472

      *           620           *           640           *           660
TrDFRg1: ----- : -
TrDFRg2: AAATGGAAACCTATTGTTGATGAATCTTGCCAAACAAAAACTGAGATTCTGTGGAATACA : 537
TrDFRg3: AAATGGAAACCTATTGTTGATGAATCTTGCCAAACAAAAACTGAGATTCTGTGGAATACA : 532

      *           680           *           700           *
TrDFRg1: ----- : -
TrDFRg2: CAACCAAGTGGATGGGTTTATGCACTTTCAAAGCTTCATGCAGAAGAAGCGGCT : 591
TrDFRg3: CAACCAAGTGGATGGGTTTATGCACTTTCAAAGCTTCATG----- : 572
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FIGURE 61 (cont)

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TrDFRh : GNNNGTCTTCCGTTNAATTTNAGNCTATATTGAAAAGGAAAAAAGAGTAGAGAAGTGA : 60

TrDFRh : AGTGAAGTGAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA : 120

TrDFRh : GGTTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 180

TrDFRh : ACCGTTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTGTGGTGAAGTCCCGGGTGCA : 240

TrDFRh : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA : 300

TrDFRh : ATTAAAGGGTGACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC : 360

TrDFRh : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC : 420

TrDFRh : GAAAAGGCAAAAACAGTTAGAAAATTGGTTTTCACATCATCGGCTGGAAGTGTGGACGTT : 480

TrDFRh : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 540

TrDFRh : AGAGTCAAGATGACCGGTTGGATGTATTTTGTTCAAAGACCCTAGCAGAGCAAGAAGCT : 600

TrDFRh : TGGAAGTATTTCGAAAGAGCACAAACATAGACTTTGTCTCCATCATTCCACCTCTTGTTGTT : 660

TrDFRh : GGCCCTTTCTTATGGCCTCAATGCCACCTAGTCTAATCACTGCTCTTTCTCTTATCACA : 720

TrDFRh : GGAAATGAGGCCCATTAATCATAAAGCAAGGGCAATACGTCCATTTAGATGACCTT : 780

TrDFRh : TGTCTTGCTCATATATTTCTGTATGAGAATCCAAAAGCTCAAGGGAGATACATTTGCTGT : 840

FIGURE 62

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TrDFRh : TCACATGAAGCAACCATTCATCAAGTTGCAAACTTATTAAAGAAAAATACCCAGAGTTC : 900

TrDFRh : AATGTCCCAACAAAATTCAATGATATCCCAGATGAATTGGAAATTATTAAATTTCTAAA : 960

TrDFRh : AAGAAGATCACAGACT : 976

FIGURE 62 (cont)

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TrDFRh : MGSESEIVCVTGASGFIGSWLVMRLIERGYTVRATVRDPDNMKKVKHLVELPGAKSKLSL : 60

TrDFRh : WKADLDKEGSFDEAIKGCTGVFHVATPMDFESKDPENEVIKPTINGLIDILKACEKAKTV : 120

TrDFRh : RKLVTSSAGTVDVTEHPKSIIDETCWSVDVFCRRVKMTGWMYFVSKTLAEQEAWKYSKE : 180

TrDFRh : HNIDFVSIIPPLVVGPFLMASMPPSLITALSLITGNEAHYSIIKQGQYVHLDDLCLAHIF : 240

TrDFRh : LYENPKAQGRYICCSHEATIHQVAKLIKEKYPEFNVPTKFNDIPDELEIIKFSKKKITD : 299

FIGURE 63

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      *           20           *           40           *           60
TrDFRh1 : GNN TGTCTTCCGTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNGA : 60
TrDFRh2 : -TGTCTTAAATCAATTTAGNCTAATTTGAAAAAGAAAAAAGAGGAGAGAAGTCA : 59
TrDFRh3 : ---GNGTCTTCCGTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNGA : 57
TrDFRh4 : ---GNGTCTTCCGTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGAGAANNCN : 57
TrDFRh5 : ---GNGTCTTCCGTTNAATTTAGNCTATATTGAAAAGNAAAAAAGAGTAGNNNANNGA : 57
TrDFRh6 : ---GNGTCTTCCGTTNAATTTAGNCTATATTGAAAAGNAAAAAAGAGTAGNNNANNGA : 57
TrDFRh7 : ---GNGTCTTCCGTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGAGAAGTGA : 57
TrDFRh8 : ---GTCCTTCCTTNAATTTNAGNCTAATTTGAAAAAGAAAAAAGAGGAGAGAAGTGA : 56
TrDFRh9 : ---GTCCTTCCGTTNAATTTAGNCTATATTGAAAAAGAAAAAAGAGTAGAGAAGTGA : 56
TrDFRh10 : ---GTCCTTCCGTTNATTTAGNCTATATTGAAAAAGAAAAAAGAGTAGAGAAGTGA : 56
TrDFRh11 : ---GTCCTTCCGTTNATTTAGNCTATATTGAAAAAGAAAAAAGAGGAGAGAAGTGA : 55
TrDFRh12 : ---GTCCTTCCGTTNATTTNAGNCTATATTGAAAAGNAAAAAAGAGTAGAGAANNCN : 55
TrDFRh13 : ---GTCCTTCCGTTNATTTAGNCTATATTGAAAAAGAAAAAAGAGGAGAGAAGTGA : 52
TrDFRh14 : -----GNAGAGAAGTNA : 12
TrDFRh15 : ----- : -

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      *           80           *           100           *           120
TrDFRh1 : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :120
TrDFRh2 : AATGAGAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :119
TrDFRh3 : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :117
TrDFRh4 : AATGAGAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :117
TrDFRh5 : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :117
TrDFRh6 : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :117
TrDFRh7 : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :117
TrDFRh8 : AATGAGAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :116
TrDFRh9 : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :116
TrDFRh10 : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :116
TrDFRh11 : AATGAGAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :115
TrDFRh12 : AATGAGAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :115
TrDFRh13 : AATGAGAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA :112
TrDFRh14 : CATTGAGAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA : 72
TrDFRh15 : ----- : -

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      *           140           *           160           *           180
TrDFRh1 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :180
TrDFRh2 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :179
TrDFRh3 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :177
TrDFRh4 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :177
TrDFRh5 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :177
TrDFRh6 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :177
TrDFRh7 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :177
TrDFRh8 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :176
TrDFRh9 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :176
TrDFRh10 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :176
TrDFRh11 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :175
TrDFRh12 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :175
TrDFRh13 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :172
TrDFRh14 : GGTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC :132
TrDFRh15 : ----- : -

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FIGURE 64

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		*	200	*	220	*	240	
TrDFRh1 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	240					
TrDFRh2 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	239					
TrDFRh3 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	237					
TrDFRh4 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	237					
TrDFRh5 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	237					
TrDFRh6 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	237					
TrDFRh7 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	237					
TrDFRh8 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	236					
TrDFRh9 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	236					
TrDFRh10 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	236					
TrDFRh11 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	235					
TrDFRh12 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	235					
TrDFRh13 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	232					
TrDFRh14 :	ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA	:	192					
TrDFRh15 :	-----	:	-					
		*	260	*	280	*	300	
TrDFRh1 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	300					
TrDFRh2 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	299					
TrDFRh3 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	297					
TrDFRh4 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	297					
TrDFRh5 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	297					
TrDFRh6 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	297					
TrDFRh7 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	297					
TrDFRh8 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	296					
TrDFRh9 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	296					
TrDFRh10 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	296					
TrDFRh11 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	295					
TrDFRh12 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	295					
TrDFRh13 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	292					
TrDFRh14 :	AAAAGCAAATTGTCTCTTTTGGGAAGGCTGATCTTGATAAAAGAGGGGAGTTTTGATGAAGCA	:	252					
TrDFRh15 :	-----	:	-					
		*	320	*	340	*	360	
TrDFRh1 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	360					
TrDFRh2 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	359					
TrDFRh3 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	357					
TrDFRh4 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	357					
TrDFRh5 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	357					
TrDFRh6 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	357					
TrDFRh7 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	357					
TrDFRh8 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	356					
TrDFRh9 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	356					
TrDFRh10 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	356					
TrDFRh11 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	355					
TrDFRh12 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	355					
TrDFRh13 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	352					
TrDFRh14 :	ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC	:	312					
TrDFRh15 :	-----	:	-					

FIGURE 64 (cont)

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      *           380           *           400           *           420
TrDFRh1 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 420
TrDFRh2 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 419
TrDFRh3 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 417
TrDFRh4 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 417
TrDFRh5 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 417
TrDFRh6 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 417
TrDFRh7 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 417
TrDFRh8 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 416
TrDFRh9 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 416
TrDFRh10 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 416
TrDFRh11 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 415
TrDFRh12 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 415
TrDFRh13 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 412
TrDFRh14 : CCTGAGAATGAAGTGATAAAGCCTACAATAAAATGGATTAATAGACATACTGAAAGCATGC : 372
TrDFRh15 : -----TACTGAAAGCATGC : 14

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      *           440           *           460           *           480
TrDFRh1 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 480
TrDFRh2 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 479
TrDFRh3 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 477
TrDFRh4 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 477
TrDFRh5 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 477
TrDFRh6 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 477
TrDFRh7 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 477
TrDFRh8 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 476
TrDFRh9 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 476
TrDFRh10 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 476
TrDFRh11 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 475
TrDFRh12 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 475
TrDFRh13 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 472
TrDFRh14 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 432
TrDFRh15 : GAAAAGGCCAAAAACAGTTAATAAAATTTGGTTTTTCACATCATCGGCTGGAACGTGTGGACGTT : 74

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      *           500           *           520           *           540
TrDFRh1 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 540
TrDFRh2 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 539
TrDFRh3 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 493
TrDFRh4 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 537
TrDFRh5 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 537
TrDFRh6 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 537
TrDFRh7 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 537
TrDFRh8 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 536
TrDFRh9 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 536
TrDFRh10 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 536
TrDFRh11 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 535
TrDFRh12 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 535
TrDFRh13 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 532
TrDFRh14 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 492
TrDFRh15 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 134

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FIGURE 64 (cont)

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	*	560	*	580	*	600	
TrDFRh1 :	AGAGTCAAGATGACCGGTTGGATGTATTTTGTTCAAAGACCCTAG-----						:586
TrDFRh2 :	AGAGTCAAAATGACCGGTTGGATGTATTTT-----						:569
TrDFRh3 :	-----						: -
TrDFRh4 :	ANAGTCAANATGACCGGCTGGATGTATTTTGTTCAAANACCC-----						:580
TrDFRh5 :	AGAGTCAAGATGACCGGTTGGATGTATTTTGTTCAAAGACCCT-----						:581
TrDFRh6 :	AGAGTCAAGATGACCGGTTGGATGTATTTTGTTCAAAGACCCTAGCAGAGCAAG-----						:592
TrDFRh7 :	AGAGTCAAGATGACCGGTTGGATGTATTTTGTTCAAAGACCCTAGCAGAGCAAGAAGCT						:597
TrDFRh8 :	AGAGTCAAAATGACCGGTTGGATGTATTTTGTTCAAAGA-----						:576
TrDFRh9 :	AGAGTCAAGATGACCGGTTGGATGTATTTTGTTCAAAGACCCTAGCAGAG-----						:587
TrDFRh10:	AGAGTCAAGATGACCGGTTGGATGTATTTTGTTCAAAGACCCTAGCAGAGCAAGAAGCT						:596
TrDFRh11:	AGAGTCAAATGACCGGTTGGATGTATTTTGTTCAAAGACCCT-----						:579
TrDFRh12:	AGAGTCAAGATGACCGGTTGGATGTATTTTGTTCAAAGACCCTAGCAGAGCAAGAAGCT						:595
TrDFRh13:	AGAGTCAAATGACCGGTTGGATGTATTTTGTTCAAAGACCCTAGCAGAGCAG-----						:586
TrDFRh14:	AGAGTCAAATGACCGGTTGGATGTATTTTGTTCAAAGACCCTAGCAGAGCAAGAAGCT						:552
TrDFRh15:	AGAGTCAAATGACCGGTTGGATGTATTTTGTTCAAAGACCCTAGCAGAGCAAGAAGCT						:194

	*	620	*	640	*	660	
TrDFRh1 :	-----						: -
TrDFRh2 :	-----						: -
TrDFRh3 :	-----						: -
TrDFRh4 :	-----						: -
TrDFRh5 :	-----						: -
TrDFRh6 :	-----						: -
TrDFRh7 :	T-----						:598
TrDFRh8 :	-----						: -
TrDFRh9 :	-----						: -
TrDFRh10:	TGGAAGTATTCGAAAGAGCACAACATAGACTTTG-----						:630
TrDFRh11:	-----						: -
TrDFRh12:	TGGAAGTAT-----						:604
TrDFRh13:	-----						: -
TrDFRh14:	TGGAAGTATTCGAAAGAGCACAACATAGACTTTG-----						:586
TrDFRh15:	TGGAAGTATTCGAAAGAGCACAACATAGACTTTGTCTCCATCATTCACCTCTTGTGTT						:254

	*	680	*	700	*	720	
TrDFRh1 :	-----						: -
TrDFRh2 :	-----						: -
TrDFRh3 :	-----						: -
TrDFRh4 :	-----						: -
TrDFRh5 :	-----						: -
TrDFRh6 :	-----						: -
TrDFRh7 :	-----						: -
TrDFRh8 :	-----						: -
TrDFRh9 :	-----						: -
TrDFRh10:	-----						: -
TrDFRh11:	-----						: -
TrDFRh12:	-----						: -
TrDFRh13:	-----						: -
TrDFRh14:	-----						: -
TrDFRh15:	GGCCCCTTTCTTATGGCCTCAATGCCACCTAGTCTAATCACTGCTCTTTCTCTTATCACA						:314

FIGURE 64 (cont)

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	*	740	*	760	*	780	
TrDFRh1 :	-----		-----		-----		: -
TrDFRh2 :	-----		-----		-----		: -
TrDFRh3 :	-----		-----		-----		: -
TrDFRh4 :	-----		-----		-----		: -
TrDFRh5 :	-----		-----		-----		: -
TrDFRh6 :	-----		-----		-----		: -
TrDFRh7 :	-----		-----		-----		: -
TrDFRh8 :	-----		-----		-----		: -
TrDFRh9 :	-----		-----		-----		: -
TrDFRh10 :	-----		-----		-----		: -
TrDFRh11 :	-----		-----		-----		: -
TrDFRh12 :	-----		-----		-----		: -
TrDFRh13 :	-----		-----		-----		: -
TrDFRh14 :	-----		-----		-----		: -
TrDFRh15 :	GGAAATGAGGCCCATTTACTCAATCATAAAGCAAGGGCAATACGTCATTTAGATGACCTT						: 374

	*	800	*	820	*	840	
TrDFRh1 :	-----		-----		-----		: -
TrDFRh2 :	-----		-----		-----		: -
TrDFRh3 :	-----		-----		-----		: -
TrDFRh4 :	-----		-----		-----		: -
TrDFRh5 :	-----		-----		-----		: -
TrDFRh6 :	-----		-----		-----		: -
TrDFRh7 :	-----		-----		-----		: -
TrDFRh8 :	-----		-----		-----		: -
TrDFRh9 :	-----		-----		-----		: -
TrDFRh10 :	-----		-----		-----		: -
TrDFRh11 :	-----		-----		-----		: -
TrDFRh12 :	-----		-----		-----		: -
TrDFRh13 :	-----		-----		-----		: -
TrDFRh14 :	-----		-----		-----		: -
TrDFRh15 :	TGTCTTGCTCATATATTTCTGTATGAGAATCCAAAAGCTCAAGGGAGATACATTTGCTGT						: 434

	*	860	*	880	*	900	
TrDFRh1 :	-----		-----		-----		: -
TrDFRh2 :	-----		-----		-----		: -
TrDFRh3 :	-----		-----		-----		: -
TrDFRh4 :	-----		-----		-----		: -
TrDFRh5 :	-----		-----		-----		: -
TrDFRh6 :	-----		-----		-----		: -
TrDFRh7 :	-----		-----		-----		: -
TrDFRh8 :	-----		-----		-----		: -
TrDFRh9 :	-----		-----		-----		: -
TrDFRh10 :	-----		-----		-----		: -
TrDFRh11 :	-----		-----		-----		: -
TrDFRh12 :	-----		-----		-----		: -
TrDFRh13 :	-----		-----		-----		: -
TrDFRh14 :	-----		-----		-----		: -
TrDFRh15 :	TCACATGAAGCAACCATTTCATCAAGTTGCAAAACTTATTAAAGAAAAATACCCAGAGTTC						: 494

FIGURE 64 (cont)

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	*	920	*	940	*	960	
TrDFRh1 :	-----		-----		-----		:
TrDFRh2 :	-----		-----		-----		:
TrDFRh3 :	-----		-----		-----		:
TrDFRh4 :	-----		-----		-----		:
TrDFRh5 :	-----		-----		-----		:
TrDFRh6 :	-----		-----		-----		:
TrDFRh7 :	-----		-----		-----		:
TrDFRh8 :	-----		-----		-----		:
TrDFRh9 :	-----		-----		-----		:
TrDFRh10 :	-----		-----		-----		:
TrDFRh11 :	-----		-----		-----		:
TrDFRh12 :	-----		-----		-----		:
TrDFRh13 :	-----		-----		-----		:
TrDFRh14 :	-----		-----		-----		:
TrDFRh15 :	AATGTCCCAACAAAATTCAATGATATCCCAGATGAATTGGAAATTATTAAATTTTCTAAA						: 554

	*	
TrDFRh1 :	-----	:
TrDFRh2 :	-----	:
TrDFRh3 :	-----	:
TrDFRh4 :	-----	:
TrDFRh5 :	-----	:
TrDFRh6 :	-----	:
TrDFRh7 :	-----	:
TrDFRh8 :	-----	:
TrDFRh9 :	-----	:
TrDFRh10 :	-----	:
TrDFRh11 :	-----	:
TrDFRh12 :	-----	:
TrDFRh13 :	-----	:
TrDFRh14 :	-----	:
TrDFRh15 :	AAGAAGATCACAGACT	: 570

FIGURE 64 (cont)

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      *           20           *           40           *           60
TrLCRa : GGNCATAAAAAGTGCAGTAGTGTGTATAAGTTTNTTAGTGAAAAAAGAGTGTGTAAATTA : 60

      *           80           *           100          *           120
TrLCRa : ACATCATGGCTAGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG : 120

      *           140          *           160          *           180
TrLCRa : GTTTTGTTGCATCTATGTTGATCAAACAGTTACTTGAAAAGGGTTATGCTGTTAATACTA : 180

      *           200          *           220          *           240
TrLCRa : CTGTTAGAGACCCAGATAGTCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG : 240

      *           260          *           280          *           300
TrLCRa : GGGAAGTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG : 300

      *           320          *           340          *           360
TrLCRa : CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGAAGTTTGCTTCTCAAGATCCTG : 360

      *           380          *           400          *           420
TrLCRa : AGAATGACATGATAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 420

      *           440          *           460          *           480
TrLCRa : GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAATG : 480

      *           500          *           520          *           540
TrLCRa : AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 540

      *           560          *           580          *           600
TrLCRa : AACTGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAATGCTAGCTGAAAAGGCTG : 600

      *           620          *           640          *           660
TrLCRa : CATGGAAATTTGCTGAAGAAAAATGACATTGATCTAATCACTGTGATACCTAGTTTAACAA : 660

      *           680          *           700          *           720
TrLCRa : CTGGTCCTTCTCTCACACCAGATATCCCATCTAGTGTGGCTTGGCAATGTCTCTAATAA : 720

      *           740          *           760          *           780
TrLCRa : CAGGCAATGATTTCTCATAAATGCTCTGAAAGGAATGCAATTTCTGTGCGGGTTCGTTAT : 780

      *           800          *           820          *
TrLCRa : CCATCACTCATGTTGAGGATATTTGCCGAGCTCATATATTTCTGGCAGAGAAG : 833

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FIGURE 65

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TrLCRa : * 20 * 40 * 60
MASIKQIGNKKACVIGGTGFVASMLIKQLLEKGYAVNTTVRDPDSPKKISHLVALQSLGE : 60

TrLCRa : * 80 * 100 * 120
LNLFRADLTVEEDFDAPAGCELVFQLATPVNFASQDPENDMIKPAIKGVNLNVLKASARA : 120

TrLCRa : * 140 * 160 * 180
KEVKRVILTSSAAAVTINELKGTGHVMDETNWSDFEFLNTAKPPTWGYPAKMLAEKAAW : 180

TrLCRa : * 200 * 220 * 240
KFAEENDIDLITVIPSLTTGPSLTPDIPSSVGLAMSLITGNDFLINALKGMQFLSGSLSI : 240

TrLCRa : *
THVEDICRAHIFLAEK : 256

FIGURE 66

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		*	20	*	40	*	60	
TrLCRa1:	GGNCATAAAAACTGCACTAGTGTGTATAAGTTTNTAGTGAAAAAAGAGTGTGTAAATTA	:	60					
TrLCRa2:	GGNCNTAAAAACTGCACTAGTGTGTATAAGTTTNTAGTGAAAAAAGAGTGTGTAAATTA	:	60					
TrLCRa3:	-----TAAAAACTGTTACTNGTGTGTATAAGTTTNTAGTGAAAAAAGAGTGTGTAAATTA	:	55					
TrLCRa4:	-----TAAAAACTGCACTAGTGTGTATAAGTTTCTTGCTGAAAAAAGAGTTTGTAAATTA	:	55					
TrLCRa5:	-----GACCTCGTGTGNANTAGTTTCTTGCTGAAAAAAGAGTTTGTAAANTA	:	47					
TrLCRa6:	-----	:	-					
TrLCRa7:	-----	:	-					
		*	80	*	100	*	120	
TrLCRa1:	ACATCATGGCTAGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG	:	120					
TrLCRa2:	ACATCATGGCTAGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG	:	120					
TrLCRa3:	ACATCATGGCTAGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG	:	115					
TrLCRa4:	ACATCATGGCTAGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG	:	115					
TrLCRa5:	ACATCNTGGCTNGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG	:	107					
TrLCRa6:	-----	:	-					
TrLCRa7:	-----	:	-					
		*	140	*	160	*	180	
TrLCRa1:	GTTTTGTTGCATCTATGTTGATCAAACAGTTACTTGAAAAGGGTTATGCTGTTAATACTA	:	180					
TrLCRa2:	GTTTTGTTGCATCTATGTTGATCAAACAGTTACTTGAAAAGGGTTATGCTGTTAATACTA	:	180					
TrLCRa3:	GTTTTGTTGCATCTATGTTGATCAAACAGTTACTTGAAAAGGGTTATGCTGTTAATACTA	:	175					
TrLCRa4:	GTTTTGTTGCATCTATGTTGATCAAACAGTTACTTGAAAAGGGTTATGCTGTTAATACTA	:	175					
TrLCRa5:	GTTTTGTTGCATCTATGTTGATCAAACAGTTACTTGAAAAGGGTTATGCTGTTAATACTA	:	167					
TrLCRa6:	-----	:	-					
TrLCRa7:	-----	:	-					
		*	200	*	220	*	240	
TrLCRa1:	CTGTTAGAGACCCAGATAGTCCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG	:	240					
TrLCRa2:	CTGTTAGAGACCCAGATAGTCCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG	:	240					
TrLCRa3:	CTGTTAGAGACCCAGATAGTCCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG	:	235					
TrLCRa4:	CTGTTAGAGACCCAGATAGTCCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG	:	235					
TrLCRa5:	CTGTTAGAGACCCAGATAGTCCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG	:	227					
TrLCRa6:	-----G	:	1					
TrLCRa7:	-----	:	-					
		*	260	*	280	*	300	
TrLCRa1:	GGGAACCTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG	:	300					
TrLCRa2:	GGGAACCTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG	:	300					
TrLCRa3:	GGGAACCTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG	:	295					
TrLCRa4:	GGGAACCTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG	:	295					
TrLCRa5:	GGGAACCTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG	:	287					
TrLCRa6:	NGNACCTGAATCTATTTAGAGNAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG	:	61					
TrLCRa7:	-----TTAACAGTTGAAGAAGATTTTGATGCTCCTATAG	:	34					
		*	320	*	340	*	360	
TrLCRa1:	CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG	:	360					
TrLCRa2:	CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG	:	360					
TrLCRa3:	CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG	:	355					
TrLCRa4:	CAGGATGTGAACTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG	:	355					
TrLCRa5:	CAGGATGTGAACTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG	:	347					
TrLCRa6:	CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG	:	121					
TrLCRa7:	CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG	:	94					

FIGURE 67

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          *           380           *           400           *           420
TrLCRa1: AGAATGACATGATAAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 420
TrLCRa2: AGAATGACATGATAAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 420
TrLCRa3: AGAATGACATGATAAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 415
TrLCRa4: AGAATGACATGATAAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAATTGCAA : 415
TrLCRa5: AGAATGACATGATAAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAATTGCAA : 407
TrLCRa6: AGAATGACATGATAAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 181
TrLCRa7: AGAATGACATGATAAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 154

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          *           440           *           460           *           480
TrLCRa1: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAAATG : 480
TrLCRa2: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAAATG : 480
TrLCRa3: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAAATG : 475
TrLCRa4: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAAATG : 475
TrLCRa5: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAAATG : 467
TrLCRa6: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAAATG : 241
TrLCRa7: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAAATG : 214

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          *           500           *           520           *           540
TrLCRa1: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 540
TrLCRa2: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 540
TrLCRa3: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 535
TrLCRa4: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 535
TrLCRa5: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 527
TrLCRa6: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 301
TrLCRa7: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 274

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          *           560           *           580           *           600
TrLCRa1: ACAC TGCAAAGCCACCCACTTGGGGTTATCCTGCTT----- : 576
TrLCRa2: ACAC TGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAN----- : 580
TrLCRa3: ACAC TGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAAAT----- : 578
TrLCRa4: ACAC TGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAAATGCTAGCTGAAAAGGCTG : 595
TrLCRa5: ACAC TGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAAATGCTAGCTGAAAAGGCTG : 587
TrLCRa6: ACAC TGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAAATGCTAGCTGAAAAGGCTG : 361
TrLCRa7: ACAC TGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAAATGCTAGCTGAAAAGGCTG : 334

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```

          *           620           *           640           *           660
TrLCRa1: ----- : -
TrLCRa2: ----- : -
TrLCRa3: ----- : -
TrLCRa4: CATGGAAATTTGCTGAAGAAAATG----- : 619
TrLCRa5: CATGGAAATTTGCTGAAGAAAATGACNTTGAT----- : 619
TrLCRa6: CATGGAAATTTGCTGAAGAAAATGACATTGATCTAATCACTGTGATACCTAGTTTAACAA : 421
TrLCRa7: CATGGAAATTTGCTGAAGAAAATGACATTGATCTAATCACTGTGATACCTAGTTTAACAA : 394

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          *           680           *           700           *           720
TrLCRa1: ----- : -
TrLCRa2: ----- : -
TrLCRa3: ----- : -
TrLCRa4: ----- : -
TrLCRa5: ----- : -
TrLCRa6: CTGGTCCTTCTCTCACACCAGATATCCCATCTAGTGTGGCTTGGCAATGTCTCTAATAA : 481
TrLCRa7: CTGGTCCTTCTCTCACACCAGATATCCCATCTAGTGTGGCTTGGCAATGTCTCTAATAA : 454

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FIGURE 67 (cont)

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	*	740	*	760	*	780		
TrLCRa1:	-----		-----		-----		:	-
TrLCRa2:	-----		-----		-----		:	-
TrLCRa3:	-----		-----		-----		:	-
TrLCRa4:	-----		-----		-----		:	-
TrLCRa5:	-----		-----		-----		:	-
TrLCRa6:		CAGGCAATGATTTTCCTCATAAATGCTCTGAAAGGAATGCAATTTCTGTCGGGTTTCGTTAT					:	541
TrLCRa7:		CAGGCAATGATTTTCCTCATAAATGCTCTGAAAGGAATGCAATTTCTGTCGGGTTTCGTTAT					:	514

	*	800	*	820	*		
TrLCRa1:	-----		-----		-----	:	-
TrLCRa2:	-----		-----		-----	:	-
TrLCRa3:	-----		-----		-----	:	-
TrLCRa4:	-----		-----		-----	:	-
TrLCRa5:	-----		-----		-----	:	-
TrLCRa6:		CCATCACTCATGTTGAGGATATTTGCCGAGCTCATATATTTCTGG				:	586
TrLCRa7:		CCATCACTCATGTTGAGGATATTTGCCGAGCTCATATATTTCTGGCAGAGAAG				:	567

FIGURE 67 (cont)

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TrF3'5'Ha: GGAACCAATTGTCTCGGACTTTTTTCCCGGGTTGGCCCGATTTCGATTTGCAGGGTGTGGTG : 60

TrF3'5'Ha: AAAGAGATGGATGTCTTGGTTCCACGTTTTGATAGCATATTTGAAAAAATGATTGGTGAA : 120

TrF3'5'Ha: CGTAAGAAGAAGGAAGTGGAGGGGAAAGAAAATGAAAGTAAGGATTTTCTGCAGTTTTTG : 180

TrF3'5'Ha: TTGAATTTGAAGGATGAGGGTGATTCTAAGACTCCATTACACAATTACCCATGTTAAGGCT : 240

TrF3'5'Ha: CTACTCATGGACATGGTTGTGGGTGGATCAGACACATCCTCCAACACAATTGAGTTTGCA : 300

TrF3'5'Ha: TTGGCAGAAATGATGAACAACCCAGAAGTAATGAGGAAGGTTCAAGAGGAATTAGAAGAT : 360

TrF3'5'Ha: GTAGTTGGGAAAGATAACTTAGTAGAAGAGTCTCACATTCATAAGCTACCCCTACTTGCAT : 420

TrF3'5'Ha: GCAGTGATGAAAGAAACACTTCGTTTACACCCAGCACTTCCACTTTTAGTCCCTCACTGT : 480

TrF3'5'Ha: CCAAGTGAAACCACCAATGTTGGAGGCTACACAATTCCAAAGGGATCTCGTGTTGTTGTG : 540

TrF3'5'Ha: AACGTTTGGGCTATTCATAGAGACCCCTTCATTTGGGAGAAACCACTAGAATTTGAT : 597

FIGURE 68

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      *           20           *           40           *           60
TrF3'5'Ha: GTNLSDFFPGLARFDLQGVVKEMDVLVPRFDSIFEKMI GERKKKEVEGKENESKDFLQFL : 60

      *           80           *           100          *           120
TrF3'5'Ha: LNLKDEGDSKTPFTITHVKALLMDMVVGSDTSSNTIEFALAEMMNPEVMRKVQEELED :120

      *           140          *           160          *           180
TrF3'5'Ha: VVGKDNLVEESHIHKLPYLHAVMKETLRLHPALPLLVP HCPSETTNVGGYTIPKGSRVFV :180

      *
TrF3'5'Ha: NVWAIHRDPSIWEKPLEFD :199

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FIGURE 69

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TrF3'5'Hb: GNAATCCACNAATCTCTTGAANTAATACCATTTCTTTACAAGAACTTAACCATGGTGATG : 60

TrF3'5'Hb: ATCACTCAATACCAAACCTTCCTTTACAAAGAACTTTCTATATCCTTTTTCATTTTCTTG : 120

TrF3'5'Hb: ATAACCCATTTTCATCATAAGTTTCTCTTCAAAAAAATCTCAAAAAACTTCCACCAGGC : 180

TrF3'5'Hb: CCAAAGGTTTTCAGTTGTTGGTGCACCTCCACTAATGGGATCCATGCCTCATGTTACC : 240

TrF3'5'Hb: CTATTCAAAATGTCACAAAAATATGGTCCCATAATGTACCTAAAAATGGGATCAAATAAC : 300

TrF3'5'Hb: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTCTCTCAAAACACTTGACCTAAAT : 360

TrF3'5'Hb: TTCTCCAATAGACCGCCGAACGCTGGCGCAACTCACCTAGCTTATGATTCACAAGACTTG : 420

TrF3'5'Hb: GTTTTCGCCGACTATGGATCTAGGTGGAAATTACTTAGGAACTAAGTAAGTTCACATG : 480

TrF3'5'Hb: CTCGGCGGAAAAGCCCTCGAAAATGGTTCGAAAGTTCGTGAGATTGAAATGGGTCACATG : 540

TrF3'5'Hb: ATTCGTACAATGTACGATTGTAGCAAGAAAGACGAATCCGTTGTTGTGGCCGAAATGTTG : 600

TrF3'5'Hb: ACATATGCTATGGCCAATATGATAGGTCAAGTTATATTGAGTCGTCGCGTGTTTCGAGACA : 660

TrF3'5'Hb: AAAGGTAGTGACTCAAATGAATTTAAGGATATGGTTGNTG : 700

FIGURE 70

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      *      20      *      40      *      60
TrF3'5'Hb: MVMITQYQTFLYKELSSISFFIFLITHFIISFLFKKNLKKLPFGPKGFPVVGALPLMGSM : 60

      *      80      *      100     *      120
TrF3'5'Hb: HVTLFKMSQKYGPIMYLKMGSNNMVVASTPSSAKAFLKTLDLNFSNRPPNAGATHLAYDS :120

      *      140     *      160     *      180
TrF3'5'Hb: QDLVFADYGSRWKLLRKLSNLHMLGGKALENWSKVREIEMGHMIRTMYDCSKKDESVVVA :180

      *      200     *
TrF3'5'Hb: EMLTYAMANMIGQVILSRRVFETKGSDSNEFKDMVX :216

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FIGURE 71

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      *           20           *           40           *           60
TrF3 '5' Hb1: GNAATCCACNAATCTCTTGAAATAATNCCATTTCCTTTACAAGAACTTAACCATGGTGATG : 60
TrF3 '5' Hb2: -----GNCAAATCTCTTGCAANTAANNCCATTTCCTTTACAAGAACTTAACCATGGTGATG : 54
TrF3 '5' Hb3: -----CNAATCTCTTGGAANTATACCATTTCCTTTACAAGAACTTAACCATGGTGATG : 52
TrF3 '5' Hb4: -----TCTCTTGNAATNATACCATTTCCTTTACAAGAACTTAACCATGGTGATG : 48

      *           80           *           100          *           120
TrF3 '5' Hb1: ATCACTCAATACCAAACCTTCCTTTCAAAGAACTTTCTATATCCTTTTTTCATTTTCTTG : 120
TrF3 '5' Hb2: ATCACTCAAACCAAACCTTCCTTTCAAAGAACTTTCTATATCCTTTTTTCATTTTCTTG : 114
TrF3 '5' Hb3: ATNNCTCAATACCAAACCTTCCTTTCAAAGAACTTTCTATATCCTTTTTTCATTTTCTTG : 112
TrF3 '5' Hb4: ATNNCTCNATACCAAACCTTCCTTTCAAAGAACTTTCTATATCCTTTTTTCATTTTCTTG : 108

      *           140          *           160          *           180
TrF3 '5' Hb1: ATAACCCATTTTCATCATAAGTTTCTCTTCAAAAAAATCTCAAAAAACTTCCACCAGGC : 180
TrF3 '5' Hb2: ATAACCCATTTTCATCATAGTTTCTCTTCAAAAAAATCTCAAAAAACTTCCACCAGGC : 174
TrF3 '5' Hb3: ATAACCCATTTTCATCATAAGTTTCTCTTCAAAAAAATCTCAAAAAACTTCCACCAGGC : 172
TrF3 '5' Hb4: ATAACCCATTTTCATCATAGTTTCTCTTCAAAAAAATCTCAAAAAACTTCCACCAGGC : 168

      *           200          *           220          *           240
TrF3 '5' Hb1: CCAAAAGGTTTTCCAGTTGTTGGTGCACCTCCACTAATGGGATCCATGCCCTCATGTTACC : 240
TrF3 '5' Hb2: CCAAAAGGTTTTCCAGTTGTTGGTGCACCTCCACTAATGGGATCCATGCCCTCATGTTACC : 234
TrF3 '5' Hb3: CCAAAAGGTTTTCCAGTTGTTGGTGCACCTCCACTAATGGGATCCATGCCCTCATGTTACC : 232
TrF3 '5' Hb4: CCAAAAGGTTTTCCAGTTGTTGGTGCACCTCCACTAATGGGATCCATGCCCTCATGTTACC : 228

      *           260          *           280          *           300
TrF3 '5' Hb1: CTATTCAAAAATGTCACAAAAATATGGTCCCATAATGTACCTAAAAATGGGATCAAATAAC : 300
TrF3 '5' Hb2: CTATTCAAAAATGTCACAAAAATATGGTCCATAATGTACCTAAAAATGGGATCAAATAAC : 294
TrF3 '5' Hb3: CTATTCAAAAATGTCACAAAAATATGGTCCCATAATGTACCTAAAAATGGGATCAAATAAC : 292
TrF3 '5' Hb4: CTATTCAAAAATGTCACAAAAATATGGTCCATAATGTACCTAAAAATGGGATCAAATAAC : 288

      *           320          *           340          *           360
TrF3 '5' Hb1: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTTCTCAAAACACTTGACCTAAAT : 360
TrF3 '5' Hb2: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTTCTCAAAACACTTGACCTAAAT : 354
TrF3 '5' Hb3: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTTCTCAAAACACTTGACCTAAAT : 352
TrF3 '5' Hb4: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTTCTCAAAACACTTGACCTAAAT : 348

      *           380          *           400          *           420
TrF3 '5' Hb1: TTCTCCAATAGACCGCCGAACGCTGGCGCACTCACCTAGCTTATGATTCACAAGACTTG : 420
TrF3 '5' Hb2: TTCTCCAATAGACCGCCGAACGCTGGCGCACTCACCTAGCTTATGATTCACAAGACTTG : 414
TrF3 '5' Hb3: TTCTCCAATAGACCGCCGAACGCTGGCGCACTCACCTAGCTTATGATTCACAAGACTTG : 412
TrF3 '5' Hb4: TTCTCCAATAGACCGCCGAACGCTGGCGCACTCACCTAGCTTATGATTCACAAGACTTG : 408

      *           440          *           460          *           480
TrF3 '5' Hb1: GTTTTCGCCCGACTATGGATCTAGGTGGAAATTACTTAGGAAACTAAGTAACCTTGCACATG : 480
TrF3 '5' Hb2: GTTTTCGCCCGACTATGGATCTAGGTGGAAATTACTTAGGAAACTAAGTAACCTTGCACATG : 474
TrF3 '5' Hb3: GTTTTCGCCCGACTATGGATCTAGGTGGAAATTCTTAGGAAACTAAGTAACCTTGCACATG : 472
TrF3 '5' Hb4: GTTTTCGCCCGACTATGGATCTAGGTGGAAATTACTTAGGAAACTAAGTAACCTTGCACATG : 468

      *           500          *           520          *           540
TrF3 '5' Hb1: CTCGGCGGAAAAGCCCTCGAAATTTGGTTCGAAAGTTCGTGAGATTGAAATGGGTCACATG : 540
TrF3 '5' Hb2: CTCGGCGGAAAAGCCCTCGAAATTTGGTTCGAAAGTTCGTGAGATTGAAATGGGTCACATG : 534
TrF3 '5' Hb3: CTCGGCGGAAAAGCCCTCGAAATTTGGTTCGAAAGTTCGTGAGATTGAAATGGGTCACATG : 532
TrF3 '5' Hb4: CTCGGCGGAAAAGCCCTCGAAATTTGGTTCGAAAGTTCGTGAGATTGAAATGGGTCACATG : 528

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FIGURE 72

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	*	560	*	580	*	600	
TrF3 '5' Hb1:	ATTCGTACAATGTATGATTGTAGCAAGAAAGACGAATCCGTTGT-----						: 584
TrF3 '5' Hb2:	ATTCGTACAATGTACGATTGTAGCAAGAAAGACGAATCCGTTGTTGTGGCCGAAATGTTG						: 594
TrF3 '5' Hb3:	ATTCGTACAATGTACGATTGTAGCAAGAAAGACGAATATGTTGTTGTC-----						: 580
TrF3 '5' Hb4:	ATTCGTACAATGTACGATTGTAGCAAGAAAGACGAATCCGNTGNTG-----						: 74
	*	620	*	640	*	660	
TrF3 '5' Hb1:	-----						: -
TrF3 '5' Hb2:	ACATATGCTATGGCCAATATGATAGGTCAAGTTATATTGAGTCGTCGCGTGTTCGAGACA						: 654
TrF3 '5' Hb3:	-----						: -
TrF3 '5' Hb4:	-----						: -
	*	680	*	700			
TrF3 '5' Hb1:	-----					: -	
TrF3 '5' Hb2:	AAAGGTAGTGACTCAAATGAATTTAAGGATATGGTTGNTG					: 694	
TrF3 '5' Hb3:	-----					: -	
TrF3 '5' Hb4:	-----					: -	

FIGURE 72 (cont)

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      *           20           *           40           *           60
TrF3Ha : GCACACNTCTATTTATTTCTACTTAAACCTNACAAAAAATAANACCCACAAAACACAAAC : 60

      *           80           *           100          *           120
TrF3Ha : ACCACAAACACCAAAACCGAGTCCGTTTCCTNNTCNAACATGGCACCAAGCCAAACTCTA : 120

      *           140          *           160          *           180
TrF3Ha : AGTTATCTCTCACAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT : 180

      *           200          *           220          *           240
TrF3Ha : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTCTCTTGCTGGAATT : 240

      *           260          *           280          *           300
TrF3Ha : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT : 300

      *           320          *           340          *           360
TrF3Ha : TGGGGTATTTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC : 360

      *           380          *           400          *           420
TrF3Ha : CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC : 420

      *           440          *           460          *           480
TrF3Ha : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 480

      *           500          *           520          *           540
TrF3Ha : TGGAGAGAGCTAGTGACATATTTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG : 540

      *           560          *           580          *           600
TrF3Ha : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT : 600

      *           620          *           640          *           660
TrF3Ha : TTAGCTTGCAAACCTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 660

      *           680          *           700          *           720
TrF3Ha : ACAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT : 720

      *           740          *           760          *           780
TrF3Ha : GAACCTGACCTCACACTTGGCCTTAAACGTCACACTGACCCTGGCACAATTACTCTTTTG : 780

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FIGURE 73

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      *           800           *           820           *           840
TrF3Ha : CTTCAAGATCAAGTTGGTGGCCTTCAAGCTACCAAAGATAATGGTAAGACGTGGATTACA : 840

      *           860           *           880           *           900
TrF3Ha : GTTCAACCAGTTGAAGGTGCTTTTGTGTGTTAATCTTGGAGACCATGGTCACTATCTAAGT : 900

      *           920           *           940           *           960
TrF3Ha : AATGGACGGTTCAAAAATGCTGACCACCAAGCAGTGGTGAATTCGAACTACAGCCGNTTA : 960

      *           980           *          1000           *          1020
TrF3Ha : TCAATAGCAACATTTCAAATCCAGCTCCCGATGCAACTGTATACCCTTTGAAGATTAGA : 1020

      *          1040           *          1060           *          1080
TrF3Ha : GAGGGTGAAAAATCTGTGTTGGAAGAACCAATCACTTTTGCTGAAATGTATAGAAGGAAG : 1080

      *          1100           *          1120           *          1140
TrF3Ha : ATGACCAAAGACCTTGAAATTGCTAGGATGAAGAAGTTGGCTAAGGAACAACAACCTTAGG : 1140

      *          1160           *          1180           *          1200
TrF3Ha : GACTTGGAGGAGAACAAGACTAAATATGAGGCCAAACCTTTGAATGAGATCTTTGCTTAA : 1200

      *          1220           *          1240           *          1260
TrF3Ha : TTAATTAGTCTTAATTTAAATAATTAATAAATTTTAGACTTAATTTACATATAATAATTT : 1260

TrF3Ha : T : 1261

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FIGURE 73 (cont)

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      *      20      *      40      *      6
TrF3Ha : MAPSQTLSYLSQQNTLESSFVREEDERPKVAYNNFSNEIPIISLAGIDEVDGRRTEICNK : 59

      *      80      *      100     *      120
TrF3Ha : IVEACENWGIFQVVDHGVDTKLVSEMTRFAREFFALPPEEKLRFDMSGGKKGGFIVSSHL : 120

      *      140     *      160     *      180
TrF3Ha : QGEAVKDWRELVTYFSYPIKQRDYSRWPDKPEGWKEVTEKYSENLMNLACKLLEVLSEAM : 180

      *      200     *      220     *      240
TrF3Ha : GLEKEALTKACVDMDQKVVINYYPKCPEPDLTLGLKRHTDPGTITLLQLDQVGGLQATKD : 240

      *      260     *      280     *      300
TrF3Ha : NGKTWITVQPVGEAFVVNLGDHGHYLSNGRFRKNADHQAVVNSNYSXLSIATFQNPAPDAT : 300

      *      320     *      340     *      360
TrF3Ha : VYPLKIREGEKSVLEEPITFAEMYRRKMTKDLEIARMKKLAKEQQLRDLEENKTKYEAKP : 360

TrF3Ha : LNEIFA : 366

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FIGURE 74

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		*	20	*	40	*	60	
TrF3Ha1	:	GCACACNTCTATTTATTTCTACTTAAACCTCACAAAAAATAA	-	ACCCACAACACACAAAC	:	59		
TrF3Ha2	:	GCACNGNTCTATTTATTTCTACTTAAACCT---	NAAAAATAA	-	ACCCACAA--CAC-AA-	: 52		
TrF3Ha3	:	-CACACNTCTATTTATTTCTACTTAAACCTNACAAAAAATAAN	ACCCACAACACACAAAC	:	59			
TrF3Ha4	:	--TCCGCTCTANTTATTTCTTCTTAAACCTNNCAAAAAATNANN	ACCCACAACACACNAAN	:	58			
TrF3Ha5	:	-----	GTAAACACAC-N	CAACACAAAC	:	22		
TrF3Ha6	:	-----	GNA-ACCCACAACACACAAAC	:	20			
TrF3Ha7	:	-----	CACACNAABNCAAAC	:	16			
TrF3Ha8	:	-----	CACNACNACACAAAC	:	16			
TrF3Ha9	:	-----	CCACANGACAC-AA-	:	13			
TrF3Ha10	:	-----	GAANCCACNAAC	:	13			
TrF3Ha11	:	-----	GNACGACACAAAC	:	13			
TrF3Ha12	:	-----	GGGA--CAC-AA-	:	9			
TrF3Ha13	:	-----	TGTAACACAAAC	:	12			
TrF3Ha14	:	-----	CNCAACACAAAC	:	12			
TrF3Ha15	:	-----	GNNAATCACA	:	11			
TrF3Ha16	:	-----	GAACCCAA	:	10			
TrF3Ha17	:	-----	AACCCAG	:	9			
TrF3Ha18	:	-----	GCACNAAC	:	8			
TrF3Ha19	:	-----	AC-ANC	:	5			
TrF3Ha20	:	-----	GCNNGA	:	6			
TrF3Ha21	:	-----	GNACCC	:	6			
TrF3Ha22	:	-----	CTAGA	:	5			
TrF3Ha23	:	-----	CA	:	4			
TrF3Ha24	:	-----	AA	:	3			
TrF3Ha25	:	-----	GA	:	3			
TrF3Ha26	:	-----	GC	:	2			
TrF3Ha27	:	-----	GC	:	2			
TrF3Ha28	:	-----	GC	:	2			
TrF3Ha29	:	-----	A	:	1			
TrF3Ha30	:	-----		:	-			
TrF3Ha31	:	-----		:	-			
TrF3Ha32	:	-----		:	-			
TrF3Ha33	:	-----		:	-			
TrF3Ha34	:	-----		:	-			
TrF3Ha35	:	-----		:	-			
TrF3Ha36	:	-----		:	-			
TrF3Ha37	:	-----		:	-			
TrF3Ha38	:	-----		:	-			
TrF3Ha39	:	-----		:	-			
TrF3Ha40	:	-----		:	-			
TrF3Ha41	:	-----		:	-			

FIGURE 75

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      *           80           *           100           *           120
TrF3Ha1 : ACCA AAAACAG-AG-ACCGTTTCCATCATC-----A--AACATGGCACCAAGCCAAACTCTA :113
TrF3Ha2 : ACCA AAAACAG-AG-ACCGTTTCCATCATC-----A--AACATGGCACCAAGCCAAACCTA :106
TrF3Ha3 : ACCA AAAACAGNAG-ACCGTTTCCATCATC-----A--AACATGGCACCAAGCCAAACTCTA :119
TrF3Ha4 : ANCAC AAAANANACAGNAG-ACCGTTTCCATCATCAACATGGCACCAAGCCAAACTCTA :118
TrF3Ha5 : ACCA AAAACAGNAN-ACCGTTTCC-A-TNCA-T:CAAACATGGCACCAAGCCAAACTCTA : 78
TrF3Ha6 : A-CA AAAACAG-AG-NCCGTTTCN-TNATC-----A--AACATGGCACCAAGCCAAACTCTA : 71
TrF3Ha7 : ACCA AAAACAGNAN-ACCGTTTCC-A-TNCA-TNCAAACATGGCACCAAGCCAAACTCTA : 73
TrF3Ha8 : ACCA AAAACAGNAN-ACCGTTTCC-A-TNCA-T:CAAACATGGCACCAAGCCAAACTCTA : 72
TrF3Ha9 : A-CACCAAA-A-ACAGAGCAGCCGTTTCCATCATCAACATGGCACCAAGCCAAACTCTA : 70
TrF3Ha10 : ANCACAAACNCAAAAANAGAGACCGTTTCCCTNNTNNAACATGGCACCAAGCCAAACTCTA : 73
TrF3Ha11 : ACCA AAAACAG-AG-ACCGTTTCC-TNATC-----A--AACATGGCACCAAGCCAAACTCTA : 66
TrF3Ha12 : ACC-AAAAC-C-AGC-CCGTTTCC-T-NT-----A--AACATGGCACCAAGCCAAACTCTA : 57
TrF3Ha13 : ACCA AAAACAG-AGNACCGTTTCC-TNTCC-----A--A-CATGGCACCAAGCCAAACTCTA : 64
TrF3Ha14 : ACCA AAAACAG-AG-ACCGTTTCC-A-TNCA-TNCAAACATGGCACCAAGCCAAACTCTA : 69
TrF3Ha15 : AC-TNCAAAAC-CCA-AA-CGAG-CCGTTTCCCTNCTNNAACATGGCACCAAGCCAAACTCTA : 71
TrF3Ha16 : AC-CCAA-CCA-AA-CGAGNCCGTTTCCCT-NTC-AACATGGCACCAAGCCAAACTCTA : 67
TrF3Ha17 : AC-TNCAAA-CCA-AA-CGAG-CCGTTTCCCTNNTCNAACATGGCACCAAGCCAAACTCTA : 69
TrF3Ha18 : ANCACAAAC-CC-AAA-NGAGACCGTTTCCCT-NTNNAACATGGCACCAAGCCAAACTCTA : 68
TrF3Ha19 : A-CAAAAC-N-C-AAA-CGAGTCCGTTCCCT-NT-NAACATGGCACCAAGCCAAACTCTA : 60
TrF3Ha20 : ANCACAAAC-C-AAAACGAGCACCCTTTCCCTANTNNAACATGGCACCAAGCCAAACTCTA : 66
TrF3Ha21 : AC-TNCAAA-CCA-AA-CGAG-CCGTTTCCCTNCTNNAACATGGCACCAGCCAAACTCTA : 66
TrF3Ha22 : AC-TNCAAA-CCA-AA-CGAGNCCGTTTCCCT-CTC-AACATGGCACCAAGCCAAACTCTA : 62
TrF3Ha23 : AC-CAAAAC-CCA-AA-CGAG-CCGTTTCCCT-CTN-AACATGGCACCAAGCCAAACTCTA : 60
TrF3Ha24 : AC-CAAAAC-CCA-AA-CGAG-CCGTTTCCCT-NTC-AACATGGCACCAAGCCAAACTCTA : 58
TrF3Ha25 : AC-CAAAACCA-AA-CGAGNCCGTTTCCCT-NTC-AACATGGCACCAAGCCAAACTCTA : 59
TrF3Ha26 : AC-CAAAAC-ACCAAAA-CGAG-CCGTTTCC-----ATCAACATGGCACCAAGCCAAACCTA : 59
TrF3Ha27 : AC-TNCAAA-CCA-AA-CGAG-CCGTTTCC-TNCTCNAACATGGCACCAAGCCAAACTCTA : 62
TrF3Ha28 : AC-TNCAAAACCA-AA-CGAGNCCGTTTCCCTNNTCNAACATGGCACCAAGCCAAACTCTA : 62
TrF3Ha29 : ACCA AAAACAG-AGN-CCGTTTCN-TNNTN-----A--A-CATGGC-CC-AGCCAAACTCTA : 51
TrF3Ha30 : A-CAAAAC-T-NAAACCGAGACCGTTTCCCT-NT-NAACATGGCACCAAGCCAAACTCTA : 55
TrF3Ha31 : -GCNNAAAACACCA-AA-CGAG-CCGTTTCCCTNNTCGAACATGGCACCAAGCCAAACTCTA : 59
TrF3Ha32 : -CAAAAC-CCA-AA-CGAG-CCGTTTCCCT-NTC-AACATGGCACCAAGCCAAACTCTA : 56
TrF3Ha33 : -----CAAAC-C-AAAACNGAGNCCGTTTCCCTA-TN-AACATGGCACCAAGCCAAACTCTA : 52
TrF3Ha34 : -----NAAAC-C-AAAACG-AGNCCGTTTCC-TNCTC-AACATGGCTCCTAGCCAAACTCTA : 51
TrF3Ha35 : -----CAACCAAAACNGAG-CCGTTTTCNNNTNNAACATGGCACCAGCCAAACCTA : 54
TrF3Ha36 : -----A-CACAAAC-AGAGNCCGTTTCC-TNNTNNAACATGGCACCAGCCAAACTCTA : 53
TrF3Ha37 : -----AACCAAA-CCGAGNCCGTTTCCNNNTNNAACATGGCACCAGCCAAACCTA : 52
TrF3Ha38 : -----AACCAAAACGAGNCCGTTTTCNNNTNNAACATGGCACCAGCCAAACCTA : 52
TrF3Ha39 : ----- : 1
TrF3Ha40 : ----- : -
TrF3Ha41 : ----- : -

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FIGURE 75 (cont)

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		*	140	*	160	*	180	
TrF3Ha1	:	AGTTATCTCTCACAACAAAA	CACTCTC	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	173		
TrF3Ha2	:	AGTTATCTCTCACAACAAAA	GACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	166			
TrF3Ha3	:	AGTTATCTCTCACAACAAAA	CACTCTC	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	179		
TrF3Ha4	:	AGTTATCTCTCACAACAAAA	CACTCTC	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	178		
TrF3Ha5	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	138		
TrF3Ha6	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	131		
TrF3Ha7	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	133		
TrF3Ha8	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	132		
TrF3Ha9	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	130		
TrF3Ha10	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	133		
TrF3Ha11	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	126		
TrF3Ha12	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	116		
TrF3Ha13	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	124		
TrF3Ha14	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	129		
TrF3Ha15	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	131		
TrF3Ha16	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	127		
TrF3Ha17	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	129		
TrF3Ha18	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	128		
TrF3Ha19	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	120		
TrF3Ha20	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	126		
TrF3Ha21	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	126		
TrF3Ha22	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	122		
TrF3Ha23	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	119		
TrF3Ha24	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	117		
TrF3Ha25	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	118		
TrF3Ha26	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	119		
TrF3Ha27	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	122		
TrF3Ha28	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	122		
TrF3Ha29	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	110		
TrF3Ha30	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	115		
TrF3Ha31	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	119		
TrF3Ha32	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	116		
TrF3Ha33	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	112		
TrF3Ha34	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	109		
TrF3Ha35	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	114		
TrF3Ha36	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	113		
TrF3Ha37	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	112		
TrF3Ha38	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	112		
TrF3Ha39	:	AGTTATCTCTCACAACAAAA	CACTCTT	GAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT	:	61		
TrF3Ha40	:	-----	-----	-----	:	-		
TrF3Ha41	:	-----	-----	-----	:	-		

FIGURE 75 (cont)

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	*	200	*	220	*	240	
TrF3Ha1	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 233
TrF3Ha2	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 226
TrF3Ha3	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 239
TrF3Ha4	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 238
TrF3Ha5	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 198
TrF3Ha6	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 191
TrF3Ha7	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 193
TrF3Ha8	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 192
TrF3Ha9	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 190
TrF3Ha10	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 193
TrF3Ha11	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 186
TrF3Ha12	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 176
TrF3Ha13	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 184
TrF3Ha14	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 189
TrF3Ha15	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 191
TrF3Ha16	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 187
TrF3Ha17	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 189
TrF3Ha18	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 188
TrF3Ha19	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 180
TrF3Ha20	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 186
TrF3Ha21	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 186
TrF3Ha22	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 182
TrF3Ha23	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 179
TrF3Ha24	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 177
TrF3Ha25	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 178
TrF3Ha26	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 179
TrF3Ha27	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 182
TrF3Ha28	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 182
TrF3Ha29	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 170
TrF3Ha30	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 175
TrF3Ha31	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 179
TrF3Ha32	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 176
TrF3Ha33	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 172
TrF3Ha34	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 169
TrF3Ha35	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 174
TrF3Ha36	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 173
TrF3Ha37	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 172
TrF3Ha38	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 172
TrF3Ha39	:	CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCCTCTTGCTGGAATT	:				: 121
TrF3Ha40	:	-----	:				: -
TrF3Ha41	:	-----	:				: -

FIGURE 75 (cont)

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	*	260	*	280	*	300	
TrF3Ha1	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	293			
TrF3Ha2	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	286			
TrF3Ha3	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	299			
TrF3Ha4	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	298			
TrF3Ha5	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	258			
TrF3Ha6	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	251			
TrF3Ha7	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	253			
TrF3Ha8	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	252			
TrF3Ha9	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	250			
TrF3Ha10	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	253			
TrF3Ha11	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	246			
TrF3Ha12	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	236			
TrF3Ha13	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	244			
TrF3Ha14	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	249			
TrF3Ha15	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	251			
TrF3Ha16	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	247			
TrF3Ha17	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	249			
TrF3Ha18	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	236			
TrF3Ha19	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	240			
TrF3Ha20	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	246			
TrF3Ha21	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	246			
TrF3Ha22	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	242			
TrF3Ha23	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	239			
TrF3Ha24	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	237			
TrF3Ha25	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	238			
TrF3Ha26	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	239			
TrF3Ha27	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	242			
TrF3Ha28	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	242			
TrF3Ha29	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	230			
TrF3Ha30	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	235			
TrF3Ha31	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	239			
TrF3Ha32	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	236			
TrF3Ha33	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	232			
TrF3Ha34	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	229			
TrF3Ha35	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	234			
TrF3Ha36	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	233			
TrF3Ha37	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	232			
TrF3Ha38	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	232			
TrF3Ha39	:	GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT	:	181			
TrF3Ha40	:	-----GTAACAGATTGTTG-ANCTTGTGAGNAT	:	28			
TrF3Ha41	:	-----	:	-			

FIGURE 75 (cont)

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*          320          *          340          *          360
TrF3Ha1 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 353
TrF3Ha2 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 346
TrF3Ha3 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 359
TrF3Ha4 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 358
TrF3Ha5 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 318
TrF3Ha6 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 311
TrF3Ha7 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 313
TrF3Ha8 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 312
TrF3Ha9 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 309
TrF3Ha10 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 267
TrF3Ha11 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 306
TrF3Ha12 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 296
TrF3Ha13 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 304
TrF3Ha14 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 309
TrF3Ha15 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 311
TrF3Ha16 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 307
TrF3Ha17 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 309
TrF3Ha18 : ----- : -
TrF3Ha19 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 273
TrF3Ha20 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 306
TrF3Ha21 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 306
TrF3Ha22 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 302
TrF3Ha23 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 299
TrF3Ha24 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 297
TrF3Ha25 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 298
TrF3Ha26 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 299
TrF3Ha27 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 302
TrF3Ha28 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 302
TrF3Ha29 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 290
TrF3Ha30 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 295
TrF3Ha31 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 299
TrF3Ha32 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 296
TrF3Ha33 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 292
TrF3Ha34 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 289
TrF3Ha35 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 294
TrF3Ha36 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 293
TrF3Ha37 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 292
TrF3Ha38 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 292
TrF3Ha39 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 241
TrF3Ha40 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACCTGTTTCTGAGATGACC : 88
TrF3Ha41 : ----- : -

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FIGURE 75 (cont)

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	*	380	*	400	*	420	
TrF3Ha1	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 413
TrF3Ha2	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 406
TrF3Ha3	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 419
TrF3Ha4	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 418
TrF3Ha5	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 378
TrF3Ha6	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 371
TrF3Ha7	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 373
TrF3Ha8	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 372
TrF3Ha9	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 369
TrF3Ha10	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: -
TrF3Ha11	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 366
TrF3Ha12	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 356
TrF3Ha13	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 364
TrF3Ha14	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 369
TrF3Ha15	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 371
TrF3Ha16	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 367
TrF3Ha17	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 369
TrF3Ha18	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: -
TrF3Ha19	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: -
TrF3Ha20	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 366
TrF3Ha21	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 366
TrF3Ha22	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 362
TrF3Ha23	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 359
TrF3Ha24	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 357
TrF3Ha25	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 358
TrF3Ha26	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 359
TrF3Ha27	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 362
TrF3Ha28	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 362
TrF3Ha29	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 350
TrF3Ha30	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 355
TrF3Ha31	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 359
TrF3Ha32	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 356
TrF3Ha33	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 352
TrF3Ha34	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 349
TrF3Ha35	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 354
TrF3Ha36	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 353
TrF3Ha37	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 352
TrF3Ha38	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 352
TrF3Ha39	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 301
TrF3Ha40	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: 148
TrF3Ha41	:	CGTTTTGCTAGAGAGTTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC	:				: -

FIGURE 75 (cont)

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      *           440           *           460           *           480
TrF3Ha1 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT : 473
TrF3Ha2 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 466
TrF3Ha3 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT : 479
TrF3Ha4 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 478
TrF3Ha5 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 438
TrF3Ha6 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 431
TrF3Ha7 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 433
TrF3Ha8 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 432
TrF3Ha9 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 428
TrF3Ha10 : ----- : -
TrF3Ha11 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT : 426
TrF3Ha12 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 416
TrF3Ha13 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTNCAAGGAGAAGCAGTGAAGGAT : 424
TrF3Ha14 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 429
TrF3Ha15 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 431
TrF3Ha16 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 427
TrF3Ha17 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT : 429
TrF3Ha18 : ----- : -
TrF3Ha19 : ----- : -
TrF3Ha20 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 426
TrF3Ha21 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 426
TrF3Ha22 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 422
TrF3Ha23 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 419
TrF3Ha24 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 417
TrF3Ha25 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 418
TrF3Ha26 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 419
TrF3Ha27 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 422
TrF3Ha28 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT : 422
TrF3Ha29 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 410
TrF3Ha30 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 415
TrF3Ha31 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 419
TrF3Ha32 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 416
TrF3Ha33 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT : 412
TrF3Ha34 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTNCAAGGAGAAGCAGTGAAGGAT : 409
TrF3Ha35 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 414
TrF3Ha36 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 413
TrF3Ha37 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 412
TrF3Ha38 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 412
TrF3Ha39 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTNNTCATCTCCAAGGAGAAGCAGTGAAGGAT : 361
TrF3Ha40 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 208
TrF3Ha41 : ----- : -

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FIGURE 75 (cont)

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	*	500	*	520	*	540	
TrF3Ha1	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	533			
TrF3Ha2	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	526			
TrF3Ha3	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	539			
TrF3Ha4	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	492			
TrF3Ha5	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	498			
TrF3Ha6	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	491			
TrF3Ha7	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	493			
TrF3Ha8	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	492			
TrF3Ha9	:	ANNNAAG-CNT-TGGGAANNNCNNNN	:	453			
TrF3Ha10	:		:	-			
TrF3Ha11	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	486			
TrF3Ha12	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	476			
TrF3Ha13	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	450			
TrF3Ha14	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	489			
TrF3Ha15	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	491			
TrF3Ha16	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	487			
TrF3Ha17	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	489			
TrF3Ha18	:		:	-			
TrF3Ha19	:		:	-			
TrF3Ha20	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	486			
TrF3Ha21	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	486			
TrF3Ha22	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	482			
TrF3Ha23	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	479			
TrF3Ha24	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	477			
TrF3Ha25	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	478			
TrF3Ha26	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	479			
TrF3Ha27	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	482			
TrF3Ha28	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	482			
TrF3Ha29	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	470			
TrF3Ha30	:	TG	:	418			
TrF3Ha31	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	479			
TrF3Ha32	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	476			
TrF3Ha33	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	472			
TrF3Ha34	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	469			
TrF3Ha35	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	474			
TrF3Ha36	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	473			
TrF3Ha37	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	472			
TrF3Ha38	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	472			
TrF3Ha39	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	421			
TrF3Ha40	:	TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG	:	268			
TrF3Ha41	:		:	-			

FIGURE 75 (cont)

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	*	560	*	580	*	600	
TrF3Ha1	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCT	-----				: 586
TrF3Ha2	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 586
TrF3Ha3	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 599
TrF3Ha4	:	-----					: -
TrF3Ha5	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 558
TrF3Ha6	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 551
TrF3Ha7	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 553
TrF3Ha8	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 552
TrF3Ha9	:	-----					: -
TrF3Ha10	:	-----					: -
TrF3Ha11	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 546
TrF3Ha12	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 536
TrF3Ha13	:	-----					: -
TrF3Ha14	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 549
TrF3Ha15	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 551
TrF3Ha16	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 547
TrF3Ha17	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 549
TrF3Ha18	:	-----					: -
TrF3Ha19	:	-----					: -
TrF3Ha20	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 546
TrF3Ha21	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 546
TrF3Ha22	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 542
TrF3Ha23	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 539
TrF3Ha24	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 535
TrF3Ha25	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 538
TrF3Ha26	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 539
TrF3Ha27	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 542
TrF3Ha28	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 542
TrF3Ha29	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 530
TrF3Ha30	:	-----					: -
TrF3Ha31	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 539
TrF3Ha32	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 536
TrF3Ha33	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 532
TrF3Ha34	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 529
TrF3Ha35	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 534
TrF3Ha36	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 533
TrF3Ha37	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 532
TrF3Ha38	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 532
TrF3Ha39	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 481
TrF3Ha40	:	CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT					: 328
TrF3Ha41	:	-----					: -

FIGURE 75 (cont)

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	*	620	*	640	*	660		
TrF3Ha1	:	-----					:	-
TrF3Ha2	:	TTAGCTTGCAG-----					:	597
TrF3Ha3	:	TTAGCT-----					:	605
TrF3Ha4	:	-----					:	-
TrF3Ha5	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA					:	618
TrF3Ha6	:	TTAGCTTGCAAACCTATTGGAAG-----					:	573
TrF3Ha7	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA					:	613
TrF3Ha8	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA					:	612
TrF3Ha9	:	-----					:	-
TrF3Ha10	:	-----					:	-
TrF3Ha11	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAG-----					:	580
TrF3Ha12	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGATTAGAAAN-----					:	586
TrF3Ha13	:	-----					:	-
TrF3Ha14	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA					:	609
TrF3Ha15	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAG-----					:	582
TrF3Ha16	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA					:	607
TrF3Ha17	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTN-----					:	593
TrF3Ha18	:	-----					:	-
TrF3Ha19	:	-----					:	-
TrF3Ha20	:	TTAGCTTGCAAACCTATTGGAAGTTT-----					:	572
TrF3Ha21	:	TTAGCTTGCAAACCTATTGGAAGTTTATC-----					:	575
TrF3Ha22	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAC-----					:	596
TrF3Ha23	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA					:	599
TrF3Ha24	:	-----					:	-
TrF3Ha25	:	TTAGCTTGCAAACCTATTGGAN-----					:	559
TrF3Ha26	:	TTAGCTTGCAAACCTATTGGAAGTTT-----					:	565
TrF3Ha27	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAN-----					:	591
TrF3Ha28	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA					:	602
TrF3Ha29	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA					:	590
TrF3Ha30	:	-----					:	-
TrF3Ha31	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAG-----					:	570
TrF3Ha32	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA					:	596
TrF3Ha33	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGCAAGCAN-----					:	592
TrF3Ha34	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGCAAGCAN-----					:	536
TrF3Ha35	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAAT-----					:	572
TrF3Ha36	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGG-----					:	573
TrF3Ha37	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGG-----					:	573
TrF3Ha38	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAG-----					:	584
TrF3Ha39	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGCAAGCAATGGGTTTAGAAG-----					:	529
TrF3Ha40	:	TTAGCTTGCAAACCTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA					:	388
TrF3Ha41	:	-----					:	-

FIGURE 75 (cont)

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		*	680	*	700	*	720	
TrF3Ha1	:	-----		-----		-----		:
TrF3Ha2	:	-----		-----		-----		:
TrF3Ha3	:	-----		-----		-----		:
TrF3Ha4	:	-----		-----		-----		:
TrF3Ha5	:	ACAAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT						: 678
TrF3Ha6	:	-----		-----		-----		:
TrF3Ha7	:	ACAAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT						: 673
TrF3Ha8	:	ACAAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT						: 672
TrF3Ha9	:	-----		-----		-----		:
TrF3Ha10	:	-----		-----		-----		:
TrF3Ha11	:	-----		-----		-----		:
TrF3Ha12	:	-----		-----		-----		:
TrF3Ha13	:	-----		-----		-----		:
TrF3Ha14	:	ACAAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT						: 669
TrF3Ha15	:	-----		-----		-----		:
TrF3Ha16	:	ACA-----		-----		-----		: 610
TrF3Ha17	:	-----		-----		-----		:
TrF3Ha18	:	-----		-----		-----		:
TrF3Ha19	:	-----		-----		-----		:
TrF3Ha20	:	-----		-----		-----		:
TrF3Ha21	:	-----		-----		-----		:
TrF3Ha22	:	-----		-----		-----		:
TrF3Ha23	:	ACAAAAGCATGTG-----		-----		-----		: 612
TrF3Ha24	:	-----		-----		-----		:
TrF3Ha25	:	-----		-----		-----		:
TrF3Ha26	:	-----		-----		-----		:
TrF3Ha27	:	-----		-----		-----		:
TrF3Ha28	:	ACAAAAG-----		-----		-----		: 609
TrF3Ha29	:	ACAAAAG-----		-----		-----		: 597
TrF3Ha30	:	-----		-----		-----		:
TrF3Ha31	:	-----		-----		-----		:
TrF3Ha32	:	ACAAAAGCATGT-----		-----		-----		: 608
TrF3Ha33	:	ACAAANANCNT-----		-----		-----		: 602
TrF3Ha34	:	-----		-----		-----		:
TrF3Ha35	:	-----		-----		-----		:
TrF3Ha36	:	-----		-----		-----		:
TrF3Ha37	:	-----		-----		-----		:
TrF3Ha38	:	-----		-----		-----		:
TrF3Ha39	:	-----		-----		-----		:
TrF3Ha40	:	ACAAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT						: 448
TrF3Ha41	:	-----ATCMAAAAAGTTGTTATAAATTATTACCCMAAATGCCCT						: 38

FIGURE 75 (cont)

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	*	740	*	760	*	780	
TrF3Ha1	:	-----		-----		-----	:
TrF3Ha2	:	-----		-----		-----	:
TrF3Ha3	:	-----		-----		-----	:
TrF3Ha4	:	-----		-----		-----	:
TrF3Ha5	:	GAACCTGACCTT		-----		-----	: 690
TrF3Ha6	:	-----		-----		-----	:
TrF3Ha7	:	GAACCTGACCTCCCACTT		GCCGTAAACGNCACACTGACCCNGA		-----	: 716
TrF3Ha8	:	GAACCTGACCTCACACTTGGCCTTAAACGTCACACTGACCCTGGCACAN		-----		-----	: 721
TrF3Ha9	:	-----		-----		-----	:
TrF3Ha10	:	-----		-----		-----	:
TrF3Ha11	:	-----		-----		-----	:
TrF3Ha12	:	-----		-----		-----	:
TrF3Ha13	:	-----		-----		-----	:
TrF3Ha14	:	GAACCTGACCTC		-----		-----	: 681
TrF3Ha15	:	-----		-----		-----	:
TrF3Ha16	:	-----		-----		-----	:
TrF3Ha17	:	-----		-----		-----	:
TrF3Ha18	:	-----		-----		-----	:
TrF3Ha19	:	-----		-----		-----	:
TrF3Ha20	:	-----		-----		-----	:
TrF3Ha21	:	-----		-----		-----	:
TrF3Ha22	:	-----		-----		-----	:
TrF3Ha23	:	-----		-----		-----	:
TrF3Ha24	:	-----		-----		-----	:
TrF3Ha25	:	-----		-----		-----	:
TrF3Ha26	:	-----		-----		-----	:
TrF3Ha27	:	-----		-----		-----	:
TrF3Ha28	:	-----		-----		-----	:
TrF3Ha29	:	-----		-----		-----	:
TrF3Ha30	:	-----		-----		-----	:
TrF3Ha31	:	-----		-----		-----	:
TrF3Ha32	:	-----		-----		-----	:
TrF3Ha33	:	-----		-----		-----	:
TrF3Ha34	:	-----		-----		-----	:
TrF3Ha35	:	-----		-----		-----	:
TrF3Ha36	:	-----		-----		-----	:
TrF3Ha37	:	-----		-----		-----	:
TrF3Ha38	:	-----		-----		-----	:
TrF3Ha39	:	-----		-----		-----	:
TrF3Ha40	:	GAACCTGACCTCACACTTGGCCTTAAACGTCACACTGACCCTGGCACAATTACTCTTTTG		-----		-----	: 508
TrF3Ha41	:	GAACCTGACCTCACACTTGGCCTTAAACGTCACACTGACCCTGGCACAATTACTCTTTTG		-----		-----	: 98

FIGURE 75 (cont)

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	*	800	*	820	*	840	
TrF3Ha1	:	-----	:	-----	:	-----	:
TrF3Ha2	:	-----	:	-----	:	-----	:
TrF3Ha3	:	-----	:	-----	:	-----	:
TrF3Ha4	:	-----	:	-----	:	-----	:
TrF3Ha5	:	-----	:	-----	:	-----	:
TrF3Ha6	:	-----	:	-----	:	-----	:
TrF3Ha7	:	-----	:	-----	:	-----	:
TrF3Ha8	:	-----	:	-----	:	-----	:
TrF3Ha9	:	-----	:	-----	:	-----	:
TrF3Ha10	:	-----	:	-----	:	-----	:
TrF3Ha11	:	-----	:	-----	:	-----	:
TrF3Ha12	:	-----	:	-----	:	-----	:
TrF3Ha13	:	-----	:	-----	:	-----	:
TrF3Ha14	:	-----	:	-----	:	-----	:
TrF3Ha15	:	-----	:	-----	:	-----	:
TrF3Ha16	:	-----	:	-----	:	-----	:
TrF3Ha17	:	-----	:	-----	:	-----	:
TrF3Ha18	:	-----	:	-----	:	-----	:
TrF3Ha19	:	-----	:	-----	:	-----	:
TrF3Ha20	:	-----	:	-----	:	-----	:
TrF3Ha21	:	-----	:	-----	:	-----	:
TrF3Ha22	:	-----	:	-----	:	-----	:
TrF3Ha23	:	-----	:	-----	:	-----	:
TrF3Ha24	:	-----	:	-----	:	-----	:
TrF3Ha25	:	-----	:	-----	:	-----	:
TrF3Ha26	:	-----	:	-----	:	-----	:
TrF3Ha27	:	-----	:	-----	:	-----	:
TrF3Ha28	:	-----	:	-----	:	-----	:
TrF3Ha29	:	-----	:	-----	:	-----	:
TrF3Ha30	:	-----	:	-----	:	-----	:
TrF3Ha31	:	-----	:	-----	:	-----	:
TrF3Ha32	:	-----	:	-----	:	-----	:
TrF3Ha33	:	-----	:	-----	:	-----	:
TrF3Ha34	:	-----	:	-----	:	-----	:
TrF3Ha35	:	-----	:	-----	:	-----	:
TrF3Ha36	:	-----	:	-----	:	-----	:
TrF3Ha37	:	-----	:	-----	:	-----	:
TrF3Ha38	:	-----	:	-----	:	-----	:
TrF3Ha39	:	-----	:	-----	:	-----	:
TrF3Ha40	:	CTTCAAGATCAAGTTGGTGGG	:	CTTCAAGCTACCAAAGATAATGGTAAGACGTGGATTACA	:		: 568
TrF3Ha41	:	CTTCAAGATCAAGTTGGTGGCCTTCAAGCTACCAAAGATAATGGTAAGACGTGGATTACA	:		:		: 158

FIGURE 75 (cont)

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	*	860	*	880	*	900	
TrF3Ha1	:	-----	-----	-----	-----	-----	:
TrF3Ha2	:	-----	-----	-----	-----	-----	:
TrF3Ha3	:	-----	-----	-----	-----	-----	:
TrF3Ha4	:	-----	-----	-----	-----	-----	:
TrF3Ha5	:	-----	-----	-----	-----	-----	:
TrF3Ha6	:	-----	-----	-----	-----	-----	:
TrF3Ha7	:	-----	-----	-----	-----	-----	:
TrF3Ha8	:	-----	-----	-----	-----	-----	:
TrF3Ha9	:	-----	-----	-----	-----	-----	:
TrF3Ha10	:	-----	-----	-----	-----	-----	:
TrF3Ha11	:	-----	-----	-----	-----	-----	:
TrF3Ha12	:	-----	-----	-----	-----	-----	:
TrF3Ha13	:	-----	-----	-----	-----	-----	:
TrF3Ha14	:	-----	-----	-----	-----	-----	:
TrF3Ha15	:	-----	-----	-----	-----	-----	:
TrF3Ha16	:	-----	-----	-----	-----	-----	:
TrF3Ha17	:	-----	-----	-----	-----	-----	:
TrF3Ha18	:	-----	-----	-----	-----	-----	:
TrF3Ha19	:	-----	-----	-----	-----	-----	:
TrF3Ha20	:	-----	-----	-----	-----	-----	:
TrF3Ha21	:	-----	-----	-----	-----	-----	:
TrF3Ha22	:	-----	-----	-----	-----	-----	:
TrF3Ha23	:	-----	-----	-----	-----	-----	:
TrF3Ha24	:	-----	-----	-----	-----	-----	:
TrF3Ha25	:	-----	-----	-----	-----	-----	:
TrF3Ha26	:	-----	-----	-----	-----	-----	:
TrF3Ha27	:	-----	-----	-----	-----	-----	:
TrF3Ha28	:	-----	-----	-----	-----	-----	:
TrF3Ha29	:	-----	-----	-----	-----	-----	:
TrF3Ha30	:	-----	-----	-----	-----	-----	:
TrF3Ha31	:	-----	-----	-----	-----	-----	:
TrF3Ha32	:	-----	-----	-----	-----	-----	:
TrF3Ha33	:	-----	-----	-----	-----	-----	:
TrF3Ha34	:	-----	-----	-----	-----	-----	:
TrF3Ha35	:	-----	-----	-----	-----	-----	:
TrF3Ha36	:	-----	-----	-----	-----	-----	:
TrF3Ha37	:	-----	-----	-----	-----	-----	:
TrF3Ha38	:	-----	-----	-----	-----	-----	:
TrF3Ha39	:	-----	-----	-----	-----	-----	:
TrF3Ha40	:	GTTCAACCAGTTGAAGGTGCTTTTGTGTTAATCTTGGAGACCATGGTCACTATCTAAGT					: 628
TrF3Ha41	:	GTTCAACCAGTTGAAGGTGCTTTTGTGTTAATCTTGGAGACCATGGTCACTATCTAAGT					: 218

FIGURE 75 (cont)

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	*	920	*	940	*	960	
TrF3Ha1	:	-----	-----	-----	-----	-----	:
TrF3Ha2	:	-----	-----	-----	-----	-----	:
TrF3Ha3	:	-----	-----	-----	-----	-----	:
TrF3Ha4	:	-----	-----	-----	-----	-----	:
TrF3Ha5	:	-----	-----	-----	-----	-----	:
TrF3Ha6	:	-----	-----	-----	-----	-----	:
TrF3Ha7	:	-----	-----	-----	-----	-----	:
TrF3Ha8	:	-----	-----	-----	-----	-----	:
TrF3Ha9	:	-----	-----	-----	-----	-----	:
TrF3Ha10	:	-----	-----	-----	-----	-----	:
TrF3Ha11	:	-----	-----	-----	-----	-----	:
TrF3Ha12	:	-----	-----	-----	-----	-----	:
TrF3Ha13	:	-----	-----	-----	-----	-----	:
TrF3Ha14	:	-----	-----	-----	-----	-----	:
TrF3Ha15	:	-----	-----	-----	-----	-----	:
TrF3Ha16	:	-----	-----	-----	-----	-----	:
TrF3Ha17	:	-----	-----	-----	-----	-----	:
TrF3Ha18	:	-----	-----	-----	-----	-----	:
TrF3Ha19	:	-----	-----	-----	-----	-----	:
TrF3Ha20	:	-----	-----	-----	-----	-----	:
TrF3Ha21	:	-----	-----	-----	-----	-----	:
TrF3Ha22	:	-----	-----	-----	-----	-----	:
TrF3Ha23	:	-----	-----	-----	-----	-----	:
TrF3Ha24	:	-----	-----	-----	-----	-----	:
TrF3Ha25	:	-----	-----	-----	-----	-----	:
TrF3Ha26	:	-----	-----	-----	-----	-----	:
TrF3Ha27	:	-----	-----	-----	-----	-----	:
TrF3Ha28	:	-----	-----	-----	-----	-----	:
TrF3Ha29	:	-----	-----	-----	-----	-----	:
TrF3Ha30	:	-----	-----	-----	-----	-----	:
TrF3Ha31	:	-----	-----	-----	-----	-----	:
TrF3Ha32	:	-----	-----	-----	-----	-----	:
TrF3Ha33	:	-----	-----	-----	-----	-----	:
TrF3Ha34	:	-----	-----	-----	-----	-----	:
TrF3Ha35	:	-----	-----	-----	-----	-----	:
TrF3Ha36	:	-----	-----	-----	-----	-----	:
TrF3Ha37	:	-----	-----	-----	-----	-----	:
TrF3Ha38	:	-----	-----	-----	-----	-----	:
TrF3Ha39	:	-----	-----	-----	-----	-----	:
TrF3Ha40	:	AATGGACGGTTCAAAAATGCTGACCAATCAAGCAGTGCTGAATTTCGAACCTACAGCCGNTTA					: 688
TrF3Ha41	:	AATGGACGGTTCAAAAATGCTGACCACCAAGCAGTGCTGAATTTCGAACCTACAGCCGTTTA					: 278

FIGURE 75 (cont)

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	*	980	*	1000	*	1020	
TrF3Ha1	:	-----		-----		-----	:
TrF3Ha2	:	-----		-----		-----	:
TrF3Ha3	:	-----		-----		-----	:
TrF3Ha4	:	-----		-----		-----	:
TrF3Ha5	:	-----		-----		-----	:
TrF3Ha6	:	-----		-----		-----	:
TrF3Ha7	:	-----		-----		-----	:
TrF3Ha8	:	-----		-----		-----	:
TrF3Ha9	:	-----		-----		-----	:
TrF3Ha10	:	-----		-----		-----	:
TrF3Ha11	:	-----		-----		-----	:
TrF3Ha12	:	-----		-----		-----	:
TrF3Ha13	:	-----		-----		-----	:
TrF3Ha14	:	-----		-----		-----	:
TrF3Ha15	:	-----		-----		-----	:
TrF3Ha16	:	-----		-----		-----	:
TrF3Ha17	:	-----		-----		-----	:
TrF3Ha18	:	-----		-----		-----	:
TrF3Ha19	:	-----		-----		-----	:
TrF3Ha20	:	-----		-----		-----	:
TrF3Ha21	:	-----		-----		-----	:
TrF3Ha22	:	-----		-----		-----	:
TrF3Ha23	:	-----		-----		-----	:
TrF3Ha24	:	-----		-----		-----	:
TrF3Ha25	:	-----		-----		-----	:
TrF3Ha26	:	-----		-----		-----	:
TrF3Ha27	:	-----		-----		-----	:
TrF3Ha28	:	-----		-----		-----	:
TrF3Ha29	:	-----		-----		-----	:
TrF3Ha30	:	-----		-----		-----	:
TrF3Ha31	:	-----		-----		-----	:
TrF3Ha32	:	-----		-----		-----	:
TrF3Ha33	:	-----		-----		-----	:
TrF3Ha34	:	-----		-----		-----	:
TrF3Ha35	:	-----		-----		-----	:
TrF3Ha36	:	-----		-----		-----	:
TrF3Ha37	:	-----		-----		-----	:
TrF3Ha38	:	-----		-----		-----	:
TrF3Ha39	:	-----		-----		-----	:
TrF3Ha40	:	TCAATAGCAA		-----		-----	: 698
TrF3Ha41	:	TCAATAGCAACATTTCAAAATCCAGCTCCCGATGCCAACTGTATACCCTTTGAAGATTAGA		-----		-----	: 338

FIGURE 75 (cont)

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	*	1040	*	1060	*	1080	
TrF3Ha1	:	-----		-----		-----	:
TrF3Ha2	:	-----		-----		-----	:
TrF3Ha3	:	-----		-----		-----	:
TrF3Ha4	:	-----		-----		-----	:
TrF3Ha5	:	-----		-----		-----	:
TrF3Ha6	:	-----		-----		-----	:
TrF3Ha7	:	-----		-----		-----	:
TrF3Ha8	:	-----		-----		-----	:
TrF3Ha9	:	-----		-----		-----	:
TrF3Ha10	:	-----		-----		-----	:
TrF3Ha11	:	-----		-----		-----	:
TrF3Ha12	:	-----		-----		-----	:
TrF3Ha13	:	-----		-----		-----	:
TrF3Ha14	:	-----		-----		-----	:
TrF3Ha15	:	-----		-----		-----	:
TrF3Ha16	:	-----		-----		-----	:
TrF3Ha17	:	-----		-----		-----	:
TrF3Ha18	:	-----		-----		-----	:
TrF3Ha19	:	-----		-----		-----	:
TrF3Ha20	:	-----		-----		-----	:
TrF3Ha21	:	-----		-----		-----	:
TrF3Ha22	:	-----		-----		-----	:
TrF3Ha23	:	-----		-----		-----	:
TrF3Ha24	:	-----		-----		-----	:
TrF3Ha25	:	-----		-----		-----	:
TrF3Ha26	:	-----		-----		-----	:
TrF3Ha27	:	-----		-----		-----	:
TrF3Ha28	:	-----		-----		-----	:
TrF3Ha29	:	-----		-----		-----	:
TrF3Ha30	:	-----		-----		-----	:
TrF3Ha31	:	-----		-----		-----	:
TrF3Ha32	:	-----		-----		-----	:
TrF3Ha33	:	-----		-----		-----	:
TrF3Ha34	:	-----		-----		-----	:
TrF3Ha35	:	-----		-----		-----	:
TrF3Ha36	:	-----		-----		-----	:
TrF3Ha37	:	-----		-----		-----	:
TrF3Ha38	:	-----		-----		-----	:
TrF3Ha39	:	-----		-----		-----	:
TrF3Ha40	:	-----		-----		-----	:
TrF3Ha41	:	GAGGGTGAAAAATCTGTGTTGGAAGAACCAATCACTTTTGCTGAAATGTATAGAAGGAAG					: 398

FIGURE 75 (cont)

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		*	1100	*	1120	*	1140	
TrF3Ha1	:	-----		-----		-----		:
TrF3Ha2	:	-----		-----		-----		:
TrF3Ha3	:	-----		-----		-----		:
TrF3Ha4	:	-----		-----		-----		:
TrF3Ha5	:	-----		-----		-----		:
TrF3Ha6	:	-----		-----		-----		:
TrF3Ha7	:	-----		-----		-----		:
TrF3Ha8	:	-----		-----		-----		:
TrF3Ha9	:	-----		-----		-----		:
TrF3Ha10	:	-----		-----		-----		:
TrF3Ha11	:	-----		-----		-----		:
TrF3Ha12	:	-----		-----		-----		:
TrF3Ha13	:	-----		-----		-----		:
TrF3Ha14	:	-----		-----		-----		:
TrF3Ha15	:	-----		-----		-----		:
TrF3Ha16	:	-----		-----		-----		:
TrF3Ha17	:	-----		-----		-----		:
TrF3Ha18	:	-----		-----		-----		:
TrF3Ha19	:	-----		-----		-----		:
TrF3Ha20	:	-----		-----		-----		:
TrF3Ha21	:	-----		-----		-----		:
TrF3Ha22	:	-----		-----		-----		:
TrF3Ha23	:	-----		-----		-----		:
TrF3Ha24	:	-----		-----		-----		:
TrF3Ha25	:	-----		-----		-----		:
TrF3Ha26	:	-----		-----		-----		:
TrF3Ha27	:	-----		-----		-----		:
TrF3Ha28	:	-----		-----		-----		:
TrF3Ha29	:	-----		-----		-----		:
TrF3Ha30	:	-----		-----		-----		:
TrF3Ha31	:	-----		-----		-----		:
TrF3Ha32	:	-----		-----		-----		:
TrF3Ha33	:	-----		-----		-----		:
TrF3Ha34	:	-----		-----		-----		:
TrF3Ha35	:	-----		-----		-----		:
TrF3Ha36	:	-----		-----		-----		:
TrF3Ha37	:	-----		-----		-----		:
TrF3Ha38	:	-----		-----		-----		:
TrF3Ha39	:	-----		-----		-----		:
TrF3Ha40	:	-----		-----		-----		:
TrF3Ha41	:	ATGACCAAAGACCTTGAAATTGCTAGGATGAAGAAGTTGGCTAAGGAACAACAACCTTAGG						: 458

FIGURE 75 (cont)

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	*	1160	*	1180	*	1200		
TrF3Ha1	:	-----	-----	-----	-----	-----	:	
TrF3Ha2	:	-----	-----	-----	-----	-----	:	
TrF3Ha3	:	-----	-----	-----	-----	-----	:	
TrF3Ha4	:	-----	-----	-----	-----	-----	:	
TrF3Ha5	:	-----	-----	-----	-----	-----	:	
TrF3Ha6	:	-----	-----	-----	-----	-----	:	
TrF3Ha7	:	-----	-----	-----	-----	-----	:	
TrF3Ha8	:	-----	-----	-----	-----	-----	:	
TrF3Ha9	:	-----	-----	-----	-----	-----	:	
TrF3Ha10	:	-----	-----	-----	-----	-----	:	
TrF3Ha11	:	-----	-----	-----	-----	-----	:	
TrF3Ha12	:	-----	-----	-----	-----	-----	:	
TrF3Ha13	:	-----	-----	-----	-----	-----	:	
TrF3Ha14	:	-----	-----	-----	-----	-----	:	
TrF3Ha15	:	-----	-----	-----	-----	-----	:	
TrF3Ha16	:	-----	-----	-----	-----	-----	:	
TrF3Ha17	:	-----	-----	-----	-----	-----	:	
TrF3Ha18	:	-----	-----	-----	-----	-----	:	
TrF3Ha19	:	-----	-----	-----	-----	-----	:	
TrF3Ha20	:	-----	-----	-----	-----	-----	:	
TrF3Ha21	:	-----	-----	-----	-----	-----	:	
TrF3Ha22	:	-----	-----	-----	-----	-----	:	
TrF3Ha23	:	-----	-----	-----	-----	-----	:	
TrF3Ha24	:	-----	-----	-----	-----	-----	:	
TrF3Ha25	:	-----	-----	-----	-----	-----	:	
TrF3Ha26	:	-----	-----	-----	-----	-----	:	
TrF3Ha27	:	-----	-----	-----	-----	-----	:	
TrF3Ha28	:	-----	-----	-----	-----	-----	:	
TrF3Ha29	:	-----	-----	-----	-----	-----	:	
TrF3Ha30	:	-----	-----	-----	-----	-----	:	
TrF3Ha31	:	-----	-----	-----	-----	-----	:	
TrF3Ha32	:	-----	-----	-----	-----	-----	:	
TrF3Ha33	:	-----	-----	-----	-----	-----	:	
TrF3Ha34	:	-----	-----	-----	-----	-----	:	
TrF3Ha35	:	-----	-----	-----	-----	-----	:	
TrF3Ha36	:	-----	-----	-----	-----	-----	:	
TrF3Ha37	:	-----	-----	-----	-----	-----	:	
TrF3Ha38	:	-----	-----	-----	-----	-----	:	
TrF3Ha39	:	-----	-----	-----	-----	-----	:	
TrF3Ha40	:	-----	-----	-----	-----	-----	:	
TrF3Ha41	:	GACTTGGAGGAGAACAAGACTAAATATGAGGCCAAACCTTTGAATGAGATCTTTGCTTAA					:	518

FIGURE 75 (cont)

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	*	1220	*	1240	*	1260	
TrF3Ha1	:	-----	-----	-----	-----	-----	:
TrF3Ha2	:	-----	-----	-----	-----	-----	:
TrF3Ha3	:	-----	-----	-----	-----	-----	:
TrF3Ha4	:	-----	-----	-----	-----	-----	:
TrF3Ha5	:	-----	-----	-----	-----	-----	:
TrF3Ha6	:	-----	-----	-----	-----	-----	:
TrF3Ha7	:	-----	-----	-----	-----	-----	:
TrF3Ha8	:	-----	-----	-----	-----	-----	:
TrF3Ha9	:	-----	-----	-----	-----	-----	:
TrF3Ha10	:	-----	-----	-----	-----	-----	:
TrF3Ha11	:	-----	-----	-----	-----	-----	:
TrF3Ha12	:	-----	-----	-----	-----	-----	:
TrF3Ha13	:	-----	-----	-----	-----	-----	:
TrF3Ha14	:	-----	-----	-----	-----	-----	:
TrF3Ha15	:	-----	-----	-----	-----	-----	:
TrF3Ha16	:	-----	-----	-----	-----	-----	:
TrF3Ha17	:	-----	-----	-----	-----	-----	:
TrF3Ha18	:	-----	-----	-----	-----	-----	:
TrF3Ha19	:	-----	-----	-----	-----	-----	:
TrF3Ha20	:	-----	-----	-----	-----	-----	:
TrF3Ha21	:	-----	-----	-----	-----	-----	:
TrF3Ha22	:	-----	-----	-----	-----	-----	:
TrF3Ha23	:	-----	-----	-----	-----	-----	:
TrF3Ha24	:	-----	-----	-----	-----	-----	:
TrF3Ha25	:	-----	-----	-----	-----	-----	:
TrF3Ha26	:	-----	-----	-----	-----	-----	:
TrF3Ha27	:	-----	-----	-----	-----	-----	:
TrF3Ha28	:	-----	-----	-----	-----	-----	:
TrF3Ha29	:	-----	-----	-----	-----	-----	:
TrF3Ha30	:	-----	-----	-----	-----	-----	:
TrF3Ha31	:	-----	-----	-----	-----	-----	:
TrF3Ha32	:	-----	-----	-----	-----	-----	:
TrF3Ha33	:	-----	-----	-----	-----	-----	:
TrF3Ha34	:	-----	-----	-----	-----	-----	:
TrF3Ha35	:	-----	-----	-----	-----	-----	:
TrF3Ha36	:	-----	-----	-----	-----	-----	:
TrF3Ha37	:	-----	-----	-----	-----	-----	:
TrF3Ha38	:	-----	-----	-----	-----	-----	:
TrF3Ha39	:	-----	-----	-----	-----	-----	:
TrF3Ha40	:	-----	-----	-----	-----	-----	:
TrF3Ha41	:	TTAATTAGTCTTAATTTAAATAATTAATAAATTTTAGACTTAATTTACATATAATAATTT					: 578

FIGURE 75 (cont)

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TrF3Ha1	:	-	:	-
TrF3Ha2	:	-	:	-
TrF3Ha3	:	-	:	-
TrF3Ha4	:	-	:	-
TrF3Ha5	:	-	:	-
TrF3Ha6	:	-	:	-
TrF3Ha7	:	-	:	-
TrF3Ha8	:	-	:	-
TrF3Ha9	:	-	:	-
TrF3Ha10	:	-	:	-
TrF3Ha11	:	-	:	-
TrF3Ha12	:	-	:	-
TrF3Ha13	:	-	:	-
TrF3Ha14	:	-	:	-
TrF3Ha15	:	-	:	-
TrF3Ha16	:	-	:	-
TrF3Ha17	:	-	:	-
TrF3Ha18	:	-	:	-
TrF3Ha19	:	-	:	-
TrF3Ha20	:	-	:	-
TrF3Ha21	:	-	:	-
TrF3Ha22	:	-	:	-
TrF3Ha23	:	-	:	-
TrF3Ha24	:	-	:	-
TrF3Ha25	:	-	:	-
TrF3Ha26	:	-	:	-
TrF3Ha27	:	-	:	-
TrF3Ha28	:	-	:	-
TrF3Ha29	:	-	:	-
TrF3Ha30	:	-	:	-
TrF3Ha31	:	-	:	-
TrF3Ha32	:	-	:	-
TrF3Ha33	:	-	:	-
TrF3Ha34	:	-	:	-
TrF3Ha35	:	-	:	-
TrF3Ha36	:	-	:	-
TrF3Ha37	:	-	:	-
TrF3Ha38	:	-	:	-
TrF3Ha39	:	-	:	-
TrF3Ha40	:	-	:	-
TrF3Ha41	:		:	579

FIGURE 75 (cont)

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```

      *           20           *           40           *           60
TrF3Hb : GNAGCATAACATAAACCCCTGTNCCCGATTNATGTAACACAATCTCCCCTTTTCTTATTAC : 60

      *           80           *           100          *           120
TrF3Hb : AAGTAAAATACCATAACACAATAATATGAATACCATAATCTTGAATCATACAAACAACCT : 120

      *           140          *           160          *           180
TrF3Hb : TGGATCAAACAAAACAACAACCATGGTTGATCTAGAAACAGAACCAAGTTCACCATTTAT : 180

      *           200          *           220          *           240
TrF3Hb : TCAATCCCCAGAACACAGACCAAAATCCTCAATAATCATTGCTGAAGGTATCCCTCTAAT : 240

      *           260          *           280          *           300
TrF3Hb : TGATCTCACTCCTATAAACTACAAAGATGAAATCATCACCAACCCACTTTCCATTGAAGA : 300

      *           320          *           340          *           360
TrF3Hb : CTTAGTCAAAGAAATAGGCAAAGCATGTAAAGAATGGGGTTTCTTTCAAGTGATTAATCA : 360

      *           380          *           400          *           420
TrF3Hb : CAAAGTTCCTTTTGGATAAACGTGAAAGGATTGAAGAATCTTCAAAGAAGTTTTTTGAACT : 420

      *           440          *           460          *           480
TrF3Hb : TAGTTTGGAGGAAAAACTTAAGGTGAGAAGAGATGAAGTTAATTTGCTTGGTTATTTTGA : 480

      *           500          *           520          *           540
TrF3Hb : AGCTGAGCATACAAAAAATGTTAGGGACTGGAAGGAAATTTATGATTTTAATGTGCAACA : 540

      *           560          *           580          *           600
TrF3Hb : ACCAACTTTTATACCACCTTCGGATGACCAAAGTTTTTCAGTTTCAATGGGAAAATCGATG : 600

TrF3Hb : G : 601

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FIGURE 76

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TrF3Hb : MNTIILNHTNNLGSNKTTTMDLETPSSPFIQSPEHRPKSSIIIAEGIPLIDLTPINYK : 60

TrF3Hb : DEIITNPLSIEDLVKEIGKACKEWGFFQVINHKVPLDKRERIEESSKKFFELSLEEKLV : 120

TrF3Hb : RRDEVNLLGYFEAEHTKNVRDWKEIYDFNVQQPTFIPPSDDQSFQFQWENRW : 172

FIGURE 77

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```

      *           20           *           40           *           60
TrF3Hc : TTACCCAACAATNATGTGTGACTGATGTTAGTGTACCAGGAAAGATGGGAGAGGTGGATC : 60

      *           80           *           100          *           120
TrF3Hc : CAGCTTCTTCAAATCCAGAAAATAGGCCAAAAC TTCCATAATCCAAGCTGAAGGAATT : 120

      *           140          *           160          *           180
TrF3Hc : CCTGTAATCAATCTCTCCCCATTAATTCACCACACAGTTC AAGACTCCTCTGCCATTGAA : 180

      *           200          *           220          *           240
TrF3Hc : AGCTTAGTCAAAGAAATAGGAAATGCTTGCAAGGAATGGGGTTTCTTCCAAGTAACAAAC : 240

      *           260          *           280          *           300
TrF3Hc : CATGGTGTCCCTCTAAATCTAAGGCTCAGACTCGAGGAAGCTACCAAAGTTTTCTTTGCA : 300

      *           320          *           340          *           360
TrF3Hc : CAGAGTTTGGAGGAGAAGAGGAAGCTTACCGTAGATGATAACAGTTTGCCTGGTTATCAT : 360

      *           380          *           400          *           420
TrF3Hc : GATACAGAGCACACCAAGAATGTCAGAGACTGGAAAGAAGTGTTTGATTTTTTATCCAAA : 420

      *           440          *           460          *           480
TrF3Hc : GACCCCACTTTGATTCTCTGAATTCTGATGAACATGATGATCGAGTCACTCAATGGACT : 480

      *           500          *           520          *           540
TrF3Hc : AATCCATCCCCTCAATATCCTCCAAACTTCAAAGTTATTTTGGAAGAGTATATTAAAGAG : 540

      *           560          *           580
TrF3Hc : ATGGAAAAGCTAGGCTTTAAGTTGCTAGAGCTTATAGCTTTGAGC : 585

```

FIGURE 78

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TrF3Hc : MLVYQERWERWIQLSSNPENRPKLSIIQAEGIPVINLSPLIHHTVQDSSAIESLVKEIGN : 60

TrF3Hc : ACKEWGFFQVTNHGVPLNLRRLLEEATKVFFAQSLSEKRLTVDDNSLPGYHDEHTKNV : 120

TrF3Hc : RDWKEVFDFLSKDPTLIPLNSDEHDDRVTQWTNPSPQYPPNFKVILEEYIKEMEKLGFKL : 180

TrF3Hc : LELIALS : 187

FIGURE 79

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```

      *           20           *           40           *           60
TrF3'Ha : GGGAATGGTGGAGGCGAATGTGACCCTAGGGCTGATGAATTAGTAATGGTAGTTGAGCTT : 60

      *           80           *           100          *           120
TrF3'Ha : ATGGCGTTAGCTGGAGTTTTCAATATTGGTGATTTTGTTCCTGCTTTGGAATGGTTAGAT :120

      *           140          *           160          *           180
TrF3'Ha : ATTCAAGGTGTACAAGGAAAAATGAAGAAATTACATAAAAGATTGATGCATTTTAACT :180

      *           200          *           220          *           240
TrF3'Ha : AGCATTATTGAAGATCACATGATTTCCAAGAGTGAGAAGCATAATGACTTATTGAGTACG :240

      *           260          *           280          *           300
TrF3'Ha : TTGTTATCACTAAAAGAAAAAGTTGATGAGGATGGTGACAACTTAATGATACTGAGATC :300

      *           320          *           340          *           360
TrF3'Ha : AAAGCATTACTCTTGAACATGTTTCACAGCTGGAACAGACACATCATCAAGCACAACAGAG :360

      *           380          *           400          *           420
TrF3'Ha : TGGGCTATTGCTGAACTAATAAAAAATCCAAACTAATGATTTCGTGTTCAAATGAGTTG :420

      *           440          *           460          *           480
TrF3'Ha : GACACTGTTGTGGGCCGAGACAAGCTTGTAAGTGAACAAGACTTGGCCCATCTTCCTTAC :480

      *           500          *           520          *           540
TrF3'Ha : TTAGAGGCTGTAATAAAGGAGACATTTTCGTCTCCATCCATCAACCCCTCTTTCTCTCCCA :540

      *           560          *           580          *           600
TrF3'Ha : CGTGTTGCAACAAATAGTTGTGAAATCCTCGACTATCACATTCCCAAAGGTGCAACTCTC :600

TrF3'Ha : TTGG : 604

```

FIGURE 80

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```

      *           20           *           40           *           60
TrF3'Ha : GNGGGECDPRADELVMVVELMALAGVFNIGDFVPALEWLDIQGVQGKMKKLHKRFDAFLT : 60

      *           80           *           100          *           120
TrF3'Ha : SIIEDHMISKSEKHNDLLSTLLSLKEKVDEEDGDKLNDTEIKALLNMFTAGTDTSSSTTE :120

      *           140          *           160          *           180
TrF3'Ha : WAIAELIKNPCLMIRVQNELDVTVGRDKLVTEQDLAHLPLYEAVIKETFRLHPSTPLSLP :180

      *           200
TrF3'Ha : RVATNSCEILDYHIPKGATLL :201
```

FIGURE 81

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```

      *           20           *           40           *           60
TrF3'Ha1 : G G G A A T G G T G G A G G C G A A T G T G A C C C T A G G G C T G A T G A A T T T A A G T A A T G G T A G T T G A G C : 60
TrF3'Ha2 : ---A A T G G T G G A G G C G A A T G T G A C C C T A G G G C T G A T G A A T T T A A G T A A T G G T A G T T G A G C : 57

      *           80           *           100          *           120
TrF3'Ha1 : T T A T G G C G T T A G C T G G A G T T T T C A A T A T T G G T G A T T T T G T T C C T G C T T T G G A A T G G T T A G : 120
TrF3'Ha2 : T T A T G G C G T T A G C T G G A G T T T T C A A T A T T G G T G A T T T T G T T C C T G C T T T G G A A T G G T T A G : 117

      *           140          *           160           *           180
TrF3'Ha1 : A T A T T C A A G G T G T A C A A G G A A A A T G A A G A A A T T A C A T A A A A G A T T T G A T G C A T T T T T T A A : 180
TrF3'Ha2 : A T A T T C A A G G T G T A C A A G G A A A A T G A A G A A A T T A C A T A A A A G A T T T G A T G C A T T T T T T A A : 177

      *           200          *           220           *           240
TrF3'Ha1 : C T A G C A T T A T T G A A G A T C A C A T G A T T T C C A A G A G T G A G A A G C A T A A T G A C T T A T T G A G T A : 240
TrF3'Ha2 : C T A G C A T T A T T G A A G A T C A C A T G A T T T C C A A G A G T G A G A A G C A T A A T G A C T T A T T G A G T A : 237

      *           260          *           280           *           300
TrF3'Ha1 : C G T T G T T A T C A C T A A A A G A A A A G T T G A T G A G G A T G G T G A C A A A C T T A A T G A T A C T G A G A : 300
TrF3'Ha2 : C G T T G T T A T C A C T A A A A G A A A A G T T G A T G A G G A T G G T G A C A A A C T T A A T G A T A C T G A G A : 297

      *           320          *           340           *           360
TrF3'Ha1 : T C A A A G C A T T A C T C T T G A A C A T G T T C A C A G C T G G A A C A G A C A C A T C A T C A A G C A C A A C A G : 360
TrF3'Ha2 : T C A A A G C A T T A C T C T T G A A C A T G T T C A C A G C T G G A A C A G A C A C A T C A T C A A G C A C A A C A G : 357

      *           380          *           400           *           420
TrF3'Ha1 : A G T G G G C T A T T G C T G A A C T A A T A A A A A A T C C A A A A C T A A T G A T T C G T G T T C A A A A T G A G T : 420
TrF3'Ha2 : A G T G G G C T A T T G C T G A A C T A A T A A A A A A T C C A A A A C T A A T G A T T C G T G T T C A A A A T G A G T : 417

      *           440          *           460           *           480
TrF3'Ha1 : T G G A C A C T G T T G T G G G C C G A G A C A A G C T T G T A A C T G A A C A A G A C T T G G C C C A T C T T C C T T : 480
TrF3'Ha2 : T G G A C A C T G T T G T G G G C C G A G A C A A G C T T G T A A C T G A A C A A G A C T T G G C C C A T C T T C C T T : 477

      *           500          *           520           *           540
TrF3'Ha1 : A C T T A G A G G C T G T A A T A A A G G A G A C A T T T C G T C T C C A T C C A T C A A C C C C T C T T T C T C T C C : 540
TrF3'Ha2 : A C T T A G A G G C T G T A A T A A A G G A G A C A T T T C G T C T C C A T C C A T C A A C C C C T C T T T C T C T C C : 537

      *           560          *           580           *           600
TrF3'Ha1 : C A C G T G T T G C A A C A A A T A G T T G T G A A A T C C T C G A C T A T C A C ----- : 581
TrF3'Ha2 : C A C G T G T T G C A A C A A A T A G T T G T G A A A T C C T C G A C T A T C A C A T T C C C A A A G G T G C A A C T C : 597

TrF3'Ha1 : ----- : -
TrF3'Ha2 : T C T T G G : 603

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FIGURE 82

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TrPALa : GNAGGAAATTTCAACTAAATATTGCCTTTAATTCTTTNTNATANATNTTTGAATTCNTT : 60
 TrPALa : CTCCCTAAAAATTCTATAGCTACCACATCANCAACATAACANNAATTAAGAAATATTN : 120
 TrPALa : TATNTACTATTTTAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAACAATGGCAAG : 180
 TrPALa : ATTGATTCATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTGCTGAT : 240
 TrPALa : CCTTTGAATTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG : 300
 TrPALa : CGTATGGTGGAGGAATACCGGAAACCGGTTGTCCGTCTTGGTGGCGAGACACTGACGATT : 360
 TrPALa : TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGAGCTATCGGAATCTGCT : 420
 TrPALa : AGAGCCGGCGTTAAGGCGAGCAGTGAAGGTTATGGAGAGTATGAACAAAGGTACAGAC : 480
 TrPALa : AGTTATGGTGTCACTACAGGGTTCGGCGCTACCTCGCACCGCCGAACCAACAAGGTGGT : 540
 TrPALa : GCTTTGCAGAAAGAGCTCATAAGGTNTTTTGAATGCAGGAATATTTGGAAATGGAACNTG : 600
 TrPALa : AGACAAAGCCACACACTACCC : 621

FIGURE 83

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TrPALa : MEVVA^{*}AAITKNNGKID²⁰SFCLNHANANNMKVNGADPLNWGVAAEAMKGS^{*}HLDEVKRMVEEY⁶⁰ : 60

TrPALa : RKPVVRLGGETLTISQVAAIAAHDGATVELSESARAGVKASSDWME^{*}SMNKG⁸⁰TDSYGVT^{*}T : 120

TrPALa : GFGATSHRRTKQGGALQKELIRFECRNIWKWNRQSHTLP^{*} : 159

FIGURE 84

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      *           20           *           40           *           60
TrPALa1 : GNNGGAAATTNCAACTAAATATTGCCTTTAATTCTTTNTNATANATNTTTGAATTTCCCTT : 60
TrPALa2 : GNAGGAAATTACAACATAATATTNCCCTTTAATTCTTTATNATANATNTTTGAATTTCCNTT : 60
TrPALa3 : -----TCAAGAAATTACACCTTTNTTCTTTNTAATNTTGGTTTNTATTTCCNTT : 50

      *           80           *           100          *           120
TrPALa1 : CTCCCTAAAAATTCTATAGCTACCACATCANCACAACATAACANNAATTAAGAAATATTN :120
TrPALa2 : CTCCCTAAAAATTCTATAGCTACCACATCANCACAACATAACANNAATTAAGAAATATTN :120
TrPALa3 : CTCCTCTGCAATCTATAGCTACCACATCACAACATAACAAAGTAACACTTATTACTAGGTATTA :110

      *           140          *           160          *           180
TrPALa1 : TATNTACTATTTTAAGATATGGAAGTAGTAGCANCAGCAATCACAAAAACAATGGCAAG :180
TrPALa2 : TATNTACTATTTTAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAACAATGGCAAG :180
TrPALa3 : TTTTATGCAATTTTAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAACAACGGCAAG :170

      *           200          *           220          *           240
TrPALa1 : ATTGATTCAATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTGCTGAT :240
TrPALa2 : ATTGATTCAATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTGCTGAT :240
TrPALa3 : ATTGATTCAATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTGCTGAT :230

      *           260          *           280          *           300
TrPALa1 : CCTTTGAATTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG :300
TrPALa2 : CCTTTGAATTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG :300
TrPALa3 : CCTTTGAATTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG :290

      *           320          *           340          *           360
TrPALa1 : CGTATGGTGGAGGAATACCGGAAACCGGTTGTCCGCTCTGGTGGCGAGACCTGACGATT :360
TrPALa2 : CGTATGGTGGAGGAATACCGGAAACCGGTTGTCCGCTCTGGTGGCGAGACACTGACGATT :360
TrPALa3 : CGTATGGTGGAGGAATACCGGAAACCGGTTGTCCGCTCTGGTGGCGAGACACTGACGATT :350

      *           380          *           400          *           420
TrPALa1 : TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGAGCTATCGGAATCTGCT :420
TrPALa2 : TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGAGCTATCGGAATCTGCT :420
TrPALa3 : TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGAGCTATCGGAATCTGCT :410

      *           440          *           460          *           480
TrPALa1 : AGAGCCGGCGTTAAGGCGAGCAGTGACTGGGTTATGGAGAGTATGAACAAAGGTACAGAC :480
TrPALa2 : AGAGCCGGCGTTAAGGCGAGCAGTGACTGGGTTATGGAGAGTATGAACAAAGGTACAGAC :480
TrPALa3 : AGAGCCGGCGTTAAGGCGAGCAGTGACTGGGTTATGGAGAGTATGAACAAAGGTACAGAC :470

      *           500          *           520          *           540
TrPALa1 : AGTTATGGTGTCACTACAGGGTTCGGCGCTACCTCCACCCGCCGAACCAAACAAGGTGGT :540
TrPALa2 : AGTTATGGTGTCACTACAGGGTTCGGCGCTACCTCCACCCGCCGAACCAAACAAGGTGGT :540
TrPALa3 : AGTTATGGTGTCACTACAGGGTTCGGCGCTACCTCCACCCGCCGAACCAAACAAGGTGGT :530

      *           560          *           580          *           600
TrPALa1 : GCTTTGCAGAAAGAGCTCATAAGGTATTTGCTTGTGTCAAT----- :582
TrPALa2 : GCTTTGCAGAAAGAGCTCATAAGGTNTTTTGAATGCTTGAATATTTGGAAATGGAACNTG :600
TrPALa3 : GCTTTGCAGAAAGAGCTCATAAGGTNTTTTGAATGCAGGAATATTTGGAAATGGAACNTG :590

      *           620
TrPALa1 : ----- : -
TrPALa2 : AGTCNAAGCCACACACTACCC :621
TrPALa3 : ANACAAATCC----- :600

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FIGURE 85

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TrPALb : GNAGGAAANAATTNTATTGTTATTATTTCCCCCACACAACGGAAANAATTNTATTGTTN : 60

TrPALb : CTTATTTCCCCCACACAACATAACNAATACATTNTCCTCTCCTCTCATCACAATTATTA : 120

TrPALb : CTTTCTACACACCCCCCTCTCAACTATTATTAACATAATGGAGGGAATTACCAATG : 180

TrPALb : GCCATGCTGAAGCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG : 240

TrPALb : CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT : 300

TrPALb : ACCGTAATCCATTGGTTAAATTTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA : 360

TrPALb : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCCAGGGCCGGCGTTA : 420

TrPALb : AGGCGAGTAGTGATTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 480

TrPALb : CCACCGGTTTCGGCGCCACCTCTCACCGGAGAACCAAGCAGGGTGGTGCCTTGCAGAAGG : 540

TrPALb : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAACTGTACAC : 600

TrPALb : TACCACACACAGCAACCAGAGCTGCAATGCTTGTGAGAATCAACACTCTTCTTCAAGAGG : 660

TrPALb : AATATTTCTTGAATGGCCTTTGTAAATTTTGG : 693

FIGURE 86

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TrPALb : MEGITNGHAEATFCVTKSVGDPLNWGAAAESLMGSHLDEVKRMVEEYRNPLVKIGGETLT : 60

TrPALb : IAQVAGIASHDGVRVELSESARAGVKASSDWMDSMNNGTDSYGVTGFGATSHRRTKQ : 120

TrPALb : GGALQKELIRFLNAGIFGNGTESNCTLPHTATRAAMLVRINTLLQEYFLNGLCKFL : 177

FIGURE 87

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		*	20	*	40	*	60	
TrPALb1 :	GNAGGAAANAATTNTATTGTTATTATTTCCCCCACACAAC	AAAGAAATAC	NATTATTN	:	60			
TrPALb2 :	-----	-----	-----	GGAAANAATTNTATTGTTN	:	21		
TrPALb3 :	-----	-----	-----	CCTTGAATNATTGNTTTGN	:	21		
TrPALb4 :	-----	-----	-----	GGAAANAATTATNTTGTN	:	19		
TrPALb5 :	-----	-----	-----	GGAAANAATTATATTGTT	:	19		
TrPALb6 :	-----	-----	-----	GAAANAATTNTNTTGTN	:	18		
TrPALb7 :	-----	-----	-----	CAAANAATTNTNTTGT	:	18		
TrPALb8 :	-----	-----	-----	-----	:	-		
		*	80	*	100	*	120	
TrPALb1 :	CTTCTCTCCTCACANATATTACNNTTTCNTACNACNCTNNCTCTCAACTATTA	:	120					
TrPALb2 :	TTTCTCCACCCACACAACATAACAAATACATTNTCCCTCTCCTCTCATCACAATTATTA	:	81					
TrPALb3 :	CCTCTCACACACATANACAAATACNATTTCTTCTGCTNCCTACTNGCATCACAATTATTA	:	81					
TrPALb4 :	NTTCTTCCCCCACACACATAACNAATACATTNTCTCTCCTCTNATCACAATTATTA	:	79					
TrPALb5 :	CTTATTTCCCTCCACACAACATAACAAATACATTNTCCCTCTCCTCTCATCACAATTATTA	:	79					
TrPALb6 :	ATTATTTCCCTCCACACAACATAACNAATACATTATCTCTCCTCTCATCACAATTATTA	:	78					
TrPALb7 :	CTTATTTCCCCCACACAACATAACAAATACATTNTCCCTCTCCTCTCATCACAATTATTA	:	78					
TrPALb8 :	-----	ANATAANAAATCCTTNTCTCTCCTCTANTACNATNTNN	:	42				
		*	140	*	160	*	180	
TrPALb1 :	TTCTAGCATATGAGGAAATAGAAATGCTATCTTAAATAAAACCAATG	:	180					
TrPALb2 :	CTTCTACACCTCCCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG	:	141					
TrPALb3 :	CTTCTACACCTCCCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG	:	141					
TrPALb4 :	CTTCTACACCTCCCTCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG	:	139					
TrPALb5 :	CTTCTACACCTCCCTCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG	:	139					
TrPALb6 :	CTTCTACACCTCCCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG	:	138					
TrPALb7 :	CTTCTACACCTCCCTCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG	:	138					
TrPALb8 :	CTTCTACACCTCCCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG	:	102					
		*	200	*	220	*	240	
TrPALb1 :	GCCATGCTGAACTCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG	:	240					
TrPALb2 :	GCCATGCTGAACTCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG	:	201					
TrPALb3 :	GCCATGCTGAACTCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG	:	201					
TrPALb4 :	GCCATGCTGAACTCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG	:	199					
TrPALb5 :	GCCATGCTGAACTCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG	:	199					
TrPALb6 :	GCCATGCTGAACTCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG	:	198					
TrPALb7 :	GCCATGCTGAACTCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG	:	198					
TrPALb8 :	GCCATGCTGAACTCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG	:	162					
		*	260	*	280	*	300	
TrPALb1 :	CAGCCGCGGAGTCGTTGAGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAGT	:	300					
TrPALb2 :	CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT	:	261					
TrPALb3 :	CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT	:	261					
TrPALb4 :	CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT	:	259					
TrPALb5 :	CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT	:	259					
TrPALb6 :	CAGCCGCGGAGTCGTTGAGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAGT	:	258					
TrPALb7 :	CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT	:	258					
TrPALb8 :	CAGCCGCGGAGTCGTTGAGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAGT	:	222					
		*	320	*	340	*	360	
TrPALb1 :	ACCGTAATCCCTTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA	:	360					
TrPALb2 :	ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA	:	321					
TrPALb3 :	ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA	:	321					
TrPALb4 :	ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA	:	319					
TrPALb5 :	ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA	:	319					
TrPALb6 :	ACCGTAATCCCTTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA	:	318					
TrPALb7 :	ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA	:	318					
TrPALb8 :	ACCGTAATCCCTTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA	:	282					

FIGURE 88

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      *           380           *           400           *           420
TrPALb1 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCAAGGGCCGGCGTTA : 420
TrPALb2 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCAAGGGCCGGCGTTA : 381
TrPALb3 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCAAGGGCCGGCGTTA : 381
TrPALb4 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCAAGGGCCGGCGTTA : 379
TrPALb5 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCAAGGGCCGGCGTTA : 379
TrPALb6 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCAAGGGCCGGCGTTA : 378
TrPALb7 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCAAGGGCCGGCGTTA : 378
TrPALb8 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCAAGGGCCGGCGTTA : 342

      *           440           *           460           *           480
TrPALb1 : AGGCGAGTAGTGCATTGGGTGATGGATAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 480
TrPALb2 : AGGCGAGTAGTGCATTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 441
TrPALb3 : AGGCGAGTAGTGCATTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 441
TrPALb4 : AGGCGAGTAGTGCATTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 439
TrPALb5 : AGGCGAGTAGTGCATTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 439
TrPALb6 : AGGCGAGTAGTGCATTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 438
TrPALb7 : AGGCGAGTAGTGCATTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 438
TrPALb8 : AGGCGAGTAGTGCATTGGGTGATGGATAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 402

      *           500           *           520           *           540
TrPALb1 : CCACCGGTTTTCGGTCCACCTCTCACC GGAGAACCAAGCAGGCTGGTGCCTTGCAGAAGG : 540
TrPALb2 : CCACCGGTTTTCGGTCCACCTCTCACC GGAGAACCAAGCAGGCTGGTGCCTTGCAGAAGG : 501
TrPALb3 : CCACCGGTTTTCGGTCCACCTCTCACC GGAGAACCAAGCAGGCTGGTGCCTTGCAGAAGG : 501
TrPALb4 : CCACCGGTTTTCGGTCCACCTCTCACC GGAGAACCAAGCAGGCTGGTGCCTTGCAGAAGG : 499
TrPALb5 : CCACCGGTTTTCGGTCCACCTCTCACC GGAGAACCAAGCAGGCTGGTGCCTTGCAGAAGG : 499
TrPALb6 : CCACCGGTTTTCGGTCCACCTCTCACC GGAGAACCAAGCAGGCTGGTGCCTTGCAGAAGG : 441
TrPALb7 : CCACCGGTTTTCGGTCCACCTCTCACC GGAGAACCAAGCAGGCTGGTGCCTTGCAGAAGG : 498
TrPALb8 : CCACCGGTTTTCGGTCCACCTCTCACC GGAGAACCAAGCAGGCTGGTGCCTTGCAGAAGG : 462

      *           560           *           580           *           600
TrPALb1 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAAN----- : 592
TrPALb2 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAAGTGTACAC : 561
TrPALb3 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAAGTGTACAC : 561
TrPALb4 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAAGTGTACAC : 559
TrPALb5 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAAGTGTACAC : 559
TrPALb6 : ----- : -
TrPALb7 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAAGTGTACAC : 558
TrPALb8 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAAGTGTACAC : 522

      *           620           *           640           *           660
TrPALb1 : ----- : -
TrPALb2 : TACCACACACAGCAACCAGAGCTGCAATGCTTGTGAGAATCAACACTCTTCTTCAAG--- : 618
TrPALb3 : TACCACACACAGCAACCAGAGCTGCAATGCTTGTGAGAATCAACACTCTTCTTCAAG--- : 621
TrPALb4 : TACCACACACAGCAACCAGAGCTGCAATGCTTGTGAGAATCAACACTCTTCTTCAAG--- : 590
TrPALb5 : TACCACACACAGCAACCAGAGCTGCAATGCTTGTGAGAATCAACACTCTTCTTCAAG--- : 616
TrPALb6 : ----- : -
TrPALb7 : TACCACACC----- : 567
TrPALb8 : TACCACACAC----- : 532

      *           680           *
TrPALb1 : ----- : -
TrPALb2 : ----- : -
TrPALb3 : AATATTTCTTGAATGGCCTTTGTAAATTTTTTGG : 654
TrPALb4 : ----- : -
TrPALb5 : ----- : -
TrPALb6 : ----- : -
TrPALb7 : ----- : -
TrPALb8 : ----- : -

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FIGURE 88 (cont)

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TrPALc : AACAAGATCGTTATGCCTTAGAACTTCACCTCAATGGCTTGGTCCTTTGATTGAAGTGAT : 60
 TrPALc : AAGATTTTCAACCAAATCAATTGAAAGAGAAATTAACTCGGTCAACGACAACCCCTTTGAT : 120
 TrPALc : CGATGTTTCAAGGAACAAGGCCATTCATGGTGGTAACTTTCAAGGAACACCTATTGGAGT : 180
 TrPALc : TTCAATGGATAACACACGTTTAGCTCTTGCTTCAATTGGTAAACTCATGTTTGCTCAATT : 240
 TrPALc : CTCTGAAC TTGTTAATGATTTTACAACAACGGGTTCGCCTTCGAATCTTACTGCTAGTAG : 300
 TrPALc : GAACCCGAGCTTGGACTATGGTTTCAAGGGATCGGAAATTGCCATGGCTTCGTATTGTTTC : 360
 TrPALc : CGAGTTACAATATCTTGCTAATCCTGTCACCAACCCATGTCCAAAGTGCCGAGCAACACAA : 420
 TrPALc : CCAAGATGT TAACTCTTTGGGTTTGATTTTCATCTAGAAAAACAAATGAAGCTATTGAGAT : 480
 TrPALc : TCTCAAGCTCATGTCTTCCACTTTCTTGATTGCATTATGTCAAGCAATCGACTTAAGGCA : 540
 TrPALc : CTTGGAGGAAAATCTCAGGAACACCGTCAAGAACACGGT : 579

FIGURE 89

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TrPALc : * 20 * 40 * 60
 * 80 * 100 * 120
TrPALc : SMDNTRLALASIGKLMFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGSEIAMASYCS : 120
 * 140 * 160 * 180
TrPALc : ELQYLANPVTTHVQSAEQHNQDVNSLGLISSRKTNEAIEILKLMSSTFLIALCQAIDLRH : 180
 *
TrPALc : LEENLRNTVKNT : 192

FIGURE 90

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TrPALd : GGTCAATNCAGCTTNGGAGATCTAGTCCCCCTTCTTACTNTGCTGGTTTACTAACTGGA : 60

TrPALd : AGACCNAATTCCTAAAGCTCATGGGCCTACAGGAGAAGTACTTAATGCAAAAGAAGCTTTT : 120

TrPALd : CAATTGGCTGGAATCAATACCGAGTTCTTTGAATTACAACCAAAGAAGGTCTTGCACTT : 180

TrPALd : GTTAATGGAACCTGCTGTTGGTTCTGGTTTAGCTTCTATTGTTCTTTTGGAGGCTAACATA : 240

TrPALd : TTGGCGGTGTTGTCTGAAGTTCTATCGGCAATTTTCGCTGAAGTTATGCAAGGGAAGCCC : 300

TrPALd : GAATTTACTGATCATTTGACACATAAGTTGAAGCACCACCCTGGTCAAATGAGGCTGCT : 360

TrPALd : GCTATTATGGAACACATTTTGGATGGGAGTGCTTATGTTAAAGACGCGAAGAAGTTGCAT : 420

TrPALd : GAGATGGACCCTTTACAGAAGCCAAAGCAAGATAGATATGCACTTAGAACTTCACCACAA : 480

TrPALd : TGGCTTGGTCCTTTGATTGAAGTGATTAGATTTTCAACCAAGTCAATTGAGAGAGAGATC : 540

TrPALd : AACTCTGTCAATGACAACCCCTTTGATTGATGTTTCGAGAAACAAGGCTTTG : 591

FIGURE 91

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TrPALd : GQXSXGDLVPLSYXAGLLTGRXNSKAHGPTGEVLNAKEAFQLAGINTEFFELQPKEGLAL : 60

TrPALd : VNGTAVGSGGLASIVLFEANILAVLSEVLSAIFAEVMQKPEFTDHLTHKLKHHPGQIEAA : 120

TrPALd : AIMEHILDGSAYVKDAKKLHEMDPLQKPKQDRYALRTSPQWLGPLIEVIRFSTKSIEREI : 180

TrPALd : NSVNDNPLIDVSRNKAL : 197

FIGURE 92

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TrPALe : GNNGGAAATTNCAACTCNATTTTCTTTNTATAATNTTTGAATTTTCCTTCTCTCTCAA : 60
 * 20 * 40 * 60

TrPALe : TTCTATAGCTACTCTACCACATCACACAACATAACAAATTAAGAAATATTCATTACTATA : 120
 * 80 * 100 * 120

TrPALe : CTATTAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAACAACGGCAAGATTGATTC : 180
 * 140 * 160 * 180

TrPALe : ATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGATGCTGATCCTTTGAA : 240
 * 200 * 220 * 240

TrPALe : TTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGAGATGAGGTGAAACGTATGGT : 300
 * 260 * 280 * 300

TrPALe : GGAGGAGTACCGGAAGCCGATTGTCCGTCTTGGTGGCGAGACGCTGACGATTTCTCAGGT : 360
 * 320 * 340 * 360

TrPALe : GGCTGCCATTGCTGCACACGATGGTGCGATGGTTGAGCTGTGCGAATCTGCTAGAGCCGG : 420
 * 380 * 400 * 420

TrPALe : CGTTAAGGCAAGCAGTGATTGGGTATGGAGAGTATGAACAAAGGTACTGACAGTTATGG : 480
 * 440 * 460 * 480

TrPALe : TGTCAACACAGGGTTTCGGCGCTACCTCNCACCGCCGAACCAACAAGGTGGTGCTTTACA : 540
 * 500 * 520 * 540

TrPALe : GAAAGGGCTCATAAGGTTTTTGAATGCTGGAATATTTGNAAATGNAACTGAN : 592
 * 560 * 580 *

FIGURE 93

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TrPALe : MEVVA^{*}AAITKNNGKIDS²⁰FC^{*}LNHANANNMKVNDADPLNWGVAAEAMKGS⁴⁰HLDEVKRMV^{*}EEY⁶⁰ : 60

TrPALe : RKPIVRLGGETLTISQVAAIAAHDGAMVELSESARAGVKASSDW^{*}VMESMNKG⁸⁰TDSYG^{*}VTT¹⁰⁰ : 120

TrPALe : GFGATX^{*}HRRTKQGGALQKGLIRFLNAGIFX¹⁴⁰NXTX^{*} : 154

FIGURE 94

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      *           20           *           40           *           60
TrPALf : CNATTGTTAGTNGTTTCCNCCCACCCACATAACAAATACATAATTCTCTCCTCTGATCAC : 60

      *           80           *           100          *           120
TrPALf : AATTATTACTTTACTACACCCTCCTCTCAACTATTATTAACTAGCATAATGGAGGGAATT : 120

      *           140          *           160          *           180
TrPALf : ACCAATGGCCATGCTGAAACAACCTTTTAGCGTGACCAAAAGTGNNGGNGATCCACTCAAC : 180

      *           200          *           220          *           240
TrPALf : TGGCGNGCAGCCGCGGAGTCGTCGACGGGGAGTCATTTGGATGAGGTGAAGCGTATGGNG : 240

      *           260          *           280          *           300
TrPALf : GAGGAGTACCGTAATCCGNTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTNNGGTA : 300

      *           320          *           340          *           360
TrPALf : NCTGGAATTGCTTCTCATGATAGTGAGAGTGAGGGTGGAGCTGTCCGAGTTCGCAAGGGCC : 360

      *           380          *           400          *           420
TrPALf : GGCCTTAAGGCGAGTAGTGATTGNGTGATGGATAGCATGAACAATGGGACTGATAGTTAC : 420

      *           440          *           460          *           480
TrPALf : GGTGTTACCACCGCNTTTGGTGCCACCTGTCACCGGAGAACCAAGCCANGGTGGTGCCTT : 480

      *           500          *           520          *           540
TrPALf : GCAGAAGGAGCTAAATTNNGGTGTTTTGAANGCTGGNAATANTTTGGCNNTGGTTCAGAA : 540

      *           560
TrPALf : ATCTNAACTTGTNCACTTACCACACC : 566

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FIGURE 95

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      *           20           *           40           *           60
TrPALf : MEGITNGHAETTFSVTKSXXDPLNWXAAAESSTGSHLDEVKRMXEEYRNPXVKIGGETLT : 60

      *           80           *           100          *           120
TrPALf : IAXVXGIAHDSGVRVELSEFARAGVKASSDXVMDSMNNGTDSYGVTTXFGATCHRRTKP : 120

      *           140          *
TrPALf : XWCLAEGAKXXCFEXWXXFGXGSEIXTCXLTT : 152
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FIGURE 96

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      *           20           *           40           *           60
TrPALf1 : CNATTGTTAGTNGTTTCCNCCCACCNACATAACNAATACNTANTTCTCTCCTCTGATCAC : 60
TrPALf2 : -----CCATAACAAATACATTATTCTCTCCTCTGATCAC : 35

      *           80           *           100          *           120
TrPALf1 : AATTATTACTTTTCTACACCCTCCTCTCAACTATTATTAACTAGCATAATGGAGGGAATT :120
TrPALf2 : AATTATTACTTTTACTACACCCTCCTCTCAACTATTATTAACTAGCATAATGGAGGGAATT : 95

      *           140          *           160          *           180
TrPALf1 : ACCAATGGCCATGCTGAAACAACCTTTTTCGCTGACCAAAAGTCGNGGNGATNNANTGNNC :180
TrPALf2 : ACCAATGGCCATGCTGAAACAACCTTTTTCGCTGACCAAAAGTCGNGGNGATCCACTCAAC :155

      *           200          *           220          *           240
TrPALf1 : TCGCGNG----- :188
TrPALf2 : TGCCTGCAGCCCGGAGTCGTGACGGGGAGTCATTTGATGAGGTGAAGCGTATGGNG :215

      *           260          *           280          *           300
TrPALf1 : ----- : -
TrPALf2 : GAGGAGTACCGTAATCCGNTGGTTAAATTTGGCGGCGAGACGCTTACCATTGCTNNGGTA :275

      *           320          *           340          *           360
TrPALf1 : ----- : -
TrPALf2 : NCTGGAATTGCTTCTCATGATAGTGGAGTGAGGGTGGAGCTGTCCGAGTTCGCAAGGGCC :335

      *           380          *           400          *           420
TrPALf1 : ----- : -
TrPALf2 : GGCGTTAAGGCGAGTAGTGATTGNGTGATGGATAGCATGAACAATGGGACTGATAGTTAC :395

      *           440          *           460          *           480
TrPALf1 : ----- : -
TrPALf2 : GGTGTTACCACCGCNTTTGGTGCCACCTGTCACCGGAGAACCAAGCCANGGTGGTGCCTT :455

      *           500          *           520          *           540
TrPALf1 : ----- : -
TrPALf2 : GCAGAAGGAGCTAAATTNNGGTGTTTTGAANGCTGCNAATANTTTGGCNNTGGTTCAGAA :515

      *           560
TrPALf1 : ----- : -
TrPALf2 : ATCTNAACTTGTNCACTTACCACACC :541

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FIGURE 97

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      *           20           *           40           *           60
TrVRa : GTAAGAGTTGAGAAAAAANACCAATAAAGTAAACNCTATNTAGAAAAGAGAGTCAAAAATG : 60

      *           80           *           100          *           120
TrVRa : GCTGAAGGAAAAGGAAGGGTTTGTGTTACTGGAGGAACAGGTTTCTTGTTTCATGGATC : 120

      *           140          *           160          *           180
TrVRa : ATCAAGAGTCTTCTTGAAAATGGATACTCTGTTAATACCACTATTAGAGCTGATCCAGAA : 180

      *           200          *           220          *           240
TrVRa : CGTAAGAGGGATGTAAGCTTCCTAACAAATCTACCCGGCGCATCCGAAAGGCTACATTTTC : 240

      *           260          *           280          *           300
TrVRa : TTCAACGCCGATCTAGACGACCCAGAGAGTTTCAACGAAGCAATTGAAGGTTGTGTCGGG : 300

      *           320          *           340          *           360
TrVRa : ATATTCCACACCGCTTCACCAATCGATTTGCGCGTGAGTGAGCCAGAAGAAATAGTGACA : 360

      *           380          *           400          *           420
TrVRa : AAAAGAACAGTGGATGGAGCATTAGGAATTTTAAAGCATGTGTGAATTCAAAGACAGTG : 420

      *           440          *           460          *           480
TrVRa : AAGAGATTTATTTACACTTCAAGNGGTTCTGCTGTTTCATTCATGGAAAAACAAAGAT : 480

      *           500          *           520          *           540
TrVRa : GNNTNGGATGAGAGTGATTGGAGTGATGTTGATTTGCTTAGAAGTGTTAAACCATTTGGT : 540

      *           560          *           580          *           600
TrVRa : TGGAGTTATGGNGTGTTCAAGACTTTGGCTGAGAAAGCAGTGCTTGAATTTGGTCNACAA : 600

      *           620          *           640          *           660
TrVRa : AATGGGATTGATGTTGTTACTTTGATTCTTCCTTTTATTGTTGGAGGTTTTGTTTGTCCC : 660

      *           680          *           700          *           720
TrVRa : AAGCTTCCTGATTCTGTTGAGAAAGCTCTTGTTTTGGTACTAGGCAAAAAGGAACAAATT : 720

      *           740          *           760          *           780
TrVRa : GGTATTATAAGTTTCCACATGGTACATGTAGATGATGTGGCTAGAGCACATATCTATCTA : 780

      *           800          *           820          *           840
TrVRa : CTTGAGAATCCTGTTCCAGGAGGTAGATATAATTGTTCCACCATCTTTGTATCTATTGAA : 840

      *           860          *           880          *           900
TrVRa : GAAATGTCACAGCTTCTCTCAGCCAAATATCCAGAATATCAAATACTATCAGTAGATGAG : 900

      *           920          *           940          *           960
TrVRa : TTGAAGGAAATTAAAGGGGCAAGATTGCCAGATTTGAACTCGAAGAAGCTCGTGGACGCT : 960

      *           980          *           1000         *           1020
TrVRa : GGTTTTGAGTTTAAGTATAGTGTGATGATATGTTTCGATGATGCGATTCAATGCTGCAAG : 1020

      *           1040         *           1060         *           1080
TrVRa : GAAAAAGGCTATCTCTAAGCATGTATTTGAAAATTCATGAAGTTGAGAAAACAATAATG : 1080

      *           1100         *           1120         *           1140
TrVRa : TGCCTAAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCATTAAGTTATTTGTGAT : 1140

      *           1160         *           1180
TrVRa : CAATCAAATAATGAAATAATCTGTTTCATTTTCCGAAAAAAAAA : 1185

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FIGURE 98

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TrVRa : MAEGKGRVCVTGGTGFLGSWIIKSLLENGYSVNTTIRADPERKRDVSFLTNLPGASERLH : 60

TrVRa : FFNADLDDPESFNEAIEGCVGIFHTASPIDFAVSEPEEIVTKRTVDGALGILKACVNSKT : 120

TrVRa : VKRFIYTSXGSAVSFNGKNKDXDESDWSDVDLLRSVKPFGWSYXVFKTLAEKAVLEFGX : 180

TrVRa : QNGIDVVTILLPFIVGGFVCPKLPDSVEKALVLVLGKKEQIGIISFHMVHVDDVARAHY : 240

TrVRa : LLENPVPGGRYNCSPFFVSIEEMSQLLSAKYPEYQILSVDELKEIKGARLPDLNSKKLVD : 300

TrVRa : AGFEFKYSVDDMFDDAIQCCKEKGYL : 326

FIGURE 99

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		*	20	*	40	*	60		
TrVRa1 :	GTAC	AGTTGAGAAAAAA	AC	NAATAAAAGTAAACNCTATNTAGAAAAGAGAGTCAAAAATG	:	60			
TrVRa2 :	---	AGAGTTGAGAAAAAA	NN	CCAATAAAAGTAAACNCTATNTAGAAAAGAGAGTNNAAAATG	:	57			
TrVRa3 :	-----				:	-			
TrVRa4 :	-----				:	-			
TrVRa5 :	-----				:	-			
TrVRa6 :	-----				:	-			
		*	80	*	100	*	120		
TrVRa1 :	GCTGAAGGAAAAGGAAGGGTTTGTGTTACTGGAGGAACAGGTTTTCTTGTTTCATGGATC	:	120						
TrVRa2 :	GCTGAAGGAAAAGGAAGGGTTTGTGTTACTGGAGGAACAGGTTTTCTTGTTTCATGGATC	:	117						
TrVRa3 :	-----	:	-						
TrVRa4 :	-----	:	-						
TrVRa5 :	-----	:	-						
TrVRa6 :	-----	:	-						
		*	140	*	160	*	180		
TrVRa1 :	ATCAAGAGTCTTCTTGAAAATGGATACTCTGTTAATACCACCTATTAGAGCTGATCCAGAA	:	180						
TrVRa2 :	ATCAAGAGTCTTCTTGAAAATGGATACTCTGTTAATACCACCTATTAGAGCTGATCCAGAA	:	177						
TrVRa3 :	-----	:	-						
TrVRa4 :	-----	:	-						
TrVRa5 :	-----	:	-						
TrVRa6 :	-----	:	-						
		*	200	*	220	*	240		
TrVRa1 :	CGTAAGAGGGATGTAAGCTTCCTAACAAATCTACCCGGCGCATCCGAAAGGCTACATTTTC	:	240						
TrVRa2 :	CGTAAGAGGGATGTAAGCTTCCTAACAAATCTACCCGGCGCATCCGAAAGGCTACATTTTC	:	237						
TrVRa3 :	-----	:	-						
TrVRa4 :	-----	:	-						
TrVRa5 :	-----	:	-						
TrVRa6 :	-----	:	-						
		*	260	*	280	*	300		
TrVRa1 :	TTCAACGCCGATCTAGACGACCCAGAGAGTTTCAACGAAGCAATTGAAGGTTGTGTCTGGG	:	300						
TrVRa2 :	TTCAACGCCGATCTAGACGACCCAGAGAGTTTCAACGAAGCAATTGAAGGTTGTGTCTGGG	:	297						
TrVRa3 :	-----	:	-						
TrVRa4 :	-----	:	-						
TrVRa5 :	-----	:	-						
TrVRa6 :	-----	:	-						
		*	320	*	340	*	360		
TrVRa1 :	ATATTCCACACCGCTTCACCAATCGATTTTCGCCGTGAGTGAGCCAGAAGAAATAGTGACA	:	360						
TrVRa2 :	ATATTCCACACCGCTTCACCAATCGATTTTCGCCGTGAGTGAGCCAGAAGAAATAGTGACA	:	357						
TrVRa3 :	-----	:	-						
TrVRa4 :	-----	:	-						
TrVRa5 :	-----	:	-						
TrVRa6 :	-----	:	-						
		*	380	*	400	*	420		
TrVRa1 :	AAAAGAACAGTGGATGGAGCATTAGGAATTTTAAAAGCATGTGTGAATTCAAAGACAGTG	:	420						
TrVRa2 :	AAAAGAACAGTGGATGGAGCATTAGGAATTTTAAAAGCATGTGTGAATTCAAAGACAGTG	:	417						
TrVRa3 :	-----	:	-						
TrVRa4 :	-----	:	-						
TrVRa5 :	-----	:	-						
TrVRa6 :	-----	:	-						

FIGURE 100

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		*	440	*	460	*	480	
TrVRa1 :	AAGAGATTTATTTACACTTCAAGNGGTTCTGCTGTTTCATTCAATG	AAAAANCAAAGAT	:	480				
TrVRa2 :	AAGAGATTTATTTACACTTCAAGTGGTTCTGCTGTTTCATTCAATG	AAAAAACAAAGAT	:	477				
TrVRa3 :	-----		:	-				
TrVRa4 :	-----		:	-				
TrVRa5 :	-----		:	-				
TrVRa6 :	-----		:	-				
		*	500	*	520	*	540	
TrVRa1 :	GNNTNNNATGANA	-----	:	493				
TrVRa2 :	CTTTGGATGAGAGTGATTGGAGTGATGTTGATTGCTTAGAAGTGTTAAACCATTG	GGT	:	537				
TrVRa3 :	-----		:	-				
TrVRa4 :	-----		:	-				
TrVRa5 :	-----		:	-				
TrVRa6 :	-----		:	-				
		*	560	*	580	*	600	
TrVRa1 :	-----		:	-				
TrVRa2 :	TGGAGTTATGGTGT	TTCAAGACTTTGGCTGAGAAAGCAGTGCTTGAATTTGGT	CTACAA	:	597			
TrVRa3 :	-----	GNGTGTTAAAGACTTT	GCTGAGAAAGCAGTGCTTGAATTTGGT	CTACAA	:	50		
TrVRa4 :	-----	AGAC	TTNGCTGAGAAAGC	GTGCTTGAATTTGGT	CTACAA	:	41	
TrVRa5 :	-----	-----	TTGAATTTGG	CTACAA	:	19		
TrVRa6 :	-----	-----	TTGAATTTGGT	CTACAA	:	19		
		*	620	*	640	*	660	
TrVRa1 :	-----		:	-				
TrVRa2 :	AATG	-----	:	601				
TrVRa3 :	AATGGGATTGATGTTGTTACTTTGATTCTTCCTTTTATTGTTGGAGGTTT	TGTTTGTCCC	:	110				
TrVRa4 :	AATGGGATTGATGTTGTTACTTTGATTCTTCCTTTTATTGTTGGAGGTTT	TGTTTGTCCC	:	101				
TrVRa5 :	AATGGGATTGATGTTGTTACTTTGATTCTTCCTTTT	TTGTTGGAGGTTT	TGTTTGTCCC	:	79			
TrVRa6 :	AATGGGATTGATGTTGTTACTTTGATTCTTCCTTTT	TTGTTGGAGGTTT	TGTTTGTCCC	:	79			
		*	680	*	700	*	720	
TrVRa1 :	-----		:	-				
TrVRa2 :	-----		:	-				
TrVRa3 :	AAGCTTCCTGATTCTGTTGAGAAAGCTCTTGTTTTGGTACTAGGCAAAAAGGAACAAATT		:	170				
TrVRa4 :	AAGCTTCCTGATTCTGTTGAGAAAGCTCTTGTTTTGGTACTAGGCAAAAAGGAACAAATT		:	161				
TrVRa5 :	AAGCTTCCTGATTCTGTTGAGAAAGCTCTTGTTTTGGTACTAGGCAAAAAGGAACAAATT		:	139				
TrVRa6 :	AAGCTTCCTGATTCTGTTGAGAAAGCTCTTGTTTTGGTACTAGGCAAAAAGGAACAAATT		:	139				
		*	740	*	760	*	780	
TrVRa1 :	-----		:	-				
TrVRa2 :	-----		:	-				
TrVRa3 :	GGTATTATAAGTTTCCACATGGTACATGTGGATGATGTGGCTAGAGCACATATCTATCTA		:	230				
TrVRa4 :	GGTATTATAAGTTTCCACATGGTACATGTGGATGATGTGGCTAGAGCACATATCTATCTA		:	221				
TrVRa5 :	GGTATTATAAGTTTCCACATGGTACATGTAGATGATGTGGCTAGAGCACATATCTATCTA		:	199				
TrVRa6 :	GGTATTATAAGTTTCCACATGGTACATGTAGATGATGTGGCTAGAGCACATATCTATCTA		:	199				
		*	800	*	820	*	840	
TrVRa1 :	-----		:	-				
TrVRa2 :	-----		:	-				
TrVRa3 :	CTTGAGAATCCTGTTCCAGGAGGTAGATATAAATTGTTCCACCATTCTTTGTATCTATTGAA		:	290				
TrVRa4 :	CTTGAGAATCCTGTTCCAGGAGGTAGATATAAATTGTTCCACCATTCTTTGTATCTATTGAA		:	281				
TrVRa5 :	CTTGAGAATCCTGTTCCAGGAGGTAGATATAAATTGTTCCACCATTCTTTGTATCTATTGAA		:	259				
TrVRa6 :	CTTGAGAATCCTGTTCCAGGAGGTAGATATAAATTGTTCCACCATTCTTTGTATCTATTGAA		:	259				

FIGURE 100 (cont)

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		*	860	*	880	*	900	
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	GAAATGTCACAGCTTCTTCAGCCAAATATCCAGAATATCAAATACTATCTGTAGATGAG							: 350
TrVRa4 :	GAAATGTCACAGCTTCTTCAGCCAAATATCCAGAATATCAAATACTATCTGTAGATGAG							: 341
TrVRa5 :	GAAATGTCACAGCTTCTTCAGCCAAATATCCAGAATATCAAATACTATCAGTAGATGAG							: 319
TrVRa6 :	GAAATGTCACAGCTTCTTCAGCCAAATATCCAGAATATCAAATACTATCAGTAGATGAG							: 319
		*	920	*	940	*	960	
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	TTGAAGGAAATTAAAGGGGCAAGCTTGCCAGATTTGAACTCGAAGAAGCTCGTGGACGCT							: 410
TrVRa4 :	TTGAAGGAAATTAAAGGGGCAAGCTTGCCAGATTTGAACTCGAAGAAGCTCGTGGACGCT							: 401
TrVRa5 :	TTGAAGGAAATTAAAGGGCAAGATTGCCAGATTTGAACTCGAAGAAGCTCGTGGACGCT							: 379
TrVRa6 :	TTGAAGGAAATTAAAGGGCAAGATTGCCAGATTTGAACTCGAAGAAGCTCGTGGACGCT							: 379
		*	980	*	1000	*	1020	
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	GGTTTTGAGTTTAAAGTATAGTGTTCGATGATATGTTTCGATGATGCGATTCAATGCTGCAAG							: 470
TrVRa4 :	GGTTTTGAGTTTAAAGTATAGTGTTCGATGATATGTTTCGATGATGCGATTCAATGCTGCAAG							: 461
TrVRa5 :	GGTTTTGAGTTTAAAGTATAGTGTTCGATGATATGTTTCGATGATGCGATTCAATGCTGCAAG							: 439
TrVRa6 :	GGTTTTGAGTTTAAAGTATAGTGTTCGATGATATGTTTCGATGATGCGATTCAATGCTGCAAG							: 439
		*	1040	*	1060	*	1080	
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	GAAAAAGGCTATCTCTAAGCATGTCTTTGAAAATTCCATGAAGTTGAGAAAAACAATACTG							: 530
TrVRa4 :	GAAAAAGGCTATCTCTAAGCATGTCTTTGAAAATTCCATGAAGTTGAGAAAAACAATACTG							: 521
TrVRa5 :	GAAAAAGGCTATCTCTAAGCATGTATTTGAAAATTCCATGAAGTTGAGAAAAACAATAATG							: 499
TrVRa6 :	GAAAAAGGCTATCTCTAAGCATGTATTTGAAAATTCCATGAAGTTGAGAAAAACAATAATG							: 499
		*	1100	*	1120	*	1140	
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	TGCCTAAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCATTAAGTTATTTGTGAT							: 590
TrVRa4 :	TGCCTAAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCATTAAGTTATTTGTGAT							: 581
TrVRa5 :	TGCCTAAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCATTAAGTTATTTGTGAT							: 559
TrVRa6 :	TGCCTAAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCATTAAGTTATTTGTGAT							: 559
		*	1160	*	1180			
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	CAATCAAATAATGAAATAATCTG-----							: 613
TrVRa4 :	CAATCAAATAATGAAATAATC-----							: 602
TrVRa5 :	CAATCAAATAATGAAAT-----							: 575
TrVRa6 :	CAATCAAATAATGAAATAATCTGTTTCATTTTCCGAAAAAAAAA							: 604

FIGURE 100 (cont)

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LpDFRa : GTSYWTTCGAGTTTGAGAGAATGGCTTCCAGGGCAAGGTGTGTGTTACTGGGGCCTCTGG : 60
 LpDFRa : CTTTGTTGCTTCTTGGCTTGTCAAAGACTACTCGAGTCCGGTTATAATGTTCTAGGGAC : 120
 LpDFRa : AGTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTTAGCAGGGGCCAA : 180
 LpDFRa : GGAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGAAGAAGGGAGCTTCGATGATGCTGT : 240
 LpDFRa : GATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAA : 300
 LpDFRa : GGAAGAAATGCTTGATTCTGCAATTAACGGCACTCTAAACGTGCTGAGATCGTGCAAGAA : 360
 LpDFRa : GAATCCTTTTCTCAAAGGGTTGTTCTCACGTCATCATCGTCAACCGTGAGGCTGAGGGA : 420
 LpDFRa : TGAAGCTGAATTCCCACCCAACGTGTTGCTGGATGAAACATCATGGAGCTCCGTGGAGTT : 480
 LpDFRa : CTGTGAAAGTATCCAGGTATGGTATGGTGTGCGGAAGATCCTTGCTGAGAAATCAGCTTG : 540
 LpDFRa : GGAGTTCGCCAAGGAGAACAAACATCGACCTAGTGGCTGTTCTTCCAACGTTTCGTGATTGG : 600
 LpDFRa : ACCTAATCTCTCGTCTGAATTAGGACCCACTGTTTTAGATGTCCTTGGCTTATTAAAGG : 660
 LpDFRa : AGAGACAGAGAAGTTCACCATGTTTKGGAAGGATG : 695

FIGURE 101

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LpDFRa : VFSSLREWLPGQVCVTGASGFVASWLVKRLLESGYNVLGTVRDPGNQKKVAHLWNLAGAK : 60

LpDFRa : ERLELVKADLLEEGSFDDAVMACEGVFHTASPIITKSDTKEEMLDSAINGTLNVLRSCCK : 120

LpDFRa : NPFLKRVVLTSSSSTVRLRDEAEFPPNVLLDETSWSSVEFCESIQVWYGVAKILAEKSAW : 180

LpDFRa : EFAKENNIDLVAVLPTFVIGPNLSSELGPTVLDVLGLFKGETEKFTMFGKD : 231

FIGURE 102

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      *           20           *           40           *           60
LpDFRa1 : -----GTTTCAGAGAATGGCTTCNAGGGCAGGTGTGTGTTACTGGGGCCTCTGGC : 50
LpDFRa2 : -----TCGAGTTTGAGAGAATGGCTTCNAGGGCAGGTGTGTGTTACTGGGGCCTCTGGC : 54
LpDFRa3 : -----GTTGGCTTCCAGGGCGGGTGTGTGTTACTGGGGCCTCTGGC : 41
LpDFRa4 : --GCATTTCGAGTTTGAGAGAATGGCTTCNAGGGCAGGTGTGTGTTACTGGGGCCTCTGGC : 58
LpDFRa5 : GTCTTTTCGAGTTTGAGAGAATGGCTTCNAGGGCAGGTGTGTGTTACTGGGGCCTCTGGC : 60

      *           80           *           100          *           120
LpDFRa1 : TTTGTTGCTTCTTGGCTTGTCAAAAGACTACTCGAGTCCGGTTATAATGTTCTAGGGACA :110
LpDFRa2 : TTTGTTGCTTCTTGGCTTGTCAAAAGACTACTCGAGTCCGGTTATAATGTTCTAGGGACA :114
LpDFRa3 : TTTGTTGCTTCTTGGCTTGTNAAA-GACTACTCGAGTCCGGTTATAATGTTCTAGGGACA :100
LpDFRa4 : TTTGTTGCTTCTTGGCTTGTCAAAAGACTTCTCGAGTCCGGTTATAATGTTCTAGGGACA :118
LpDFRa5 : TTTGTTGCTTCTTGGCTTGTCAAAAGACTTCTCGAGTCCGGTTATAATGTTCTAGGGACA :120

      *           140          *           160          *           180
LpDFRa1 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAAG :170
LpDFRa2 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAAG :174
LpDFRa3 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAAG :160
LpDFRa4 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAAG :178
LpDFRa5 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAAG :180

      *           200          *           220          *           240
LpDFRa1 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGAAGAAGGGAGCTTCGATGATGCTGTG :230
LpDFRa2 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGAAGAAGGGAGCTTCGATGATGCTGTG :234
LpDFRa3 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGAAGAAGGGAGCTTCGATGATGCTGTG :220
LpDFRa4 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGAAGAAGGGAGCTTCGATGATGCTGTG :238
LpDFRa5 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGAAGAAGGGAGCTTCGATGATGCTGTG :240

      *           260          *           280          *           300
LpDFRa1 : ATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG :290
LpDFRa2 : ATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG :294
LpDFRa3 : ATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG :280
LpDFRa4 : ATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG :298
LpDFRa5 : ATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG :300

      *           320          *           340          *           360
LpDFRa1 : GAAGAAATGCTTGATTCTGCAATTAACGGCACTCTAAACGTGCTGAGATCGTGCAAGAAG :350
LpDFRa2 : GAAGAAATGCTTGATTCTGCAATTAACGGCACTCTAAACGTGCTGAGATCGTGCAAGAAG :354
LpDFRa3 : GAAGAAATGCTTGATTCTGCAATTAACGGCACTCTAAACGNGCTGAGATCGNGCAAGAAG :340
LpDFRa4 : GAAGAAATGCTTGATTCTGCAATTAACGGCACTCTAAACGTGCTGAGATCGTGCAAGAAG :358
LpDFRa5 : GAAGAAATGCTTGATTCTGCAATTAACGGCNCCTCTAAACGTGCTGNNATCCGGGTNAAA :360

      *           380          *           400          *           420
LpDFRa1 : AATCCTTTTCTCAAAAGGGTTGTTCTCACGTCATCATCGTCAACCGTGAGGCTGAGGGAT :410
LpDFRa2 : AATCCTTTTCTCAAAAGGGTTGTTCTCACGTCATCATCGTCAACCGTGAGGCTGAGGGAT :414
LpDFRa3 : AATNCTTTTCTNAAAAGGGNTGNTCTCACGTCATCATCGTCAACCGNGANGCTGANGGAT :400
LpDFRa4 : AATCCTTTTCTCAAAAGGGTTGTTCTCACGTCATCATCGTCAACCGTGAGGCTGAGGGAT :418
LpDFRa5 : AAAAA----- :365

      *           440          *           460          *           480
LpDFRa1 : GAAGCTGAATTCCCACCCAACGTGTTGCTGGATGAAACATCATGGAGCTCCGTGGAGTTC :470
LpDFRa2 : GAAGCTGAATTCCCACCCAACGTGTTGCTGGATGAAACATCATGGAGCTCCGTGGAGTTC :474
LpDFRa3 : GAANCTGANTTCCCACCCAACGNGN----- :425
LpDFRa4 : GAAGCTGAATTCCCACCCAACGTGTTGCTGGATGAAACATCATGGAGCTCCGTGGAGTTC :478
LpDFRa5 : ----- : -

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FIGURE 103

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	* 500 * 520 * 540	
LpDFRa1 :	TGTGAAAGTATCCAGGTATGGTATGGTGTGCGGAAGATCCTTGCTGAGAAATCAGCTTGG	: 530
LpDFRa2 :	TGTGAAAGTATCCAGGTATGGTATGGTGTGCGGAAGATCCTTGCTGAGAAATCAGCTTGG	: 534
LpDFRa3 :	-----	: -
LpDFRa4 :	TGTGAAAGTATCCAGGTATGGTACGGTGTGCGAAAGATCCTTGCCGAGAAATCAGCCTGG	: 538
LpDFRa5 :	-----	: -
	* 560 * 580 * 600	
LpDFRa1 :	GAGTTCGCCAAGGAGAAACAACATCGACCTAGTGGCTGTTCTTCCAACGTTTCGTGATTGGA	: 590
LpDFRa2 :	GAGTTCGCCAAGGAGAAACAACATCGACCTAGTGGCTGTTCTTCCAACGTTTCGTGATTGGA	: 594
LpDFRa3 :	-----	: -
LpDFRa4 :	GAGTTCGCCAAGGAGAAACAACATCGACCTAGTGGCTGTTCTTCCAACATTTCGTGATTGGA	: 598
LpDFRa5 :	-----	: -
	* 620 * 640 * 660	
LpDFRa1 :	CCTAATCTCTCGTCTGAATTAGGACCCACTGTTTTAGATGTCCTTGGCTTATTTAAAGGA	: 650
LpDFRa2 :	CCTAATCTCTCGTCTGAATTAGGACCCACTGTTTTAGATGTCCTTGGCTTATTTAANGGA	: 654
LpDFRa3 :	-----	: -
LpDFRa4 :	CCTAATCTCTCGTCTGAATTAGGACCCACTGTTTTAGATGTCCTTGGCTTATTTAAAGGA	: 658
LpDFRa5 :	-----	: -
	* 680 *	
LpDFRa1 :	GAGACAGAGAAGTTCAG-----	: 667
LpDFRa2 :	GAGACAGAGAAGTTCACCATGTTTTGGAAGGATG	: 688
LpDFRa3 :	-----	: -
LpDFRa4 :	GAGACAGAGAAGTTCACCATGTTTGGGAAGGAN-	: 691
LpDFRa5 :	-----	: -

FIGURE 103 (cont)

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LpDFRb : * 20 * 40 * 60
 : GTCCTCGCCTACGAGCGCCCCGACGCCCGCGGCCGCTACCTCTGCATCGGGGCCGTGCTG : 60

LpDFRb : * 80 * 100 * 120
 : CACCGCGCGCACTTCCTAAAGCTTCTCAAGGACCTCTTCCCGCAGTACTCCTTCACCGCC : 120

LpDFRb : * 140 * 160 * 180
 : AAGTGCGAAGACGACGGCAAGCCCATGGCGAAGCCGTACAAGTTCTCCNACCAGAGGCTC : 180

LpDFRb : * 200 * 220 * 240
 : AGGGACCTGGGATTAAAAATCACTCCGCTGGCGGAAAGTTTGTACGAGACCGTGACGTGC : 240

LpDFRb : * 260 * 280 * 300
 : CTGCAAAAAAATGGCCACCTGCCTCTGCCCCGCTCCCATGGCGCCAAAGCGTGACATACCTA : 300

LpDFRb : * 320 * 340 * 360
 : TAATACTACAAAGACACGGCCGGGATCGACAAGCCAAGAAACAGAGGATTCTCCCGAGGT : 360

LpDFRb : * 380 * 400 * 420
 : TCACCATGGAATTGTGTATTTACAAAGTTTGAATTCTTATTTTTTTTATTATGAAGAAA : 420

LpDFRb : * 440 * 460 * 480
 : TACGGAAAACCAATACTGTATACCAGAGGCAAGTGTAACAATGTAAATAGTCGTGTAAAT : 480

LpDFRb : * 500 * 520
 : CTTGTTCAAGAATGAATGATAAAGTATTTTTTGCAAAAAAAAAA : 524

FIGURE 104

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LpDFRb : V L A Y E R P D A R G R Y L C I G A V L H R A H F L K L L K D L F P Q Y S F T A K C E D D G K P M A K P Y K F S X Q R L : 60

* 20 * 40 * 60

LpDFRb : R D L G L K F T P L A E S L Y E T V T C L Q K N G H L P L P A P M A P K R A Y L : 100

* 80 * 100

FIGURE 105

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	* 20 * 40 * 60	
LpDFRb1 :	GTCCTCGCCTACGAGCGCCCCGACGCCCGCGCCGCTACCTCTGCATCGGGGCGGTGCTG	: 60
LpDFRb2 :	-----	: -
LpDFRb3 :	-----	: -
	* 80 * 100 * 120	
LpDFRb1 :	CACCGCGCGCACTTCCTAAAGCTTCTCAAGGACCTCTTCCCGCAGTACTCCTTCACCGCC	: 120
LpDFRb2 :	-----	: -
LpDFRb3 :	-----	: -
	* 140 * 160 * 180	
LpDFRb1 :	AAGTGCGAAGACGACGCGCAAGCCCATGGCGAAGCCGTACAAGTTCTCCNACCAGAGGCTC	: 180
LpDFRb2 :	----- AAGCCGTACAAGTTCTCCNACCAGAGGCTC	: 30
LpDFRb3 :	----- GTTCTCNACCAGAGGCTC	: 19
	* 200 * 220 * 240	
LpDFRb1 :	AGGGACCTGGGATTAAATTCACCTCCGCTGGCGGAAAGTTGTACGAGACCGTGACGTGC	: 240
LpDFRb2 :	AGGGACCTGGGATTAAATTCACCTCCGCTGGCGGAAAGTTGTACGAGACCGTGACGTGC	: 90
LpDFRb3 :	AGGGACCTGGGATTAAATTCACCTCCGCTGGCGGAAAGTTGTACGAGACCGTGACGTGC	: 79
	* 260 * 280 * 300	
LpDFRb1 :	CTGCAAAAAAATGGCCACCTGCCTCTGCCCGCTCCCCTGGCGCCAAAGCGTGCATACCTA	: 300
LpDFRb2 :	CTGCAAAAAAATGGCCACCTGCCTCTGCCCGCTCCCATGGCGCCAAAGCGTGCATACCTA	: 150
LpDFRb3 :	CTGCAAAAAAATGGCCACCTGCCTCTGCCCGCTCCCATGGCGCCAAAGCGTGCATACCTA	: 139
	* 320 * 340 * 360	
LpDFRb1 :	TAATACTACAAAGACACGGCCGGGATCGACAAGCCAAGAAACAGAGGATTCTCCCGAGGT	: 360
LpDFRb2 :	TAATACTACAAAGACACGGCCGGGATCGACAAGCCAAGAAACAGAGGATTCTCCCGAGGT	: 210
LpDFRb3 :	TAATACTACAAAGACACGGCCGGGATCGACAAGCCAAGAAACAGAGGATTCTCCCGAGGT	: 199
	* 380 * 400 * 420	
LpDFRb1 :	TCACCATGGAATTGTGTATTTTCAAAAGTTTGAATTCTTATTTTTTTTATTATGAAGGAA	: 420
LpDFRb2 :	TCACCATGGAATTGTGTATTTTCAAAAGTTTGAATTCTTATTTTTTTTATTATGAAGGAA	: 270
LpDFRb3 :	TCACCATGGAATTGTGTATTTTCAAAAGTTTGAATTCTTATTTTTTTTATTATGAAGGAA	: 259
	* 440 * 460 * 480	
LpDFRb1 :	TACGGAAACCAATACTGTATACCAGAGGCAAGTGTAACAATGTAAATAGTCGTGTAAAT	: 480
LpDFRb2 :	TACGGAAACCAATACTGTATACCAGAGGCAAGTGTAACAATGTAAATAGTCGTGTAAAT	: 330
LpDFRb3 :	TACGGAAACCAATACTGTATACCAGAGGCAAGTGTAACAATGTAAATAGTCGTGTAAAT	: 319
	* 500 * 520	
LpDFRb1 :	CTTGTTCAGAATGAATGATAAAGTATTTTTTGCAAAAAA	: 524
LpDFRb2 :	CTTGTTCAGAATGAATGATAAAGTATTTTTTGCAAAAAA	: 374
LpDFRb3 :	CTTGTTCAGAATGAATGATAAAGTATTTTTTGCAAAAAA	: 363

FIGURE 106

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LpF3Ha : TCTCNAGACACACTGTGTAACCACGGTAGCGAGTGGCAAGACTAGCAGAAAGTACGGACA : 60
 LpF3Ha : TCAGCTAACCATTCTCTCAACTAGATAAGCATGGCTCCGGCGATGTCCAACCCTCTCCTC : 120
 LpF3Ha : AGTGATCGGGTGGCAGCTCCAAGAAAGTCCCATCTAGCCACGTTAGAGCGGTGGGAGAC : 180
 LpF3Ha : CGCCCAGACCTCGCCAATGTTCGACCACGAGTCCGGCGCGGGCATTCGCTCATCGACCTG : 240
 LpF3Ha : AAGCAGCTCGAAGGTCCAGGGCGCCGACGGGTCGTGAGGCCATCGGCTCCGCGTGCAG : 300
 LpF3Ha : AACGATGGGTTTTTTCATGGTGACGAATCATGGCATCCAGAGGCGGTCTGTGGAGGGGATG : 360
 LpF3Ha : CTGAGCGTGGCGAGGGAGTTCTTCCACCTGCCGGAGTCGGAGCGGCTCAAGTGCTACTCC : 420
 LpF3Ha : GACGACCCCAAGAAGGCGGTCCGGCTGTGACGAGCTTCAACGTGCGCACGGAGAAGGTG : 480
 LpF3Ha : AGCAACTGGCGCGACTTCTCCGGCTGCATTGCTACCTCTTGAGAGCTTCGTCGACCAG : 540
 LpF3Ha : TGGCCGTCGAACCCGCGCCTTCAGGCAAGTCGTGGCACCCTACTCGACGGAAGCGAGA : 600
 LpF3Ha : GCGCTGGCGCTGAGGCTCCTGGAGGCGATATCGGAGAGCCTAGGGCTGGAGAGAGGCCAC : 660
 LpF3Ha : ATGGTGAAGGCCATGGGGCGGCACGCGCAGCACATGGCGGTGAACTACTACCCGCCGTGC : 720
 LpF3Ha : CCGCAGCCGGAGCTCACCTACGGTCTGCCAGGGCACACGGACCCCAACGCCCTCACCATC : 780
 LpF3Ha : CTCCTCATGGATCCCCACGTCTCCGGCCTCCAGGTCCTCAGGGACGGCGCCAAGTGGATC : 840
 LpF3Ha : GCCGTCCACCCACGCCCCAACGCCCTGGTCATCAACCTAGGCGACCAGCTACAGGCGCTG : 900
 LpF3Ha : AGCAACGGCGCGTACAAGAGCGTGTGGCACCGGGCAGTGGTGAACGCGGAGCAGGAGCGT : 960
 LpF3Ha : CTGTCGGTGGCATCTTTCTGTGCCCCGTGCAACAGCGCGGTTATCTGCCCCGCGCCGAGG : 1020
 LpF3Ha : CTCGTGCGCGACGGGGAGGACCCCGTCTACCGGAGCTACACCTACGACGAGTACTACAAG : 1080
 LpF3Ha : AGGTTTTGGAGCAGGAACCTGGATCAGGAGCACTGCCTCGAGCTCTTCAGGAGTCAGCAC : 1140

FIGURE 107

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LpF3Ha : * 1160 * 1180 * 1200 :1200
 TGATGCTTGAACCTTGAGTTACTAGCTAGCTCTCCTTAACAGTGCAAATCCATGGCCCCAA

LpF3Ha : * 1220 * 1240 * 1260 :1260
 GAGGGCCCCGATTGCATGGTTACTTATGTTGTTTGAAC TGGTATTGCTTAAGTGCCTAAT

LpF3Ha : * 1280 * 1300 * 1320 :1320
 AACATTGCTACATTCTACTNCTATCTTGTCCGTTTAAAAATTATAAGATGGCCTAACCTTT

LpF3Ha : * 1340 * 1360 * 1380 :1380
 TTCTTAATTGTATGCATNCTGAACATATTTAAGTGTGTGTGTTTCAGACAGTTTAGTCTGC

LpF3Ha : A :1381

FIGURE 107 (cont)

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* 20 * 40 * 60
 LpF3Ha : MSNPLLSDRVARSKKVPSSHVRAVGDRPDLANVDHESGAGIPLIDLKQLEGPGRRRVVEA : 60

* 80 * 100 * 120
 LpF3Ha : IGSACENDGFFMVTNHGIPEAVVEGMLSVAREFFHLPESERLKCYSDDPKKAVRLSTSFN : 120

* 140 * 160 * 180
 LpF3Ha : VRTEKVSNNWRDFLRLHCYPLESFVDQWPSNPPAFRQVVGTYSTEARALALRLLEAISESL : 180

* 200 * 220 * 240
 LpF3Ha : GLERGHMVKAMGRHAQHMAVNYYPPCPQPELTYGLPGHTDPNALTILLMDPHVSGLQVLR : 240

* 260 * 280 * 300
 LpF3Ha : DGAKWIAVHPRPNALVINLGDQLQALSNGAYKSVWHRAVVNAEQERLSVASFLCPCNSAV : 300

* 320 * 340
 LpF3Ha : ICPAPRLVGDGEDPVYRSYTYDEYYKRFWSRNLDQEHCLFLFRSQH : 346

FIGURE 108

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      *           20           *           40           *           60
LpF3Ha1 : TCTCNAGACACACTGTGTAAACCACGGTAGCGAGTGGCAAGACTAGCAGAAAGTACGGACA : 60
LpF3Ha2 : --TCAGACACACTGTGTAAACCGGTAGCGAGTGGCAAGACTAGCAGAAAGTACGGACA : 58
LpF3Ha3 : ----- : -

      *           80           *           100          *           120
LpF3Ha1 : TCAGCTAACCATTTCCTCAACTAGAATAAGCATGGCTCCGGCGATGTCCAACCCTCTCCTC : 120
LpF3Ha2 : TCAGCTAACCATTTCCTCAACTAGAATAAGCATGGCTCCGGCGATGTCCAACCCTCTCCTC : 118
LpF3Ha3 : ----- : -

      *           140          *           160          *           180
LpF3Ha1 : AGTGATCGGGTGGCAGCTCCAAGAAAGTCCCATCTAGCCACGTTAGAGCGGTGGGAGAC : 180
LpF3Ha2 : AGTGATCGGGTGGCAGCTCCAAGAAAGTCCCATCTAGCCACGTTAGAGCGGTGGGAGAC : 178
LpF3Ha3 : ----- : -

      *           200          *           220          *           240
LpF3Ha1 : CGCCCAGACCTCGCCAATGTGCGACCACGAGTCCGGCGCGGGCATTCCGCTCATCGACCTG : 240
LpF3Ha2 : CGCCCAGACCTCGCCAATGTGCGACCACGAGTCCGGCGCGGGCATTCCGCTCATCGACCTG : 238
LpF3Ha3 : ----- : -

      *           260          *           280          *           300
LpF3Ha1 : AAGCAGCTCGAAGGTCCAGGGCGCCGCGAGGGTCGTGCGAGGCCATCGGCTCCGCGTGCGAG : 300
LpF3Ha2 : AAGCAGCTCGAAGGTCCAGGGCGCCGCGAGGGTCGTGCGAGGCCATCGGCTCCGCGTGCGAG : 298
LpF3Ha3 : ----- : -

      *           320          *           340          *           360
LpF3Ha1 : AACGATGGGTTTTTCATGGTGACGAATCATGGCATCCCAGAGCGGTCTGAGAGGGGATG : 360
LpF3Ha2 : AACGATGGGTTTTTCATGGTGACGAATCATGGCATCCCAGAGCGGTCTGAGAGGGGATG : 358
LpF3Ha3 : ----- : -

      *           380          *           400          *           420
LpF3Ha1 : CTGAGCGTGGCGAGGGAGTTCTTCCACCTGCCGGAGTCGGAGCGGCTCAAGTGCTACTCC : 420
LpF3Ha2 : CTGAGCGTGGCGAGGGAGTTCTTCCACCTGCCGGAGTCGGAGCGGCTCAAGTGCTACTCC : 418
LpF3Ha3 : ----- : -

      *           440          *           460          *           480
LpF3Ha1 : GACGACCCCAAGAAGGCGGTCCGGCTGTGCGACGAGCTTCAACGTGCGCACGGAGAAGGTG : 480
LpF3Ha2 : GACGACCCCAAGAAGGCGGTCCGGCTGTGCGACGAGCTTCAACGTGCGCACGGAGAAGGTG : 478
LpF3Ha3 : ----- : -

      *           500          *           520          *           540
LpF3Ha1 : AGCAACTGGCGCGACTTCCCTCCGGCTGCATTGCTACCCTCTTGAGAGCTTCGTCGACCAG : 540
LpF3Ha2 : AGCAACTGGCGCGACTTCCCTCCGGCTGCATTGCTACCCTCTTGAGAGCTTCGTCGACCAG : 538
LpF3Ha3 : ----- : -

      *           560          *           580          *           600
LpF3Ha1 : TGGCCGTGGAACCCGCCCCGCTTCAGGCAAGTCGTGCGGCACCTACTCGACGGAAGCGAGA : 600
LpF3Ha2 : TGGCCGTGGAACCCGCCCCGCTTCAGGCAAGTCGTGCGGCACCTACTCGACGGAAGCGAGA : 598
LpF3Ha3 : -----GGGAAGTCGG : 12

      *           620          *           640          *           660
LpF3Ha1 : GCGCTGGCGCTGAGGCTCCTGGAGGCGATATCGGAGAGCCTAGGGCTGGAGAGAGGCCAC : 660
LpF3Ha2 : GCGCTGGCGCTGAGGCTCCTGGAGGCGATATCGGAGAGCCTAGGGCTGGAGAGAGGCCAC : 658
LpF3Ha3 : CTGCTGGCGCTTCGGCTTCTGCGGCGCATGTCGCTGGCGCTGGGGCTGGAGAGAGGGTAT : 72

      *           680          *           700          *           720
LpF3Ha1 : ATGGTGAAGGCCATGGGGCGGCACGCGCAGCACATGGCGGTGAACTACTACCCGCCGTGC : 720
LpF3Ha2 : ATGGTGAAGGCCATGGGGCGGCACGCGCAGCACATGGCGGTGAACTACTACCCGCCGTGC : 718
LpF3Ha3 : CTCGAGAAGGTGCTGGGGGAGCAGCAGCAGCACATGGCGGTGAACTACTACCCGCCGTGC : 132

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FIGURE 109

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      *           740           *           760           *           780
LpF3Ha1 : CCGCAGCCGGAGCTCACCTACGGTCTGCCAGGGCA----- :755
LpF3Ha2 : CCGCAGCCGGAGCTCACCTACGGTCTGCCAGGGCACACGGACCCCAATGCCCTCACCATT :778
LpF3Ha3 : CCGCAGCCGGAGCTCACCTACGGTCTGCCCAAGCACACGGACCCCAACGCCCTCACCATC :192

      *           800           *           820           *           840
LpF3Ha1 : ----- : -
LpF3Ha2 : CT----- :780
LpF3Ha3 : CTCCTCATGGATCCCCACGTCTCCGGCCTCCAGGTCTCAGGGACGGCGCCAAGTGGATC :252

      *           860           *           880           *           900
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : GCCGTCCACCCACGCCCCAACGCCCTGGTCATCAACCTAGGCGACCAGCTACAGGCGCTG :312

      *           920           *           940           *           960
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : AGCAACGGCGCGGTACAAGAGCGTGTGGCACCGGGCAGTGGTGAACGCGGAGCAGGAGCGT :372

      *           980           *           1000           *           1020
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : CTGTGCGGTGGCATCTTTCTGTGCCCGTGCAACAGCGCGGTTATCTGCCCCGCGCCGAGG :432

      *           1040           *           1060           *           1080
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : CTCGTGCGCGACGCGGGAGGACCCCGTCTACCGGAGCTACACCTACGACGAGTACTACAAG :492

      *           1100           *           1120           *           1140
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : AGGTTTTGGAGCAGGAACCTGGATCAGGAGCACTGCCTCGAGCTCTTCAGGAGTCAGCAC :552

      *           1160           *           1180           *           1200
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : TGATGCTTGAACCTTGAGTTACTAGCTAGCTCTCCTTAACAGTGCAAAATCCATGGCCCCAA :612

      *           1220           *           1240           *           1260
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : GAGGGCCCCGATTGCATGGTTACTTATGTTGTTTGAACCTGGTATTGCTTAAGTGCCCTAAT :672

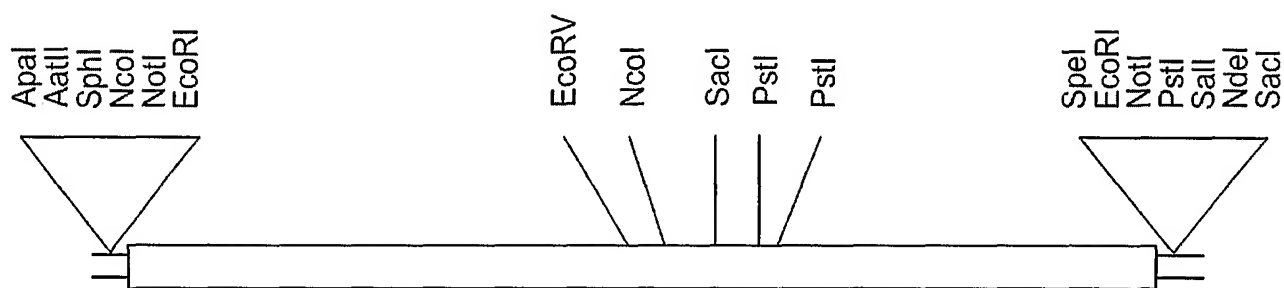
      *           1280           *           1300           *           1320
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : AACATTGCTACATTCTACTNCTATCTTGTCCGTTTAAAATTATAAGATGGCCTAACCTTT :732

      *           1340           *           1360           *           1380
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : TTCTTAATTGTATGCATNCTGAACATATTTAAGTGTGTGTGTTTCAGACAGTTTAGTCTGC :792

LpF3Ha1 : - : -
LpF3Ha2 : - : -
LpF3Ha3 : A : 793

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FIGURE 109 (cont)

183/271**LpF3OH****FIGURE 110**

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1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GACTCTCAGA
51 ACACACTGTG TAACCACGGT AGCGAGTGGC AAGACTAGCA GAAAGTACGG
101 ACATCAGCTA ACCATTCCTC AACTAGAATA AGCATGGCTC CGGCGATGTC
151 CAACCCTCTC CTCAGTGATC GGGTGGCACG CTCCAAGAAA GTCCCATCTA
201 GCCACGTTAG AGCGGTGGGA GACCGCCCAG ACCTCGCCAA TGTCGACCAC
251 GAGTCCGGCG CGGGCATTCC GCTCATCGAC CTGAAGCAGC TCGAAGGTCC
301 AGGGCGCCGC AGGGTCGTCG AGGCCATCGG CTCCGCGTGC GAGAACGATG
351 GGTTTTTTCAT GGTGACGAAT CATGGCATCC CAGAGGCGGT CGTGGAGGGG
401 ATGCTGAGCG TGGCGAGGGA GTTCTTCCAC CTGCCGGAGT CGGAGCGGCT
451 CAAGTGCTAC TCCGACGACC CCAAGAAGGC GGTCCGGCTG TCGACGAGCT
501 TCAACGTGCG CACGGAGAAG GTGAGCAACT GGCGCGACTT CCTCCGGCTG
551 CATTGCTACC CTCTTGAGAG CTTCGTCGAC CAGTGGCCGT CGAACCCGCC
601 CGCCTTCAGG CAAGTCGTCG GCACCTACTC GACGGAAGCG AGAGCGCTGG
651 CGCTGAGGCT CCTGGAGGCG ATATCGGAGA GCCTAGGGCT GGAGAGAGGC
701 CACATGGTGA AGGCCATGGG GCGGCACGCG CAGCACATGG CGGTGAACTA
751 CTACCCGCCG TGCCCGCAGC CGGAGCTCAC CTACGGTCTG CCAGGGCACA
801 AGGACCCCAA TGCCATCACG CTCCTCCTGC AGGACGGCGT CTCCGGCCTG
851 CAGGTCCAGC GCGACGGCCG GTGGGTGGCC GTCAACCCGG TGCCCAACGC
901 CCTCGTCATC AACATCGGCG ATCAGTTACA GGCGCTGAGC AACGACCGAT
951 ACAAGAGCGT GAACCACAGA GTGATCGTCA ACAGCGCGAG CGAGAGGATT
1001 TCGGTGCCGA CGTTCTACTG CCCGTCGCCG GACACGGTGG TCGCGCCGGC
1051 CGACGCGCTG GTGGACGACG CCCACCCTCG GGCCTACCAG CCCTTCACGT
1101 ACCAGGAGTA CTACGAGGAG TTCTGGAAGA TGGGCCTTCA GTCAGCAAGT
1151 TGCTTCGACA GGTTCGACG GATCGAGTGA TGGACAAGAC GTGGGCCGTT
1201 GTTATCTCCT GGGCCATGAG CGTTGCCGCA GCCGATGTGT CGCCATATGG
1251 TGGAGACGTT TCCTCCCTCC GGAAAAGAAA AATAAAACAG AGTGGAGACC
1301 ACTAGAACCG TCAGATAGCA TCCCAAAAAA AAAAAAAAAA AAAAAAAAAA
1351 AAAAGTACTC TGC GTTGT TA CCACTGCTTA ATCACTAGTG AATTC

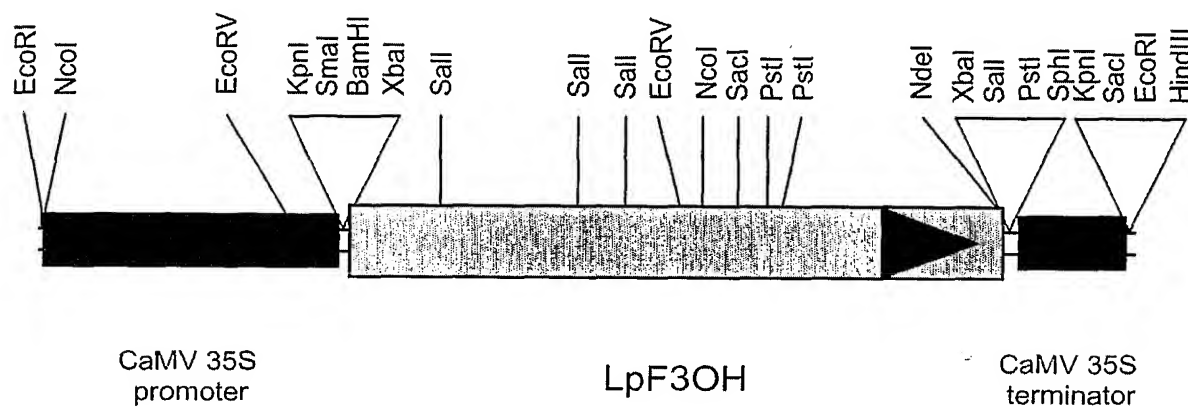
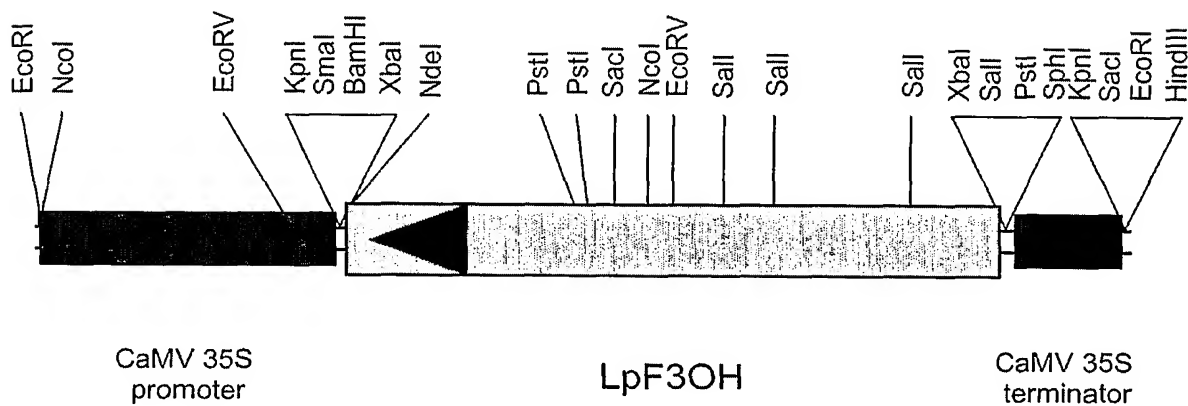
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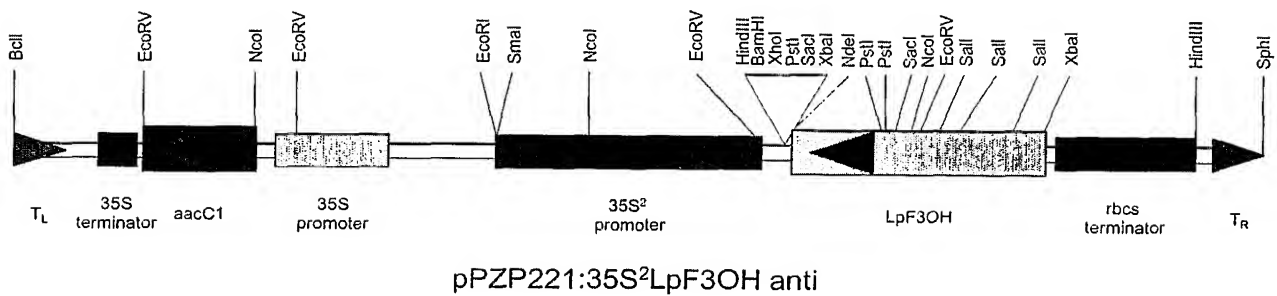
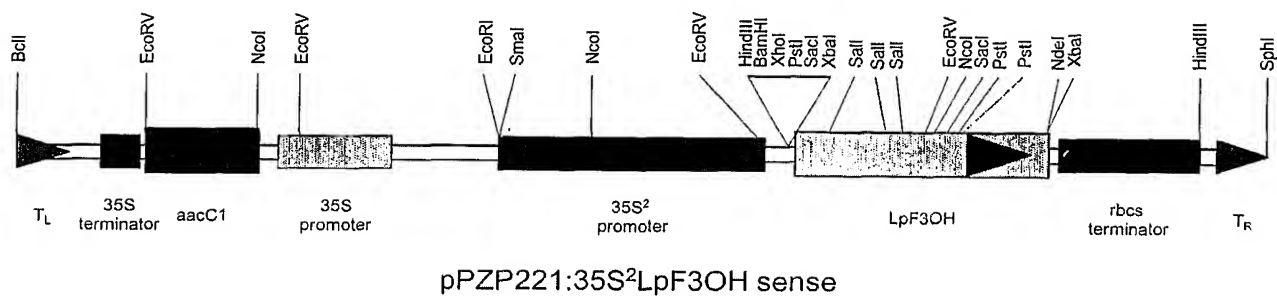
FIGURE 111

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1 MAPAMSNPLL SDRVARSKKV PSSHVRAVGD RPDLANVDHE SGAGIPLIDL
51 KQLEGPGRRR VVEAIGSACE NDGFFMVTNH GIPEAVVEGM LSVAREFFHL
101 PESERLKCYS DDPKKAVRLS TSFNV RTEKV SNWRDFLRLH CYPLESFVDQ
151 WPSNPPAFRQ VVGTYSTEAR ALALRLLEAI SESLGLERGH MVKAMGRHAQ
201 HMAVNYYPFC PQPELTYGLP GHKDPNAITL LLQDGVSGLQ VQRDGRWVAV
251 NPVPNALVIN IGDQLQALSN DRYKSVNHRV IVNSASERIS VPTFYCPSPD
301 TVVAPADALV DDAHPRAYQP FTYQEYYEEF WKMGLQSASC LDRFRRIE

FIGURE 112

186/271**pDH51LpF3OH sense****pDH51LpF3OH anti****FIGURE 113**

187/271**FIGURE 114**

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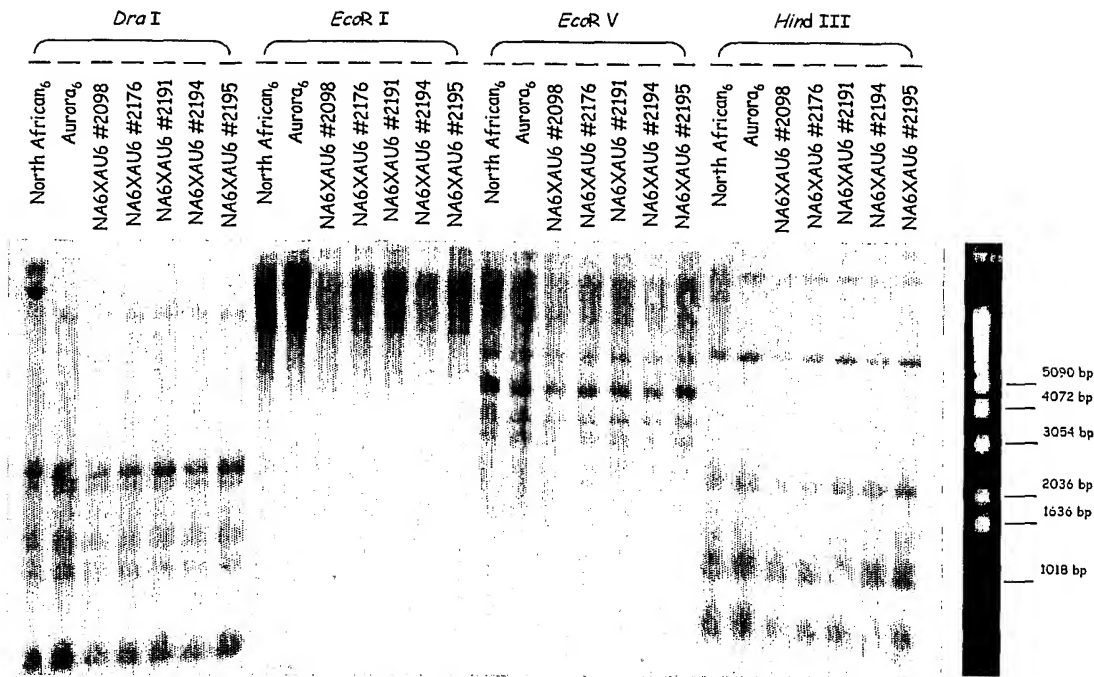


FIGURE 115

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TrBANa

FIGURE 116

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1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG ATAAAAACTG
51  CACTAGTGTG TATAAGTTTC TTGGTGAAAA AAGAGTTTGT AAATTAACAT
101 CATGGCTAGT ATCAAACAAA TTGGAAACAA GAAAGCATGT GTGATTGGTG
151 GCACTGGTTT TGTTGCATCT ATGTTGATCA AGCAGTTACT TGAAAAGGGT
201 TATGCTGTTA ATACTACCGT TAGAGACCCA GATAGCCCTA AGAAAATATC
251 TCACCTAGTG GCACTGCAAA GTTTGGGGGA ACTGAATCTA TTTAGAGCAG
301 ACTTAACAGT TGAAGAAGAT TTTGATGCTC CTATAGCAGG ATGTGAACTT
351 GTTTTTCAAC TTGCTACACC TGTGAACTTT GCTTCTCAAG ATCCTGAGAA
401 TGACATGATA AAGCCAGCAA TCAAAGGTGT GTTGAATGTG TTGAAAGCAA
451 TTGCAAGAGC AAAAGAAGTT AAAAGAGTTA TCTTAACATC TTCGGCAGCC
501 GCGGTGACTA TAAATGAACT CAAAGGGACA GGTCAATGTTA TGGATGAAAC
551 CAACTGGTCT GATGTTGAAT TTCTCAACAC TGCAAAACCA CCCACTTGGG
601 GTTATCCTGC CTCAAAAATG CTAGCTGAAA AGGCTGCATG GAAATTTGCT
651 GAAGAAAATG ACATTGATCT AATCACTGTG ATACCTAGTT TAACAACTGG
701 TCCTTCTCTC ACACCAGATA TCCCATCTAG TGTGCGCTTG GCAATGTCTC
751 TAATAACAGG CAATGATTTT CTCATAAATG CTTTGAAAGG AATGCAGTTT
801 CTGTCGGGTT CGTTATCCAT CACTCATGTT GAGGATATTT GCCGAGCTCA
851 TATATTTCTT GCAGAGAAAG AATCAGCTTC TGGTAGATAC ATTTGCTGTG
901 CTCACAATAC TAGTGTTCCC GAGCTTGCAA AGTTTCTCAA CAAACGATAT
951 CCTCAGTATA AAGTTCCAAC TGAATTTGAT GATTGCCCCA GCAAGGCAAA
1001 GTTGATAATC TCTTCTGAAA AGCTTATCAA AGAAGGGTTC AGTTTCAAGC
1051 ATGGTATTGC CGAAACTTTC GACCAGACTG TCGAGTATTT TAAGACTAAG
1101 GGGGCACTGA AGAATTAGAT TTTGATATTT CTAATTCAAT AGCAAACCTCT
1151 AAGCTTGTTA TGTGTTTGTG AAGTTCAGAG TGAAATATCA AATGAATAAG
1201 TGGAGAGAGC ACAATAAGAG GAGAGCACAA TAATTTTGGA AAAAAAAAAA
1251 AAAAAAAAAA AAAAAAAGT ACTCTGCGTT GTTACCACTG CTTAATCACT
1301 AGTGAATTC

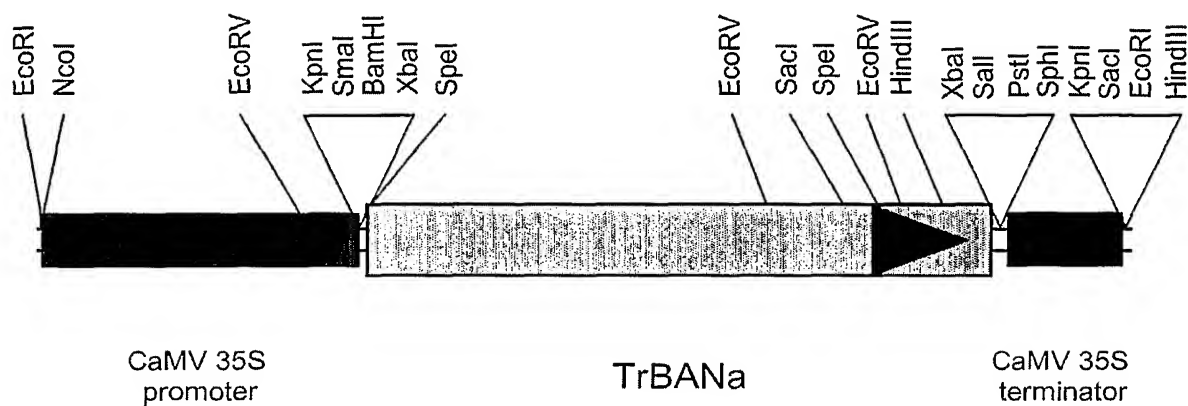
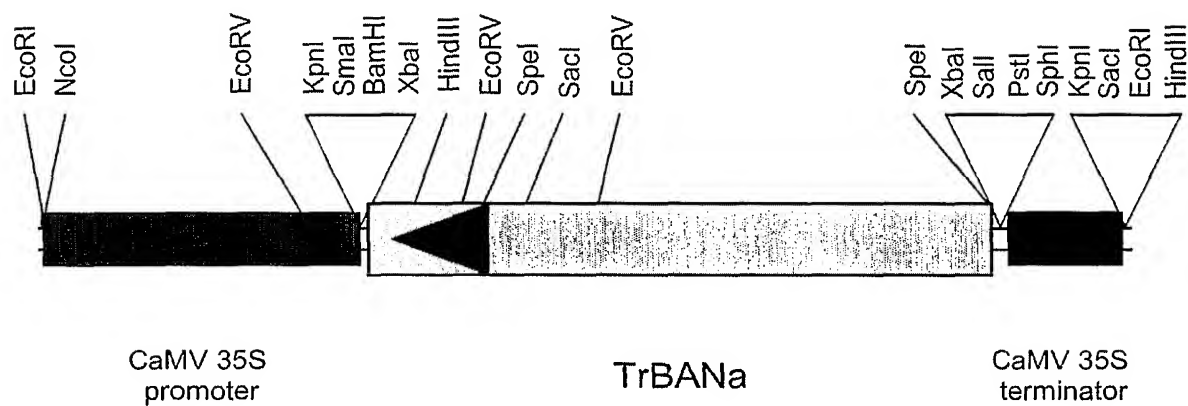
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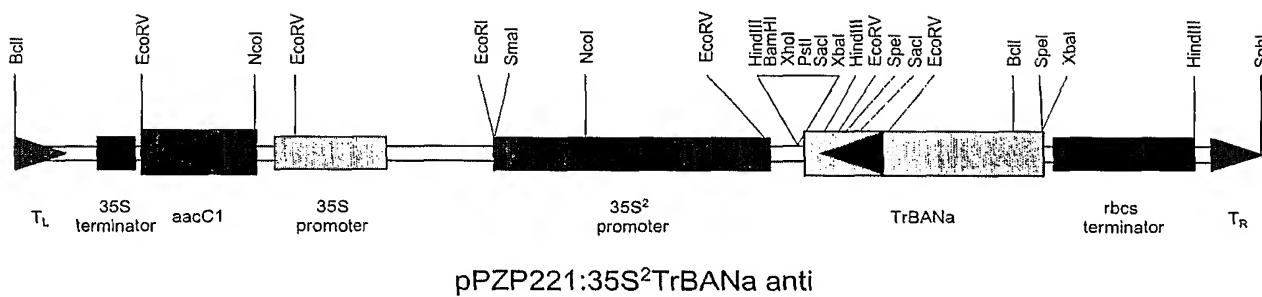
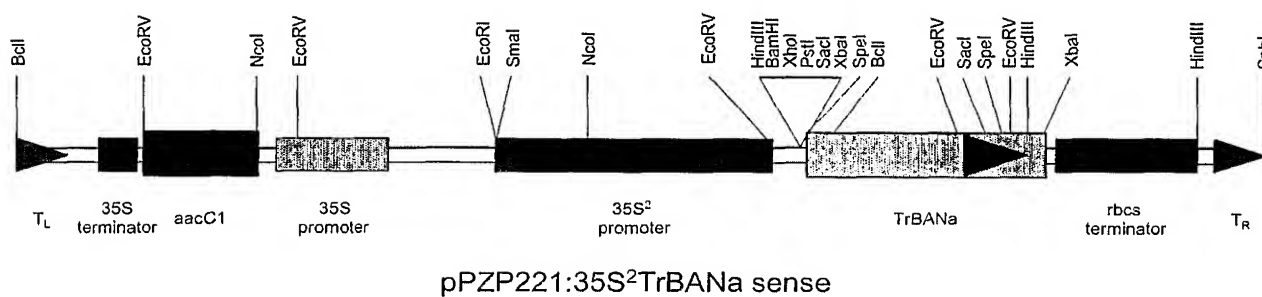
FIGURE 117

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1 MASIKQIGNK KACVIGGTGF VASMLIKQLL EKGAVNTTV RDPDSPKKIS
51 HLVALQSLGE LNLFRADLTV EEDFDAPIAG CELVFQLATP VNFASQDPEN
101 DMIKPAIKGV LNLKAIARA KEVKRVILTS SAAAVTINEL KGTGHVMDDET
151 NWSDVEFLNT AKPPTWGYP A SKMLAEKAAW KFAEENDIDL ITVIPSLTTG
201 PSLTPDIPSS VGLAMSLITG NDFLINALKG MQFLSGSLSI THVEDICRAH
251 IFLAEKESAS GRYICCAHNT SVPELAKFLN KRYPQYKVPT EFDDCPSKAK
301 LIISSEKLIK EGFSFKHGIA ETFDQTVEYF KTKGALKN

FIGURE 118

192/271**pDH51TrBANa sense****pDH51TrBANa anti****FIGURE 119**

193/271**FIGURE 120**

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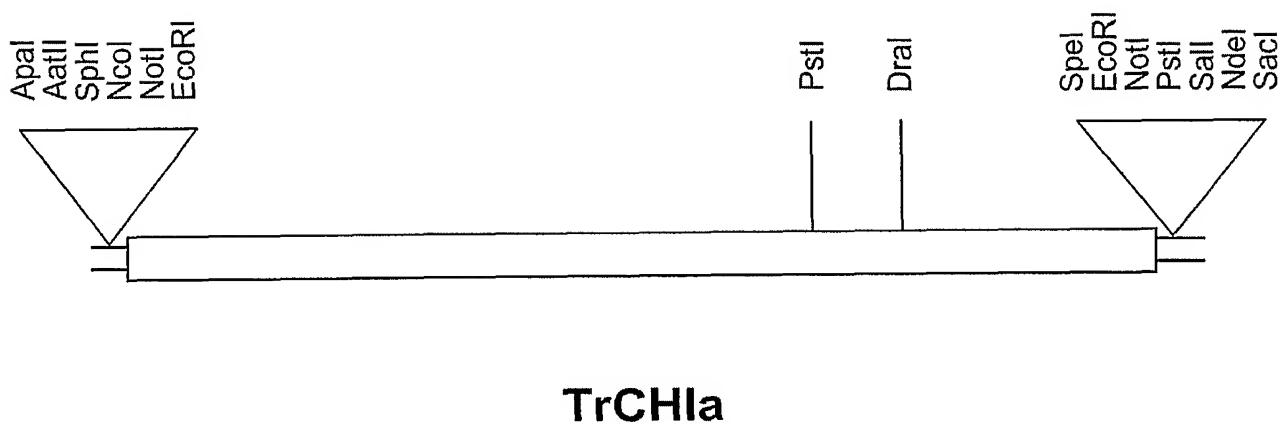


FIGURE 121

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1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GACTTAAACA
51  TTGACACAAG TCCCAAATAA AAAAGATCTG AAACAACATA GTCACCCCAT
101 TTTTAAACAT TAAACTAAAA ATATGTCGGC CATCACCGCA ATCCAAGTCG
151 AGAACCTTGA ATTTCCGGCT GTGGTTACTT CTCCGGCCAC CGGTAAGTCA
201 TATTTTCTTG GTGGTGCAGG GGAGAGAGGT TTGACTATTG AAGGAACTT
251 CATCAAGTTC ACTGCCATAG GAGTATATTT GGAAGATGTA GCAGTGGCTT
301 CACTTGCCAC TAAATGGAAG GGTAATCCTT CTGAGGAGTT GCTTGAGACT
351 CTTGACTTCT ATAGAGACAT CATTTTCAGGA CCCTTTGAAA AGTTGATTCTG
401 AGGATCGAAG ATTAGGGAAT TGAGTGGTCC TGAGTACTCA AGGAAGGTTA
451 ATGAAAACCTG CGTGGCACAC TTAAATCTG TTGGGACTTA TGGAGATGCT
501 GAAGCTGAAG CTATGCAAAA ATTTGTTGAA GCCTTCAAGC CTATTAATTT
551 TCCACCTGGT GCCTCTGTTT TTTACAGGCA ATCACCTGAT GGAATATTAG
601 GGCTTAGTTT CTCTCAAGAT GCAAGTATAC CAGAAAAGGA GGCTGCAGTA
651 ATAGAGAACA AGGCAGCTTC ATCGGCAGTG TTAGAAACTA TGATTGGTGA
701 ACATGCTGTT TCTCCTGATT TAAAGCGTTG TTTGGCTGCA AGATTACCTG
751 CCTTGTTGAA CGAGGGTACT TTCAAGATTG AATGAAACT GATTATTATT
801 ATCTCCAAAA GCATTGCAGC ACAAGATTGA GTCATTTATG AGCATGGACA
851 TTTTATATGTC CACACATGTT TAACTTTTGT ATCTCTCTTT AGATTCTCAT
901 CAATATCAAT AATACTAATA TGAAACGAAG TCAAAAAAAA AAAAAAAA
951 AAAAAAAAAA AAAAGTACTC TCGTTGTTA CCACTGCTTA ATCACTAGTG
1001 AATTC

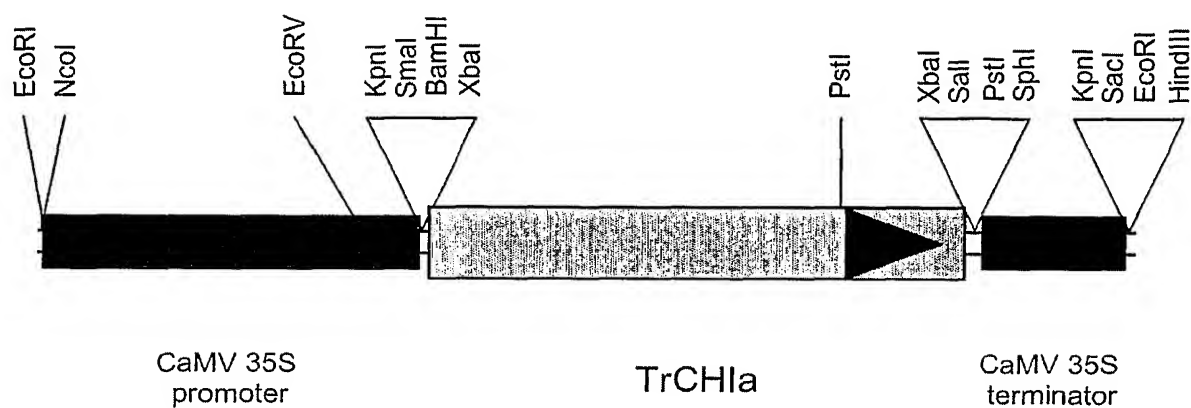
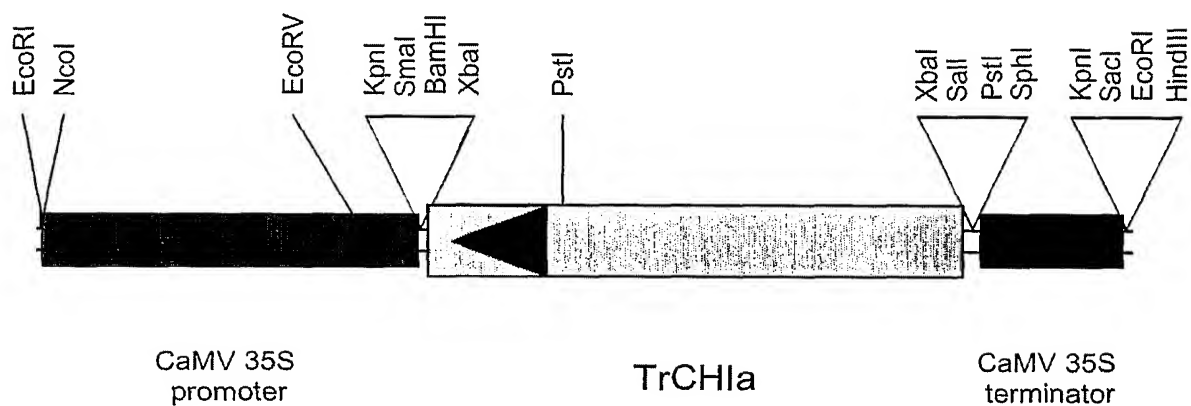
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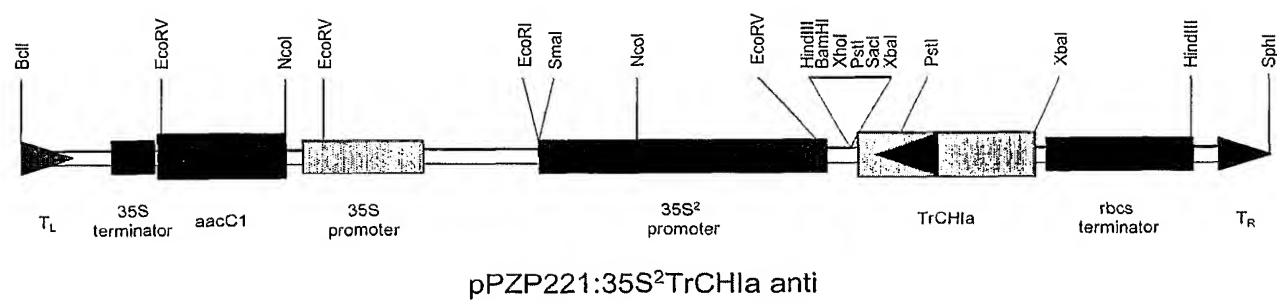
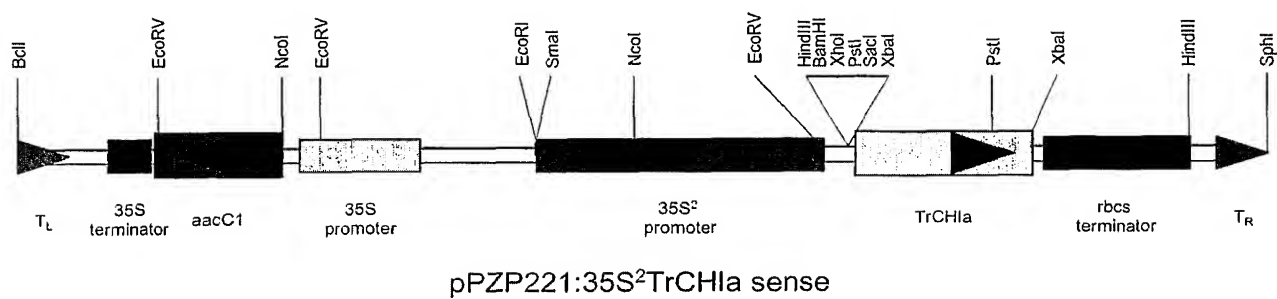
FIGURE 122

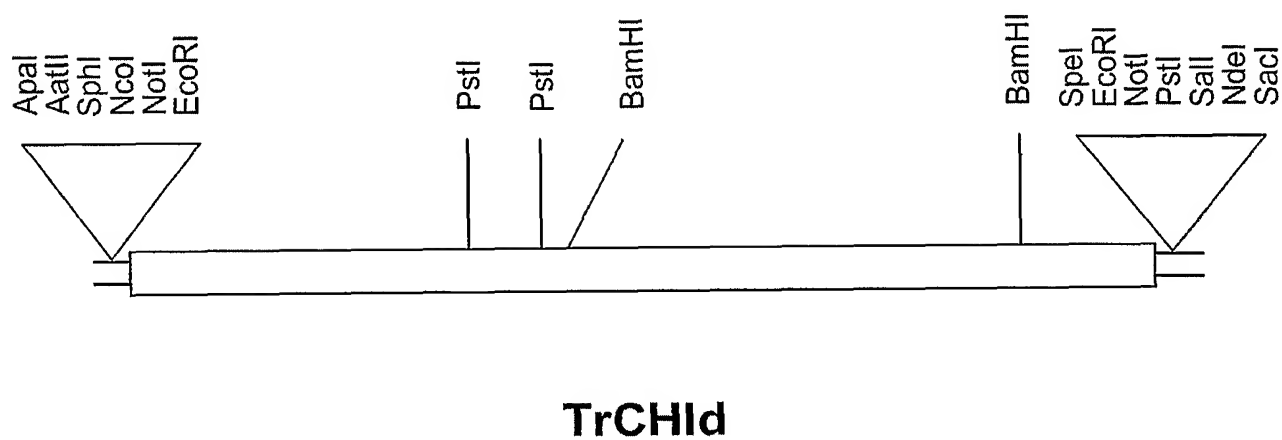
196/271

1 MSAITAIQVE NLEFPAVVTs PATGKSYFLG GAGERGLTIE GNFIKFTAIG
51 VYLEDVAVAS LATKWKGKSS EELLETLDFY RDIISGPF EK LIRGSKIREL
101 SGPEYSRKVN ENCV AHLKSV GTYGDAEAEA MQKFVEAFKP INFPPGASVF
151 YRQSPDGILG LSFSQDASIP EKEAAVIENK AASSAVLETM IGEHAVSPDL
201 KRCLAARLPA LLNEGTFKIE

FIGURE 123

197/271**pDH51TrCHla sense****pDH51TrCHla anti****FIGURE 124**

198/271**FIGURE 125**

199/271**FIGURE 126**

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1  GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGACA
51 TTACAACTCA CAACACCTTC TCCATTACCA TCTATCTTCT ACTAAGTTCA
101 ACGAGATCAA TGGCACTTCC TTCTGTCACC GCTTTGAATA TCGAGAACAA
151 TCTATTCCCT CCTACCGTCA CACCACCGGG ATCCACCAAC AATTTCTTCC
201 TCGGCGGTGC AGGAGAGCGG GGTCTTCAAA TTCAAGACAA ATTTGTCAAA
251 TTCACCGCTA TTGGTGTTTA TCTACAGGAC ATTGCTGTTC CTTACCTCGC
301 CACTAAATGG AAGGGTAAGA CTGCTCAAGA GCTAACGGAA ACTGTTTCCTT
351 TCTTCAGGGA CATCGTTACA GGTCCATTG AGAAATTTAT GCAGGTGACA
401 ATGATCTTGC CATTGACTGG GCAACAATAC TCAGAGAAAG TGTGAGAAAA
451 TTGTGTAGCT ATTTGGAAGT CTCTTGGGAT TTATACCGAC GAAGAAGCCA
501 AAGCAATTGA GAAGTTTGTT TCTGTCTTCA AAGATGAAAC ATTCCCACCA
551 GGCTCCTCTA TCCTTTTCAC AGTATTACCC AAAGGATTAG GATCACTAAC
601 GATAAGTTTC TCTAAAGATG GATCCATTCC AGAGACCGAG TCTGCAGTTA
651 TAGAGAATAA GCTACTCTCA CAAGCTGTGC TTGAGTCGAT GATAGGGGCG
701 CACGGTGTCT CCCCTGCAGC AAAACAGAGT TTGGCCACCA GGTTATCCGA
751 GTTATTCAAC GAGGTTGGTG ATGCTAGCAA CTGATTATAT CAACAAAACG
801 AAAATGAAAG TCCTTTCTGC AATAAAGACC AAGCGGAAAT TTTATTTTAG
851 GTGCACTTTG AAATGACCTC TTTGGCGACT TTTTCTTGTA CTAATAATAA
901 AGAGTG TGTT TGTATCATGT TGTAATTTTA TTTTAGAAAA AGTGAGGTAA
951 GAAAGGAGTC CTTATGTTTA TTTCAATTAT TGAAAAATTA TTTGCATGTA
1001 TAATTGATTT CAACTGATGT TATTTAATCA CGTTTTTTCT AAAAAAAAAA
1051 AAAAAAAAAA AAAAAAAAAA GTACTCTGCG TTGTTACCAC TGCTTAATCG
1101 AATTC

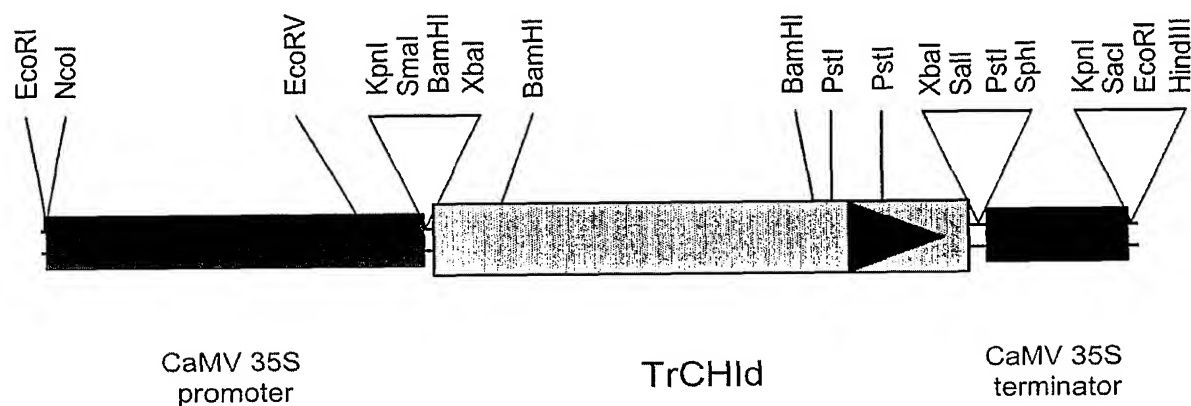
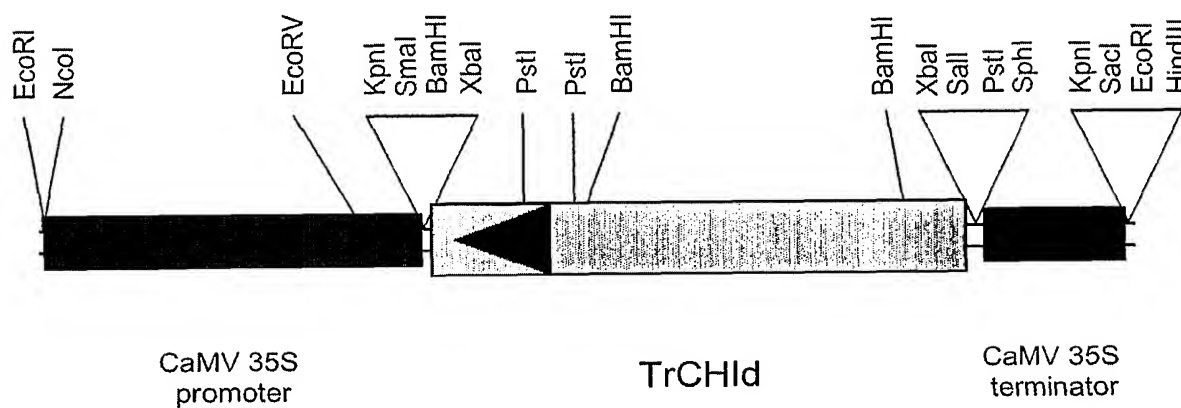
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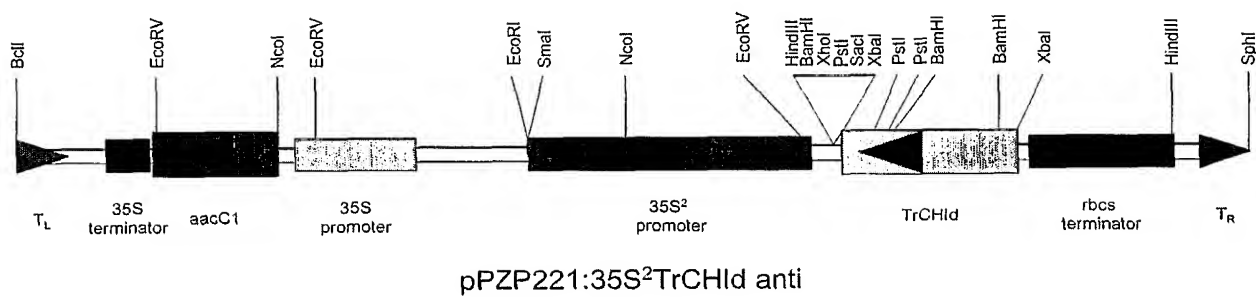
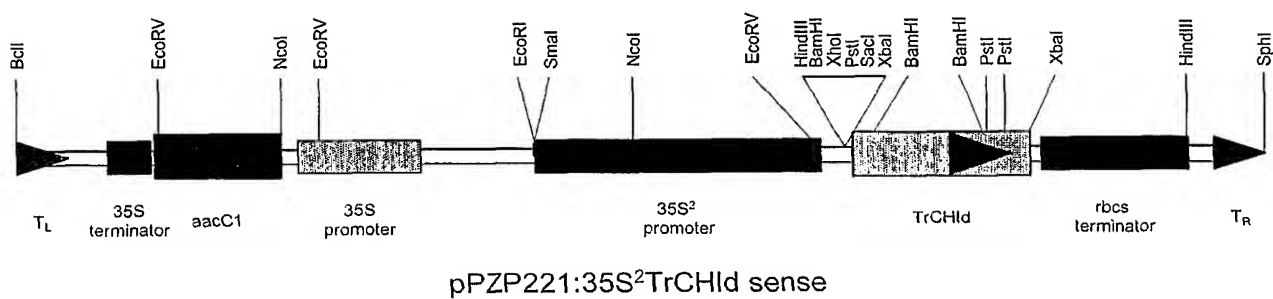
FIGURE 127

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1 MALPSVTALN IENNLFPPPTV TPPGSTNNFF LGGAGERGLQ IQDKFVKFTA
51 IGVYLQDIAV PYLATKWKGK TAQELTETVP FFRDIVTGPF EKFMQVTMIL
101 PLTGQQYSEK VSENCVAIWK SLGIYTDEEA KAIEKFVSVF KDETFFPPGSS
151 ILFTVLPKGL GSLTISFSKD GSIPETESAV IENKLLSQAV LESMIGAHGV
201 SPAAKQSLAT RLSELFNEVG DASN

FIGURE 128

202/271**pDH51TrCHId sense****pDH51TrCHId anti****FIGURE 129**

203/271**FIGURE 130**

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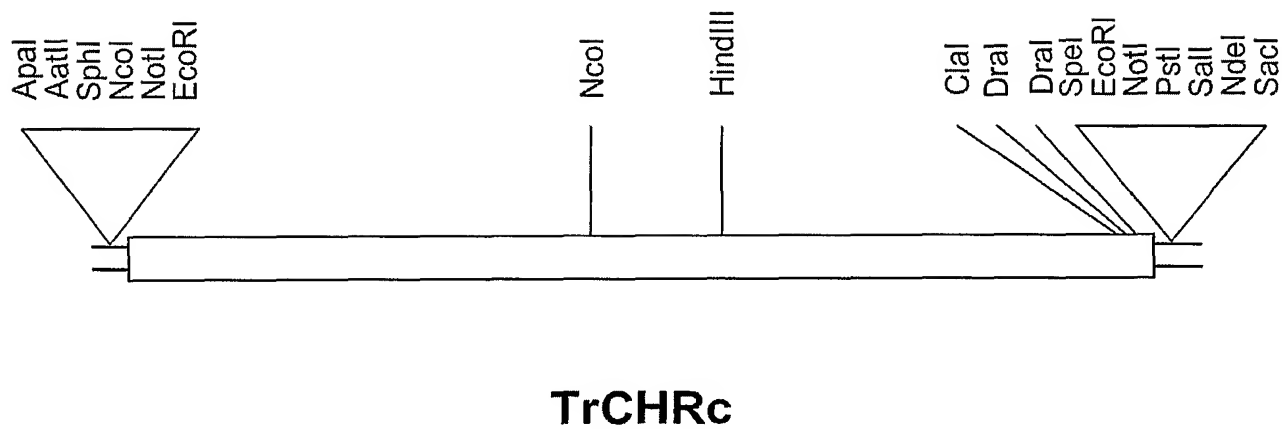


FIGURE 131

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1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GATTCAAACA
51 TAGCTCAAAG TGTGTAACAA ATTTCTTAAC TTAAAACATT TTCAACCCAA
101 CAAAAAAAAA CAAAGACAAA AACATGGGTA GTGTTGAAAT TCCAACAAAG
151 GTTCTTACTA ACAGTTCTAG TCAAGTGAAA ATGCCTGTGG TTGGAATGGG
201 ATCAGCACCT GATTTACAT GTAAAGAAAGA CACAAAAGAT GCAATCATTG
251 AAGCCATCAA ACAGGGTTAT AGACACTTTG ATACTGCTGC TGCTTATGGC
301 TCAGAACAAG CTCTTGGTGA AGGTTTGAAA GAAGCAATTG AACTTGGTCT
351 TGTCAC TAGA GAAGACCTTT TTGTTACTTC TAAACTTTGG GTCAC TGAAA
401 ATCATCCTCA TCTTGTTGTT CCTGCTCTTC AAAATCTCT CAAGACTCTT
451 CAATTGGAGT ACTTGGACTT GTATTTGATC CATTTGGCCAC TTAGTTCTCA
501 GCCTGGAAAG TTTTCATTTT CAATTGATGT GGCAGATCTC TTGCCATTTG
551 ATGTGAAGGG TGTTTGGGAA TCCATGGAAG AAGGCTTGAA ACTTGGACTC
601 ACTAAAGCTA TTGGTGTTAG TAACTTCTCT GTCAAGAAAC TTCAAAATCT
651 TGTCTCAGTT GCCACTGTTC TTCCTGCTGT CAATCAAGTG GAGATGAACC
701 TTGCATGGCA ACAAAGAAG CTTAGAGAAT TTTGCAATGC AAATGGAATA
751 GTGT TAACTG CATTTTCACC ATTGAGAAAA GGTGCAAGCA GGGGACCAA
801 TGAAGTTATG GAAAATGATA TGCTTAAAGA GATTGCAGAT GCTCATGGAA
851 AGTCTGTTGC ACAAATTTCA TTGAGATGGT TATATGAACA AGGAGTCACT
901 TTTGTTCCCA AGAGCTATGA TAAGGAAAGA ATGGGTCAAA ATTTGGCTAT
951 CTTTGATTGG ACATTGGCAA AAGAAGATCA TGAGAAAATT GATCAAATTA
1001 AGCAGAACCG TTTGATCCCT GGACCAACCA AGCCAGGACT CAGTGACCTA
1051 TGGGATGATG AAATATAAAG TGGAAGATGT TAAAAGTCCC TTAAGCTCAC
1101 TCAATATCTA TCTATTGTGT ACTTTT TGCA TTTGGGGTTT GAAATTGAGT
1151 CACCCTTGTT TCTGTATCGA TTTAAAATTT AAATAATCAA TTTTTCATTA
1201 CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AGTACTCTGC GTTGTTACCA
1251 CTGCTTAATC ACTAGTGAAT TC

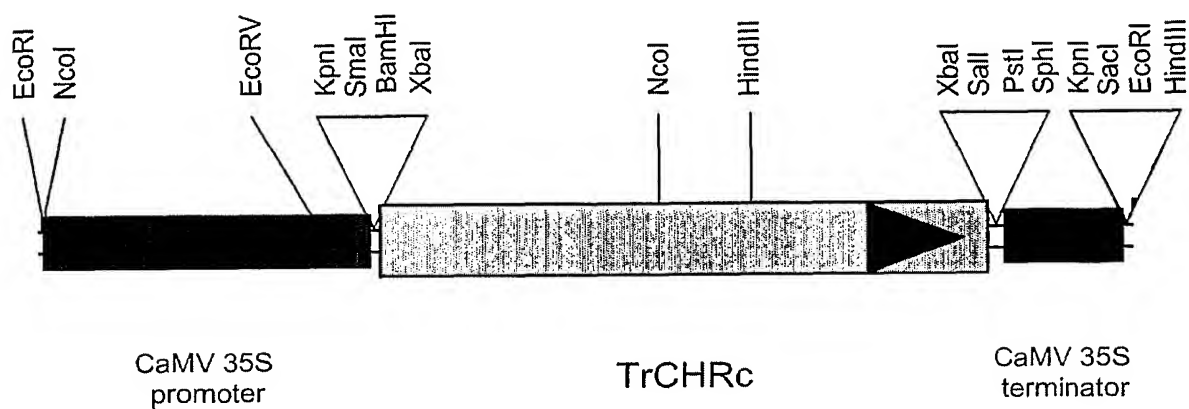
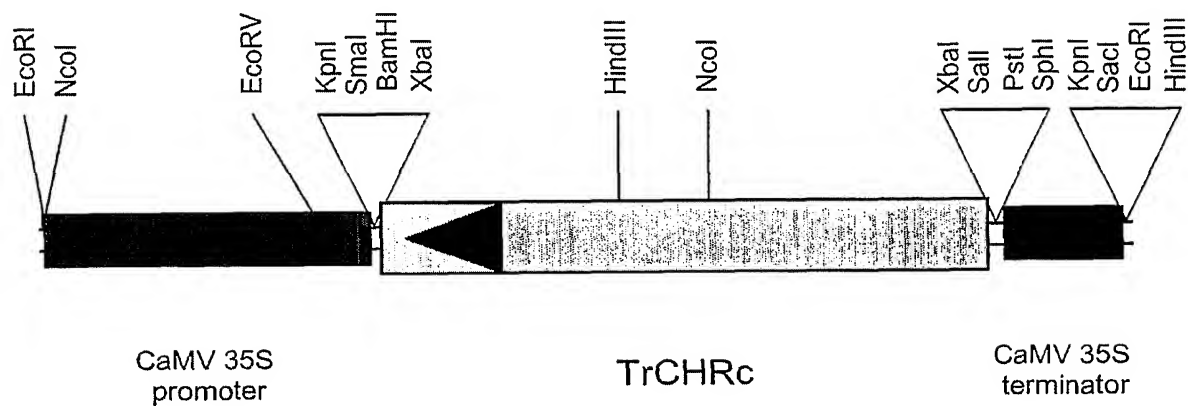
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FIGURE 132

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1 MGSVEIPTKV LTNSSSQVKM PVVGMGSAPD FTCKKDTKDA IIEAIKQGYR
51 HFDTAAAYGS EQALGEGGLKE AIELGLVTRE DLFVTSKLWV TENHPhLVVP
101 ALQKSLKTLQ LEYLDLYLIH WPLSSQPGKF SFPIDVADLL PFDVKGVWES
151 MEEGLKLGLT KAIGVSNFSV KKLQNLVSVA TVLPAVNQVE MNLAWQQKKL
201 REFNCNANGIV LTAFSPLRKG ASRGPNEVME NDMLKEIADA HGKSVAQISL
251 RWLYEQGVTF VPksYDKERM GQNLAIFDWT LAKEDHEKID QIKQNRLLPG
301 PTKPGLSDLW DDEI

FIGURE 133

207/271**pDH51TrCHRC sense****pDH51TrCHRC anti****FIGURE 134**

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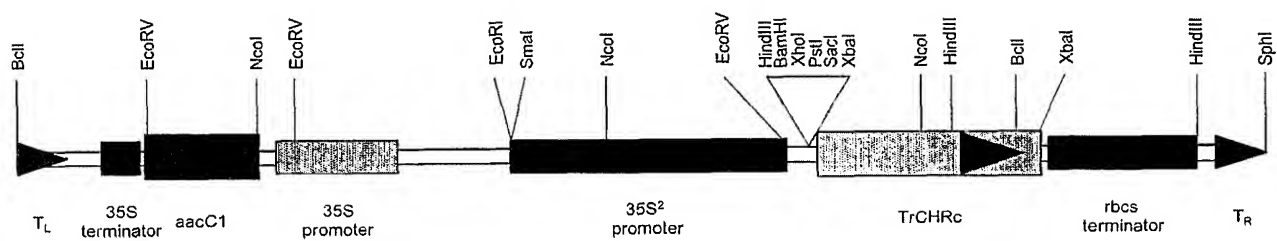
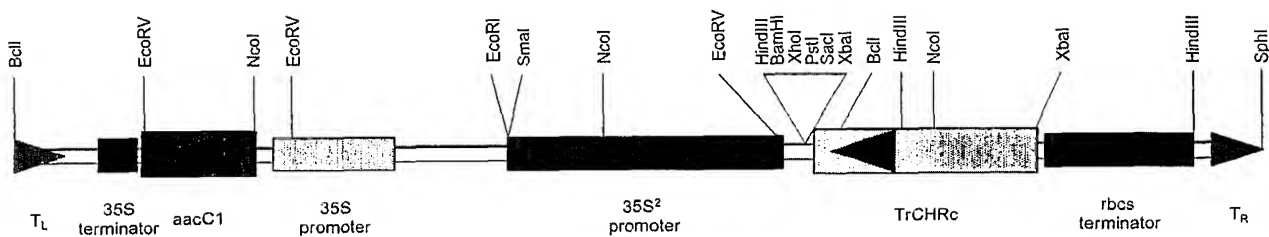
pPZP221:35S²TrCHRC sensepPZP221:35S²TrCHRC anti

FIGURE 135

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TrCHSa1

FIGURE 136

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1  GAATTCGATT AAGCAGTGGT ATCAACGCAG AGTACGCGGG GACAACAACT
51 ATAACTTCCT GTTATTAACC AATTGAGTTC AAATTACATA CATAGCAGGA
101 ACTATACTAA AGATATCAAC ATGGTTAGTG TTTCTGAAAT TCGCAAGGCT
151 CAAAGGGGCTG AAGGCCCTGC AACTATTTTG GCCATTGGTA CTGCAAATCC
201 AGCAAATCGT GTTGACCAGA GTACATATCC TGATTTCTAC TTCAAAATCA
251 CTAACAGTGA GCATAAGGTT GAGCTTAAAG AGAAATTTCA GCGCATGTGT
301 GATAAATCTA TGATCAAGAG CAGATACATG TATCTAACAG AAGAGATTTT
351 GAAAGAAAAT CCTAGTCTTT GTGAATACAT GGCACCTTCA TTGGATGCTA
401 GGCAAGACAT GGTGGTGGTT GAGGTACCTA GACTTGGGAA GGAGGCTGCA
451 GTGAAAGCTA TCAAAGAATG GGGTCAACCA AAGTCAAAGA TTACTCACTT
501 AATCTTTTGC ACCACAAGTG GTGTTGACAT GCCTGGTGCC GATTACCAAC
551 TCACAAAACT CTTAGGTCTT CGCCCATATG TGAAGAGGTA CATGATGTAC
601 CAACAAGGGT GCTTTGCAGG TGGGACGGTT CTTCGTTTGG CCAAGGATTT
651 GGCCGAGAAC AACAAAGGTG CTCGTGTGTT GGTTGTTTGC TCTGAAGTAA
701 CCGCAGTCAC ATTCCGCGGC CCCAGTGACA CTCATTTGGA CAGTCTTGTT
751 GGACAAGCAC TATTCGGAGA TGGAGCTGCT GCACTCATTG TTGGCTCAGA
801 CCCAGTACCA GAAATTGAGA AGCCAATATT TGAGATGGTT TGGACCGCAC
851 AGACAATTGC TCCAGATAGT GAAGGTGCCA TTGATGGTCA TCTTCGTGAA
901 GCTGGACTAA CATTTCATCT TCTTAAAGAT GTTCCTGGGA TTGTCTCAAA
951 GAACATTGAT AAGGCATTGG TTGAGGCATT CCAACCATTA AACATCTCTG
1001 ATTACAATTC AATCTTTTGG ATTGCTCATC CAGGTGGTCC TGCAATTCTA
1051 GACCAAGTTG AGATAAAGTT GGGCTTAAAA CCTGAAAAAA TGAAGGCCAC
1101 CAGAGATGTA CTTAGTGAAT ATGGTAACAT GTCAAGTGCA TGTGTATTGT
1151 TCATCTTAGA TGAGATGAGA AAGAAATCGG CTGAAAATGG ACTTAAAACC
1201 ACAGGAGAAG GACTTGACTG GGGTGTGTTG TTTGGATTTG GGCCCGGACT
1251 TACCATTGAA ACTGTTGTTC TACATAGTGT GGCTATATGA GAATGAGAGA
1301 CTTGATTTGT TTTTATTGTA TTGTATTGTA TTACTTTAAA TCTTGGTTGA
1351 ACCTCCATTT TAAGAATAAA TATGGAGTTC AATATGGACC ATCCTGTTAA
1401 AATAATATAT CGTTAATAGC TATTATTTTA GTGTCTGTTT CTTTTTACTA
1451 AACTATTTTA TTTTAGTATT TGTTTTTGAC CAAAAAAAA AAAAAAAAA
1501 AAAAAAGTA CTCTGCGTTG TTACCACTGC TTAATCACTA GTGAATTC

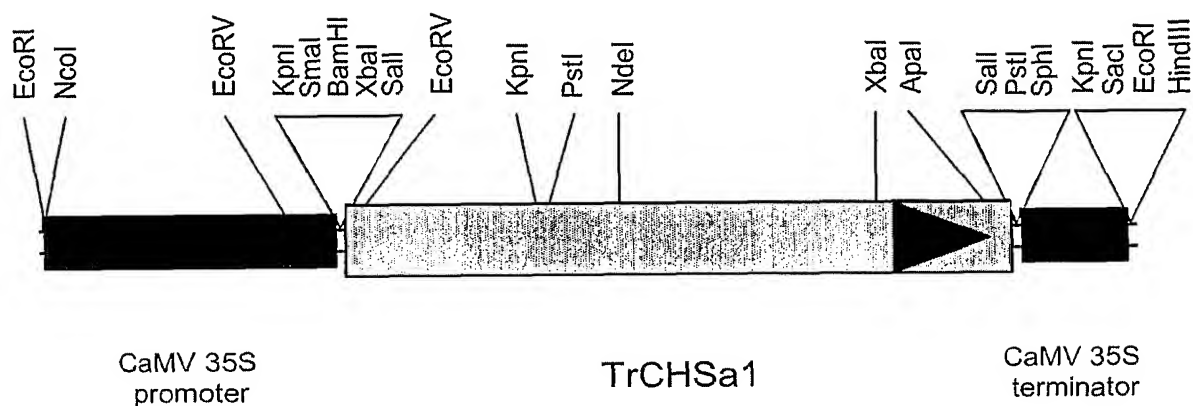
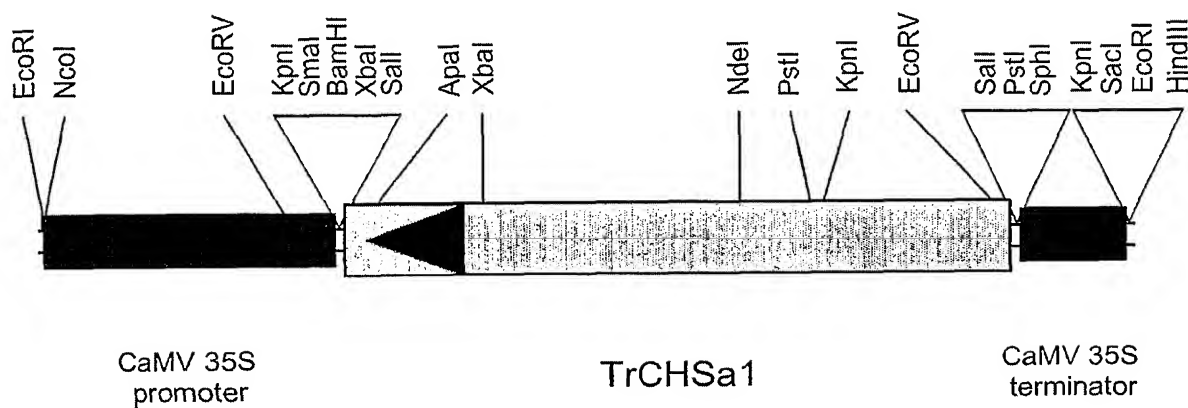
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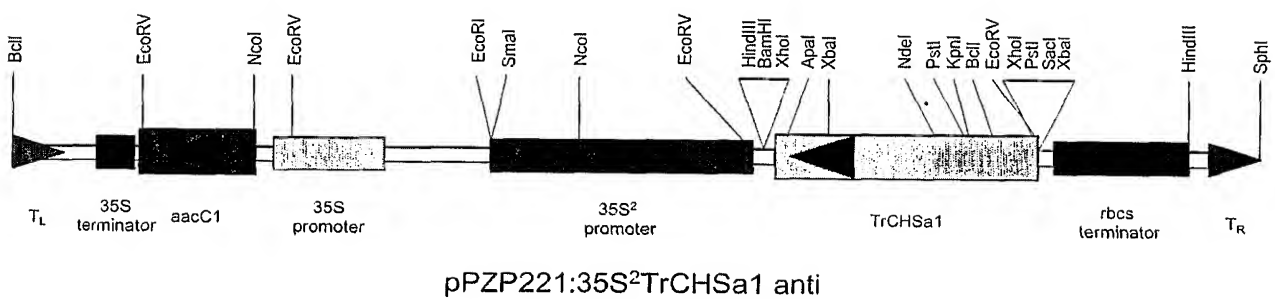
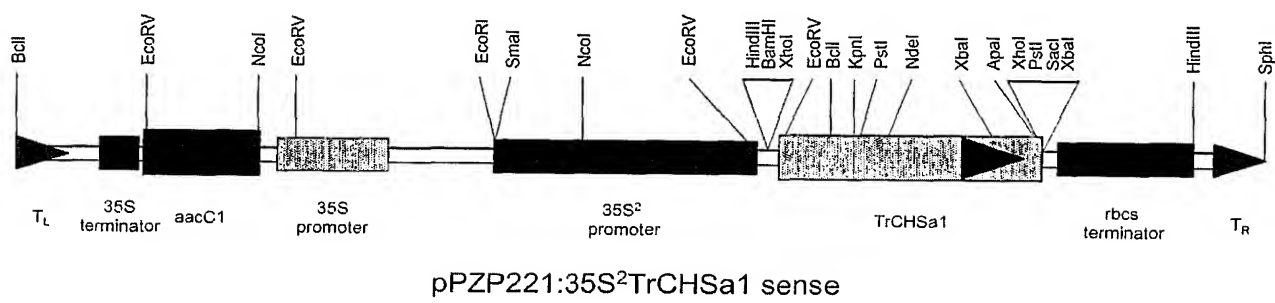
FIGURE 137

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1  MVSVSEIRKA QRAEGPATIL AIGTANPANR VDQSTYPDFY FKITNSEHKV
51  ELKEKFQRC DKSMIKSRYM YLTEEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA VKAIKEWGQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPYVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEVTAVTFRG
201 PSDTHLDSL V GQALFGDGAA ALIVGSDPVP EIEKPIFEMV WTAQTIAPDS
251 EGAIDGHLRE AGLTFHLLKD VPGIVSKNID KALVEAFQPL NISDYN SIFW
301 IAHPPGGPAIL DQVEIKLGLK PEKMKATRDV LSEYGNMSSA CVLFILDEMR
351 KKS AENGLKT TGEGLDWGVL FGFGPGLTIE TVVLHSVAI
```

FIGURE 138

212/271**pDH51TrCHSa1 sense****pDH51TrCHSa1 anti****FIGURE 139**

213/271**FIGURE 140**

214/271**TrCHSa3****FIGURE 141**

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1  GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGAAC
51  AAAAACAACT ACGCATATTA TATATATATA TATATAGTCT ATAATTGAAA
101 GAAACTGCTA AAGATATTAT TAAGATATGG TGAGTGTAGC TGAAATTCGC
151 AAGGCTCAGA GGGCTGAAGG CCCTGCAACC ATTTTGGCCA TTGGCACTGC
201 AAATCCACCA AACCGTGTTG AGCAGAGCAC ATATCCTGAT TTCTACTTCA
251 AAATTACAAA CAGTGAGCAC AAGACTGAGC TCAAAGAGAA GTTCCAACGC
301 ATGTGTGACA AATCCATGAT CAAGAGCAGA TACATGTATC TAACAGAAGA
351 GATTTTGAAA GAAAATCCTA GTCTTTGTGA ATACATGGCA CCTTCATTGG
401 ATGCTAGGCA AGACATGGTG GTGGTTGAGG TACCTAGACT TGGGAAGGAG
451 GCTGCAGTCA AGGCCATTAA AGAATGGGGT CAACCAAAGT CAAAGATTAC
501 TCACTTAATC TTTTGCACCA CAAGTGGTGT TGACATGCCT GGTGCTGATT
551 ACCAACTCAC AAAACTCTTA GGTCTTCGCC CATATGTGAA AAGGTATATG
601 ATGTACCAAC AAGGTTGTTT TGCAGGAGGC ACGGTGCTTC GTTTGGCAAA
651 AGATTTGGCC GAGAACAACA AAGGTGCTCG TGTGCTAGTT GTTTGTCTCG
701 AAGTCACCGC AGTCACATTT CGCGGCCCCA GTGATACTCA CTTGGACAGT
751 CTTGTTGGAC AAGCATTGTT TGGAGATGGA GCCGCTGCAC TAATTGTTGG
801 TTCTGATCCA GTGCCTGAAA TTGAGAAACC AATATTTGAG ATGGTTTGGA
851 CTGCACAAAC AATTGCTCCA GACAGTGAAG GTGCCATTGA TGGTCATCTT
901 CGTGAAGCTG GGCTAACATT TCATCTTCTT AAAGATGTTC CTGGGATTGT
951 ATCAAAGAAC ATTAATAAAG CATTGGTTGA GGCTTTCCAA CCATTAGGAA
1001 TTTCTGACTA CAACTCAATC TTTTGGATTG CACACCCGGG TGGACCTGCA
1051 ATTCTTGATC AAGTAGAACA AAAGCTAGCC TTGAAGCCCG AAAAGATGAG
1101 GGCCACGAGG GAAGTTCTAA GTGAATATGG AAACATGTCA AGCGCATGTG
1151 TATTGTTTCAT CTTAGATGAG ATGCGGAAGA AATCGGCTCA AAATGGACTT
1201 AAGACAACTG GAGAAGGACT TGATTGGGGT GTGTTGTTCG GCTTCGGACC
1251 AGGACTTACC ATTGAAACCG TTGTTCTTCG TAGCGTGGCT ATATAAGATG
1301 TGTGATTGTT TTTATTTTAA TGTATTACTT TTAATCTTGC TGCCTTGAAT
1351 TTCGATTTAA GAATAAATAA ATATATCTTT TGATAAAAAA AAAAAAAAAA
1401 AAAAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CGAATTC

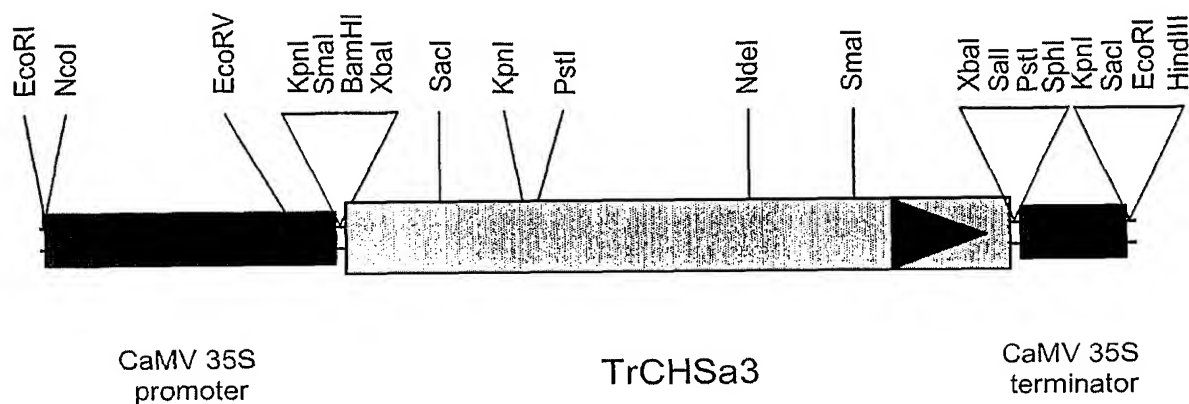
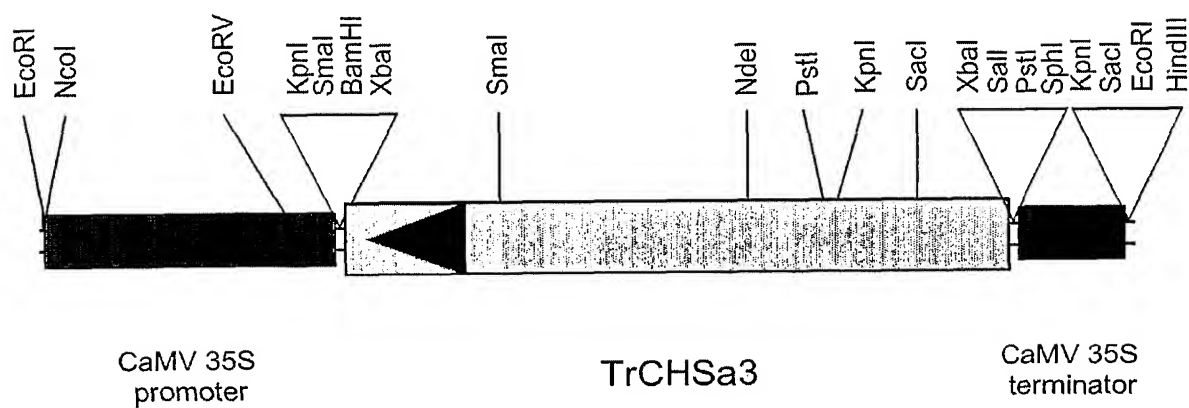
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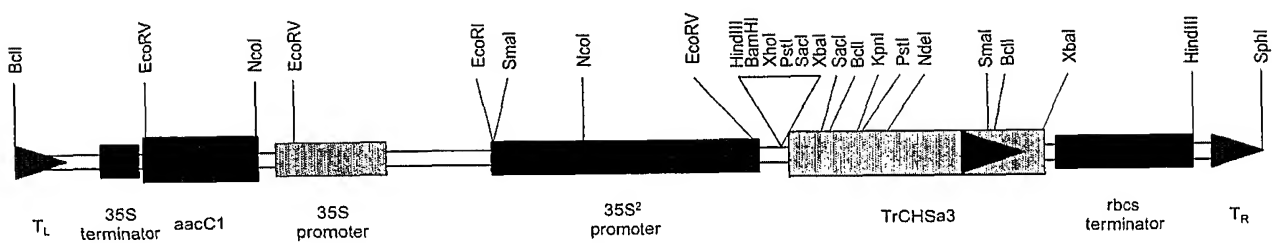
FIGURE 142

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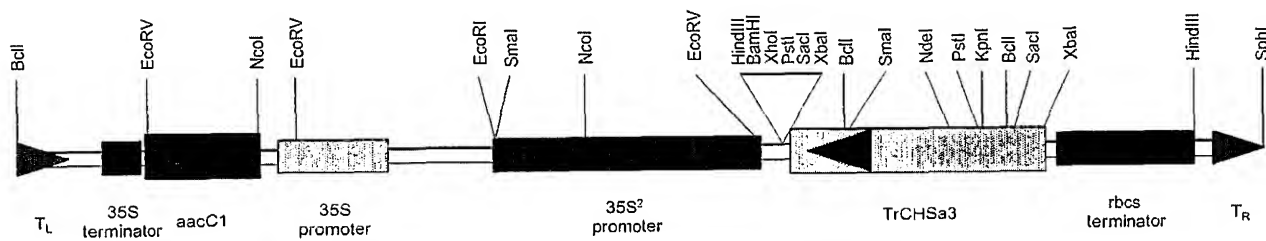
1 MVSVAEIRKA QRAEGPATIL AIGTANPPNR VEQSTYPDFY FKITNSEHKT
51 ELKEKFQRC DKSMIKSRYM YLTEEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA VKAIKEWGQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPYVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEVTAVTFRG
201 PSDTHLDSLV GQALFGDGAA ALIVGSDPVP EIEKPIFEMV WTAQTIAPDS
251 EGAIDGHLRE AGLTFHLLKD VPGIVSKNIN KALVEAFQPL GISDYNISIFW
301 IAHPGGPAIL DQVEQKLALK PEKMRATREV LSEYGNMSSA CVLFILDEMR
351 KKSAQNGLKT TGEGLDWGVL FGFGPGLTIE TVVLRSAI

FIGURE 143

217/271**pDH51TrCHSa3 sense****pDH51TrCHSa3 anti****FIGURE 144**

218/271

pPZP221:35S²TrCHSa3 sense



pPZP221:35S²TrCHSa3 anti

FIGURE 145

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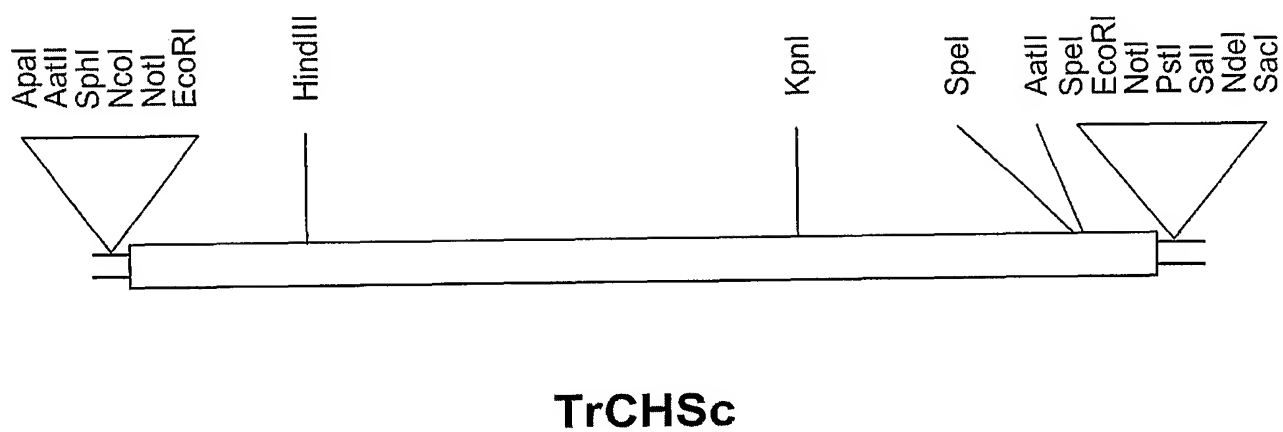


FIGURE 146

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1  GAATTCGATT AAGCAGTGGT AACACGCAG AGTACGCGGG GATTCAATCT
51  GTTGTGCATA AAATTCACCTC ATTGCATAGA AAACCATACA CATTTGATCT
101 TGCAAAGAAG AAATATGGGA GACGAAGGTA TAGTGAGAGG TGTCACAAAG
151 CAGACAACCC CTGGGAAGGC TACTATATTG GCTCTTGGCA AGGCATTCCC
201 TCACCAACTT GTGATGCAAG AGTGTTTAGT TGATGGTTAT TTTAGGGACA
251 CTAATTGTGA CAATCCTGAA CTTAAGCAGA AACTTGCTAG ACTTTGTAAG
301 ACAACCACGG TAAAAACAAG GTATGTTGTT ATGAATGAGG AGATACTAAA
351 GAAATATCCA GAACTTGTTG TCGAAGGCGC CTCAACTGTA AAACAACGTT
401 TAGAGATATG TAATGAGGCA GTAACACAAA TGGCAATTGA AGCTTCCCAA
451 GTTTGCCTAA AGAATTGGGG TAGATCCTTA TCGGACATAA CTCATGTGGT
501 TTATGTTTCA TCTAGTGAAG CTAGATTACC CGGTGGTGAC CTATACTTGT
551 CAAAAGGACT AGGACTAAAC CCTAAAATTC AAAGAACCAT GCTCTATTTT
601 TCTGGATGCT CGGGAGGCGT AGCCGGCCTT CGCGTTGCGA AAGACGTAGC
651 TGAGAACAAAC CCTGGAAGTA GAGTTTTGCT TGCTACTTCG GAAACTACAA
701 TTATTGGATT CAAGCCACCA AGTGTTGATA GACCTTATGA TCTTGTTGGT
751 GTGGCACTCT TTGGAGATGG TGCTGGTGCA ATGATAATTG GCTCAGACCC
801 GGTATTTTGA ACTGAGACAC CATTGTTTGA GCTGCATACT TCAGCTCAGG
851 AGTTTATACC AGACACCGAG AAGAAAATTG ATGGGCGGCT GACGGAGGAG
901 GGCATAAGTT TCACACTAGC AAGGGAACCT CCGCAGATAA TCGAAGACAA
951 TGTTGAGGGA TTCTGTAATA AACTAATTGA TGTTGTTGGG TTGGAGAATA
1001 AGGAGTACAA TAAGTTGTTT TGGGCTGTGC ATCCAGGTGG CCCTCGGATA
1051 TTGAATCGCG TGGAGAAGCG GCTTGAGTTG TCGCCGCAGA AGCTGAATGC
1101 TGTAGAAAA GCTCTAATGG ATTATGGAAA TGCTAGCAGC AATACTATTG
1151 TTTATGTGCT GGAATATATG CTAGAAGAGG AAAAGAAGAT TAAAAAGGCG
1201 GGTGGAGGAG ATTCTGAATG GGGATTGATA CTTGCTTTTG GACCTGGAAT
1251 TACTTTTGAG GGGATTCTAG CAAGGAACCT GTGTGCATGA AGTCTTATAC
1301 AATTGTGATG CATGACTTAT ACTCTTATTT CTACTAATTA TTATATTAAG
1351 CAAATTCAGA ACTTTTAAAGT AATGATTTAA TGAAGAATAC TTATAGTATA
1401 TTGACTTTAT TCACTTTCAA AGCAAGTTTA TGATCCTAAG ACATGGTAGA
1451 ACTTGAGCAT GTGGAATAGT TGTAACAAAA ACTCTAAGCA AATAGAGACT
1501 TTATGTAGTA TAAAGCATTT CCAGACATGA TAAATAATGG TACCTCAGAA
1551 CATAAAATAT ATTTAGCTAT CTTTCATCCC CAACTTTACA CATCCACCAA
1601 GGTACAGAAT AAGCATATGT CAACACAAAA TGTACTCTAA GTCTAACATG
1651 AGTAACCAAA CATGATGCCT GATTAAGTTA AAAGAAAAGA AAATCTGAGG
1701 GCATAGATCT TCAATCACAC CACTCCAGAG GGAAGGCGTA GAACAAGCTG
1751 TCCGCCGAAA ACACTGCAAT TCAATAAATA TCATTAGGAC AACAGTGCA
1801 AGTCATGCGG GAAATGTCTT AAGTCACTGT ACTAAAAATA TAGGATTATA
1851 TTATGAACCTA TACTAACCTT TTCACATAAT AGTAACAGAA ATCAGCTAAG
1901 ATGAATGTCT GGACAATTTC TGAGATAAGA ACCATGACGG CCATAAGCCA
1951 TACCCCAAGG CAACCAATAA ATGTCCACGG GTATCTAACA CCTGTTGCAA
2001 GAAATAGTAA GTTATTAGGA GATGTGCGGT TACGAAATTC AAGCTACACA
2051 ACAAAAGGAG GCCAGAACAA CAGCAATCTT GTAACCAGAT GACAACAATA
2101 AAATGTAAAC TTAAAGAGAC CGAACACACA AACATTGCAA CTCAGATGGA
2151 ATTGCTGCCA TGTAAGTAGT AGGAGATTTG GGACGTCAAA TCAGTATATT
2201 ATGCAAATAC AAGGTATGAC CGCCTTGTCT ATTGTAGCAT ACAACAAACG
2251 TACAGTGGGT TTGTCCCTCT CAAAATGGCA GGATCTTTAC AGCACAATAT
2301 TTGGTTTTGT CATACTTATA CCATAAAAAA AAAAAAAAAA AAAAAAAAAA
2351 AAAGTACTCT GCGTTGTTAC CACTGCTTAA TCACTAGTGA ATTC

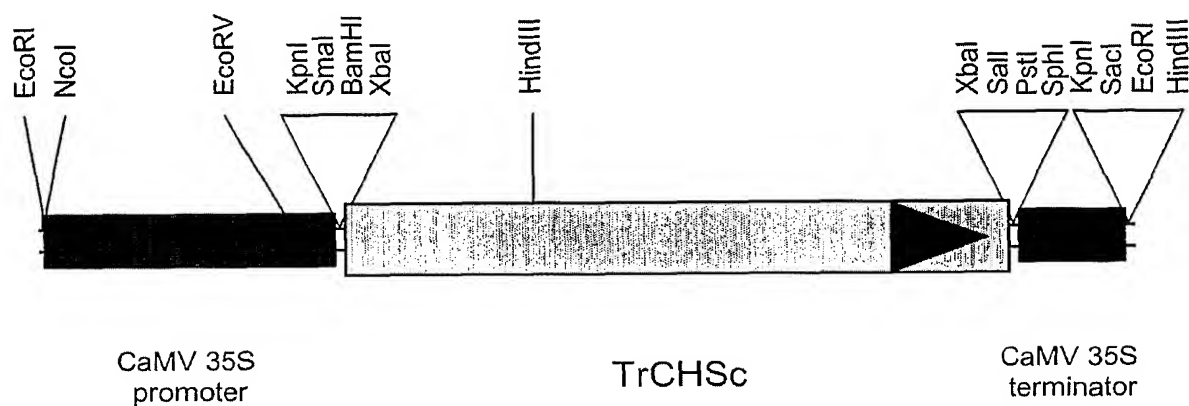
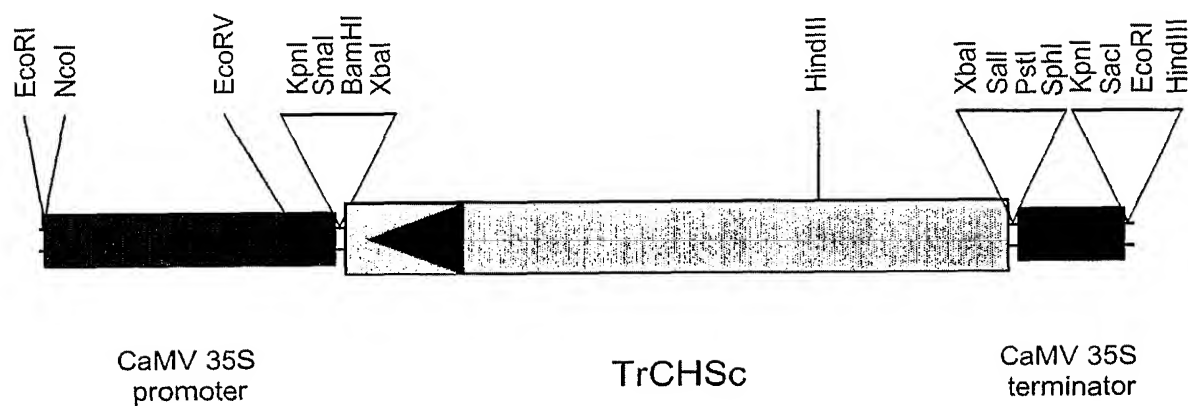
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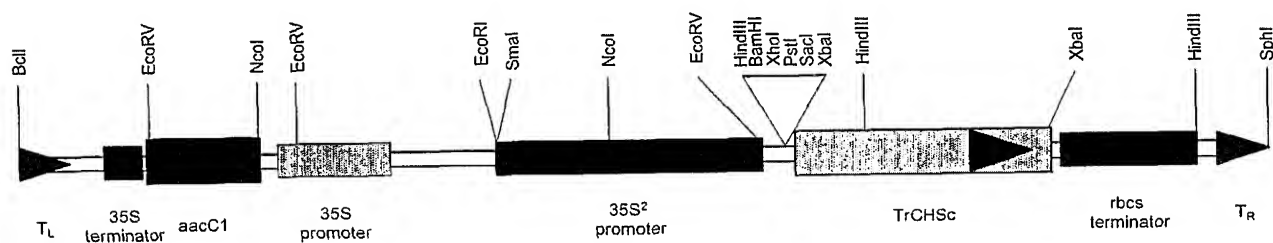
FIGURE 147

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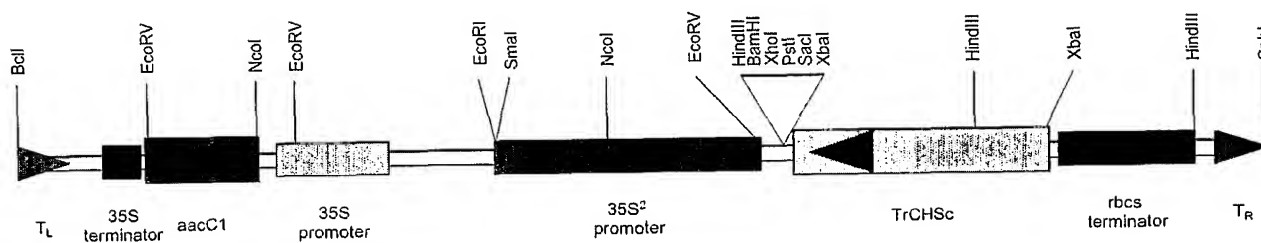
1 MGDEGIVRGV TKQTTTPGKAT ILALGKAFFH QLVMQECLVD GYFRDTNCDN
51 PELKQKLARL CKTTTVKTRY VVMNEEILKK YPELVVEGAS TVKQRLEICN
101 EAVTQMAIEA SQVCLKNWGR SLSDITHVVY VSSSEARLPG GDLYLSKGLG
151 LNPKIQRMTL YFSGCSGGVA GLRVAKDVAE NNPGSRVLLA TSETTIIGFK
201 PPSVDRPYDL VGVALFGDGA GAMIIGSDPV FETETPLFEL HTSAQEFIPD
251 TEKKIDGRLT EEGISFTLAR ELPQIIEDNV EGFCNKLIDV VGLENKEYNK
301 LFWAVHPGGP AILNRVEKRL ELSPQKLNAS RKALMDYGNA SSNTIVYVLE
351 YMLEEEKKIK KAGGGDSEWG LILAFGPGIT FEGILARNLC A

FIGURE 148

222/271**pDH51TrCHSc sense****pDH51TrCHSc anti****FIGURE 149**

223/271

pPZP221:35S²TrCHSc sense



pPZP221:35S²TrCHSc anti

FIGURE 150

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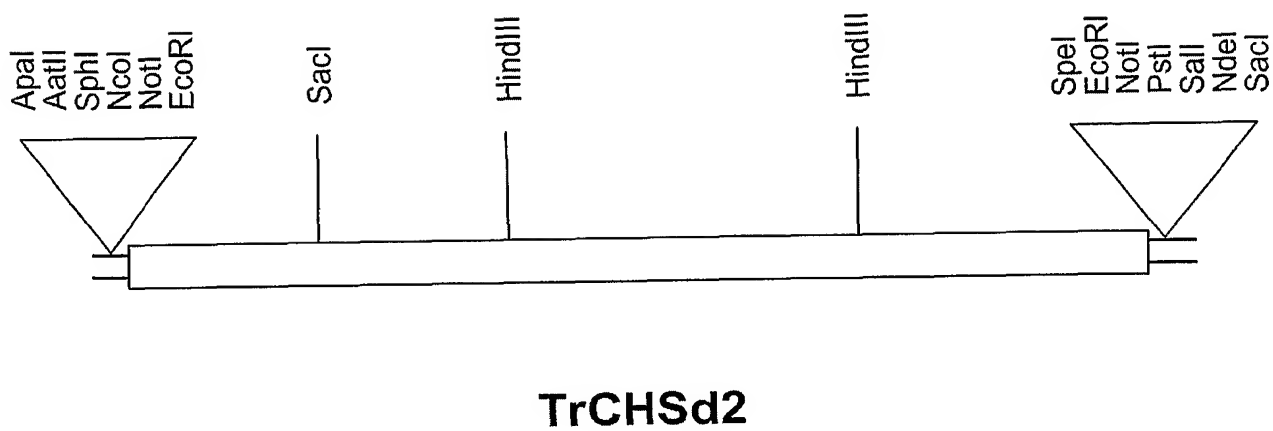


FIGURE 151

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1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GATAGCAACA
51 CACACTTTGA TTTCTTTTTG AGTCCTTGCT ACGTGGCTTT ACCAAAAAAC
101 GTTGCTAAGT CATCAACCAT TCCAATTCCT TAATATAACC TATCAGTACT
151 CACCATCTTT TCTTCCTCCC TGCTAACTTT AGACTCAGAG AAGATGGTGA
201 ATGTTAATGA GATCCGCCAG GCACAGAGAG CTGAAGGCCC TGCCACCGTG
251 TTGGCAATCG GCACTGCAAC TCCTCCAAAC TGTGTGATC AGAGTACATA
301 CCCAGACTAC TACTTCCGCA TCACAAACAG TGAGCACAAG ACAGAGCTCA
351 AAGAAAAATT CCAGCGCATG TGTGACAAAT CTATGATTAA GAAGAGATAC
401 ATGCATTTGA CAGAAGAGAT TTTGAAGGAG AATCCAAGTT TATGTGAGTA
451 CATGGCACCT TCATTGGATG CAAGACAAGA CATGGTGGTT GTGGAAGTAC
501 CAAGGCTAGG AAAAGAGGCT GCAACAAAGG CTATCAAGGA ATGGGGTCAA
551 CCTAAGTCCA AGATTACTCA CCTCATCTTT TGCACCACAA GTGGTGTGGA
601 CATGCCTGGC GCCGACTATC AGCTTACAAA GCTTTTAGGC CTTTCGTCCGC
651 ATGTGAAGCG TTATATGATG TACCAACAAG GTTGTTCGC TGGTGGTACG
701 GTGCTTCGTT TGGCTAAAGA CTTGGCTGAA AACAAACAAG GTGCCCGTGT
751 GTTGGTGGTT TGTTCAGAGA TCACTGCGGT TACTTTCCGT GGACCCAGTG
801 AACTCATCT TGATAGCCTT GTGGGGCAAG CATTGTTTGG AGATGGTGCA
851 GCAGCTGTGA TTGTAGGTTT AGACCCATTA CCACAAGTTG AGAAGCCCTT
901 GTTTGAATTG GTATGGACTG CTCAAACAAT CCTTCCAGAC AGTGAAGGAG
951 CCATTGATGG GCACCTTCGT GAAGTCGGGC TGACATTCCA TCTCCTCAAG
1001 GATGTTTCCTG GACTCATCTC AAAGAACATT GAGAAAGCTC TTGTTGAGGC
1051 CTTTCAACCT TTAGGTATCT CTGATTACAA TTCTATATTT TGGATCGCAC
1101 ATCCTGGTGG ACCTGCAATT CTGGACCAAG TGGAAGCCAA ATTAAGCTTA
1151 AAGCCAGAGA AAATGCAAGC CACCCGGCAT GTGCTTAGCG AGTATGGTAA
1201 CATGTCAAGT GCATGTGTGT TATTTATCTT GGATGAGATG AGGAGGAAGT
1251 CAAAAGAAGA TGGACTTGCC ACAACAGGCG AGGGGCTGGA ATGGGGTGTA
1301 CTATTCGGTT TTGGACCCGG ACTCACTGTT GAGACTGTAT TGCTCCATAG
1351 TGTTGCCACT TAAATTGCCT AGATATGCTA TAACTATATG CTTATTTAAT
1401 TCTTTGTTTC TGGGGGATTT TATCTTCACT TACTTCACTG AGCATTTGAA
1451 TAAAGTTTGT TTTAATTATT CATAATGTAA TATGGTGTG CTTAATGTAC
1501 CCATCCATAT AATATTTGTA ATACATATAT TAATCAACTT GCAATTTTCAT
1551 GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAGGAAAAAA
1601 AAAAAAAAAA AAAAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT
1651 CACTAGTGAA TTC

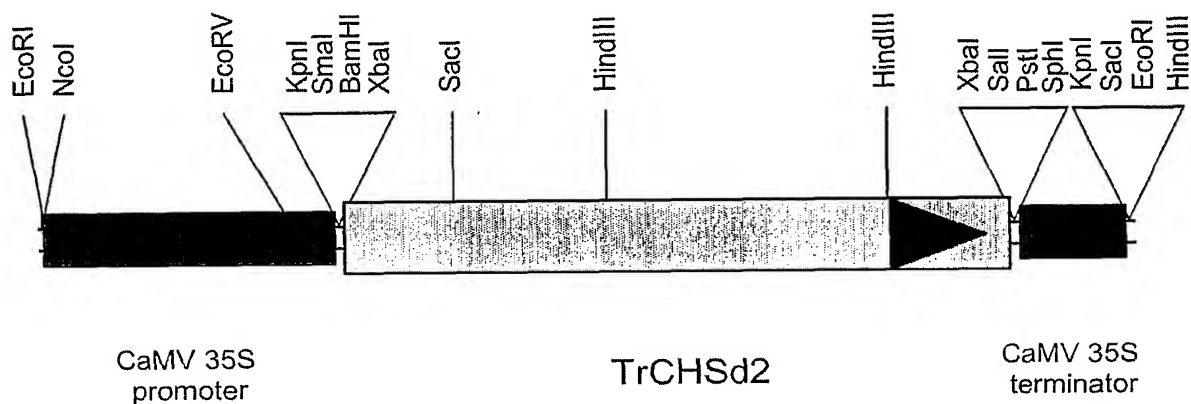
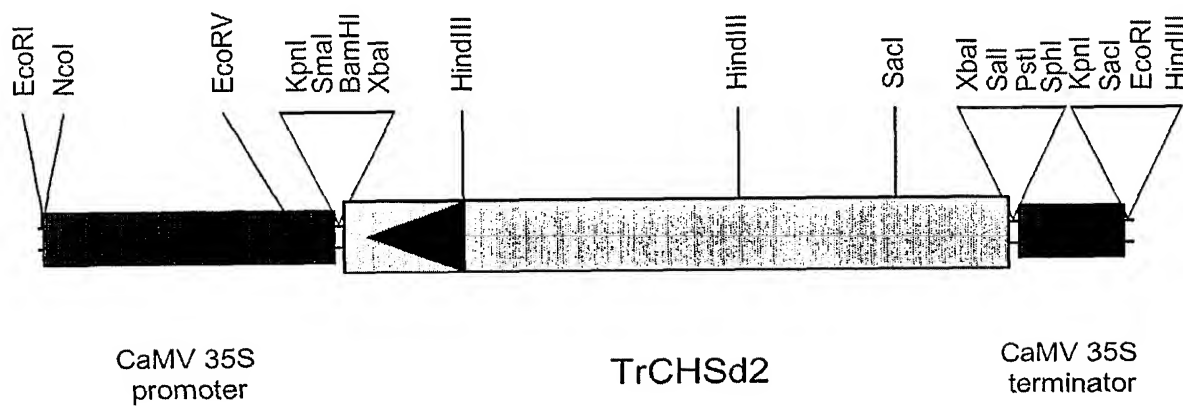
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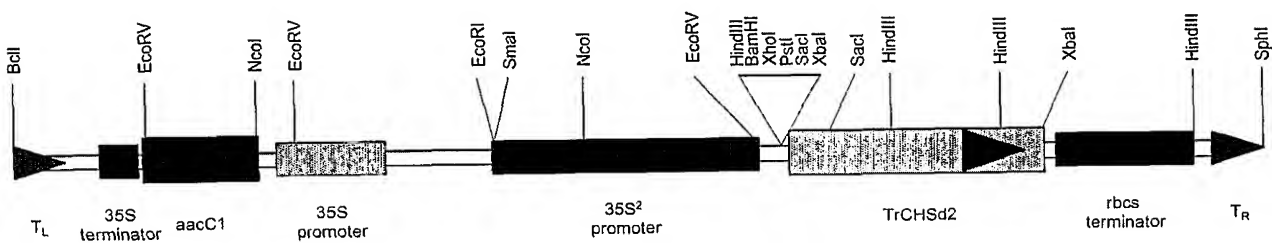
FIGURE 152

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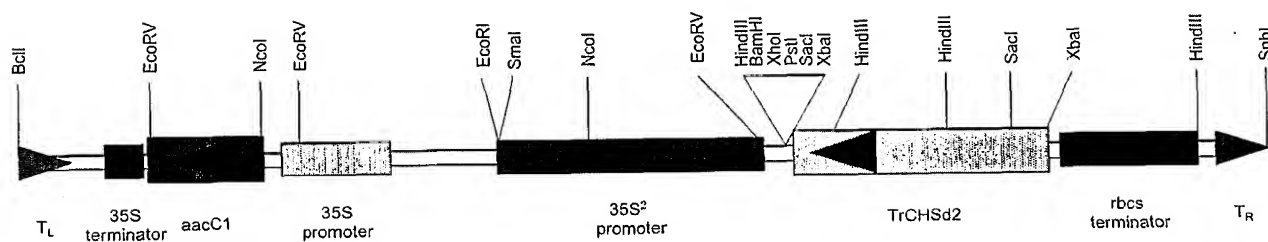
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51 ELKEKFQRM C DKSMIKKRYM HLTEEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA TKAIKEWGQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPHVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEITAVTFRG
201 PSDTHLDSL V GQALFGDGAA AVIVGSDPLP QVEKPLFELV WTAQTILPDS
251 EGAIDGHLRE VGLTFHLLKD VPGLISKNI E KALVEAFQPL GISDYN SIFW
301 IAHPGGPAIL DQVEAKLSLK PEKMQATRHV LSEYGNMSSA CVLFILDEMR
351 RKSKE DGLAT TGEGLEWGV L FGFGPGLTVE TVLLHSVAT

FIGURE 153

227/271**pDH51TrCHSd2 sense****pDH51TrCHSd2 anti****FIGURE 154**

228/271

pPZP221:35S²TrCHSd2 sense



pPZP221:35S²TrCHSd2 anti

FIGURE 155

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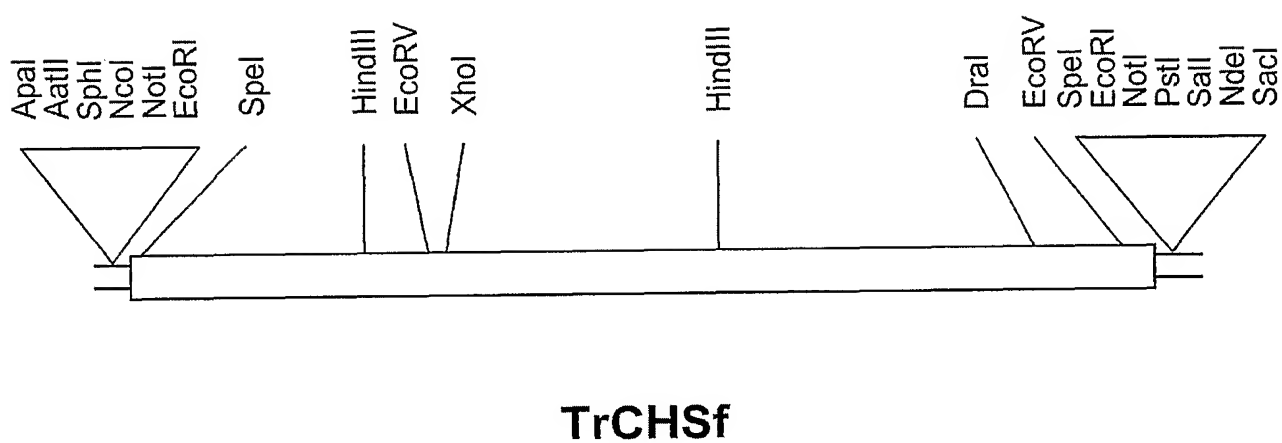


FIGURE 156

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1  GAATTCGATT AAGCAGTGGT AACACGCAG AGTACGCGGG ACTAAGCCTT
51 GATTCATTGT TTGTTTCCAT AACACAAGAA CTAGTGTTTG CTTGAATCTT
101 AAGAAAAAAT GCCTCAAGGT GATTTGAATG GAAGTTCCTC GGTGAATGGA
151 GCACGTGCTA GACGTGCTCC TACTCAGGGA AAGGCAACGA TACTTGCATT
201 AGGAAAGGCT TTCCCCGCCC AGGTCCTCCC TCAAGAGTGC TTGGTGGAAAG
251 GATTCATTTCG CGACACTAAG TGTGACGATA CTTATATTAA GGAGAAATTG
301 GAGCGTCTTT GCAAAAACAC AACTGTGAAA ACAAGATACA CAGTAATGTC
351 AAAGGAGATC TTAGACAAC TCCAGAGCT AGCCATAGAT GGAACACCAA
401 CAATAAGGCA AAAGCTTGAA ATAGCAAATC CAGCAGTAGT TGAAATGGCA
451 ACAAGAGCAA GCAAAGATTG CATCAAAGAA TGGGGAAGGT CACCTCAAGA
501 TATCACACAC ATAGTCTATG TTTCTCGAG CGAAATTCGT CTACCCGGTG
551 GTGACCTTTA TCTTGCAAAT GAACTCGGCT TAAACAGCGA TGTTAATCGC
601 GTAATGCTCT ATTTCTCGG TTGCTACGGC GGTGTCACTG GCTTACGTGT
651 CGCCAAAGAC ATCGCCGAAA ATAACCCTGG TAGTAGGGTG TTACTCACAA
701 CATCCGAGAC CACTATTCTC GGTTTTTCGAC CACCGAGTAA AGCTAGACCT
751 TATGACCTCG TTGGCGCTGC ACTTTTCGGT GATGGCGCCG CTGCTGCAAT
801 AATTGGAACA GACCCTATAT TGAATCAAGA ATCACCTTTC ATGGAATTGA
851 ACCATGCAGT CCAAAAATTC TTGCCTGATA CACAAAATGT GATTGATGGT
901 AGAATCACTG AAGAGGGTAT TAATTTTAAG CTTGGAAGAG ACCTTCCTCA
951 AAAAATTGAA GACAATATTG AAGAATTTTG CAAGAAAATT ATGGCTAAAA
1001 GTGATGTTAA GGAATTTAAT GACTTATTTT GGGCTGTTCA TCCTGGTGGG
1051 CCAGCTATAC TCAATAAGCT AGAAAATATA CTCAAATTGA AAAGTGATAA
1101 ATTGGATTGT AGTAGGAAGG CATTAATGGA TTATGGAAAT GTTAGTAGCA
1151 ATACTATATT CTATGTGATG GAGTATATGA GAGATTATTT GAAGGAAGAT
1201 GGAAGTGAAG AATGGGGATT AGGATTGGCT TTTGGACCAG GGATTACTTT
1251 TGAAGGGGTT CTCCTCCGTA GCCTTTAATC TTGAAATAAT AATTCATATG
1301 AAATTACTTG TCTTAAGATT GTGATAGGAA GATGAATATG TATTGGATTA
1351 ATATTGATAT GGTGTTATTT TAAGTTGATT TTAAAAAAG TTTATTAATA
1401 AAGTATGATG TAACAATTGT TGTTTGAATG TTAAAAGGGA AGTATACTAT
1451 TTTAAGTTCT TGACCATACT GATTTTTTCT TTACACATTT TCATATCTAA
1501 AATTGTTCTA TGATATCTTC ATTGTTGATA CTGTAATAAT ATAATATCTA
1551 ATTTGGCTGG CAAATGAAA GATTTTTTCAC CGAAAAA AAAA
1601 AAAAAA AAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CACTAGTGAA
1651 TTC

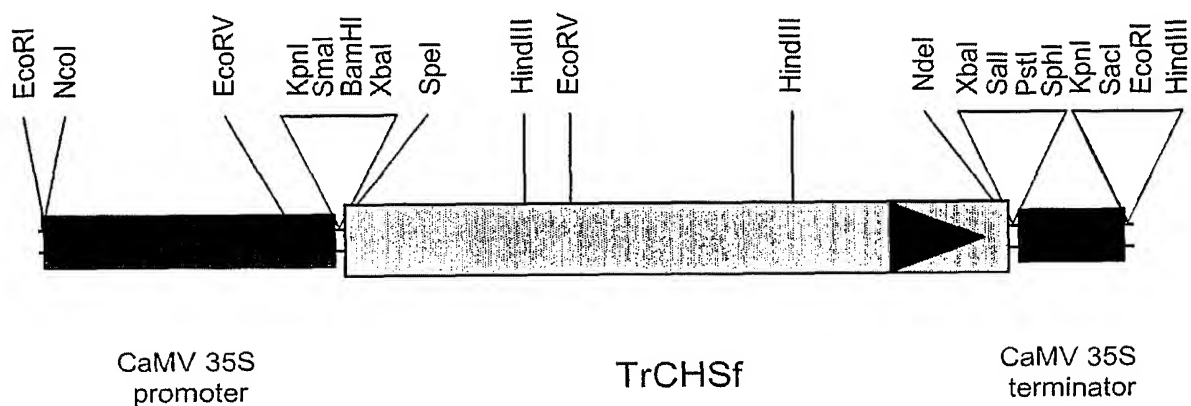
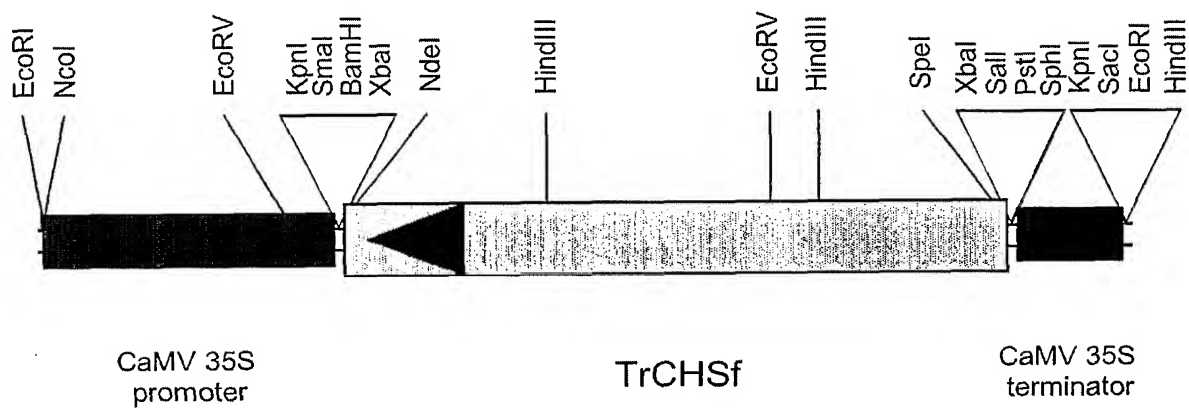
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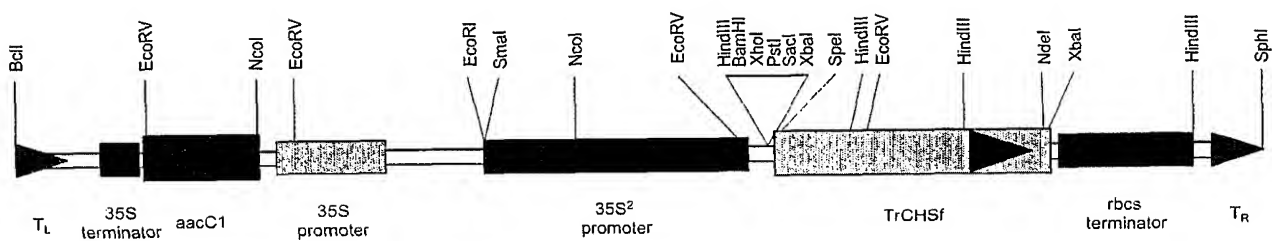
FIGURE 157

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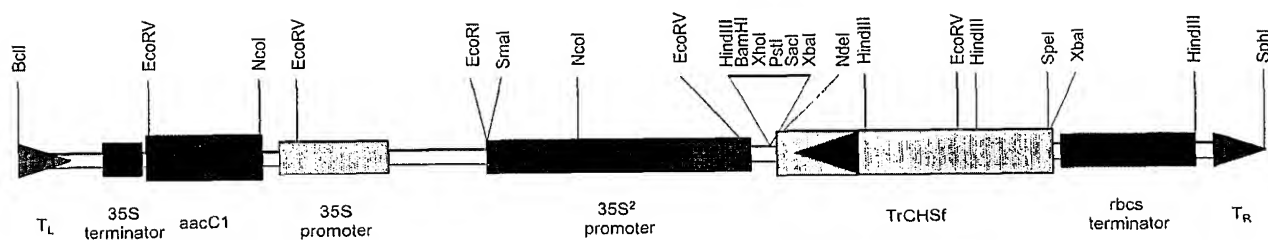
1 MPQGDNLGSS SVNGARARRA PTQ GKATILA LGKAFPAQVL PQECLVEGFI
51 RDTKCDDTYI KEKLERLCKN TTVKTRYTVM SKEILDNYPE LAIDGTPTIR
101 QKLEIANPAV VEMATRASKD CIKEWGRSPQ DITHIVYVSS SEIRLPGGDL
151 YLANELGLNS DVNRVMLYFL GCYGGVTGLR VAKDIAENNP GSRVLLTTSE
201 TTILGFRPPS KARPYDLVGA ALFGDGAAAA IIGTDPILNQ ESPFMELNHA
251 VQKFLPDTQN VIDGRITEEG INFKLGRDLP QKIEDNIEEF CKKIMAKSDV
301 KEFNDLFWAV HPGGPAILNK LENILKLKSD KLDCSRKALM DYGNVSSNTI
351 FYVMEYMRDY LKEDGSEEWG LGLAFGPGIT FEGVLLRSL

FIGURE 158

232/271**pDH51TrCHSf sense****pDH51TrCHSf anti****FIGURE 159**

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pPZP221:35S²TrCHSf sense



pPZP221:35S²TrCHSf anti

FIGURE 160

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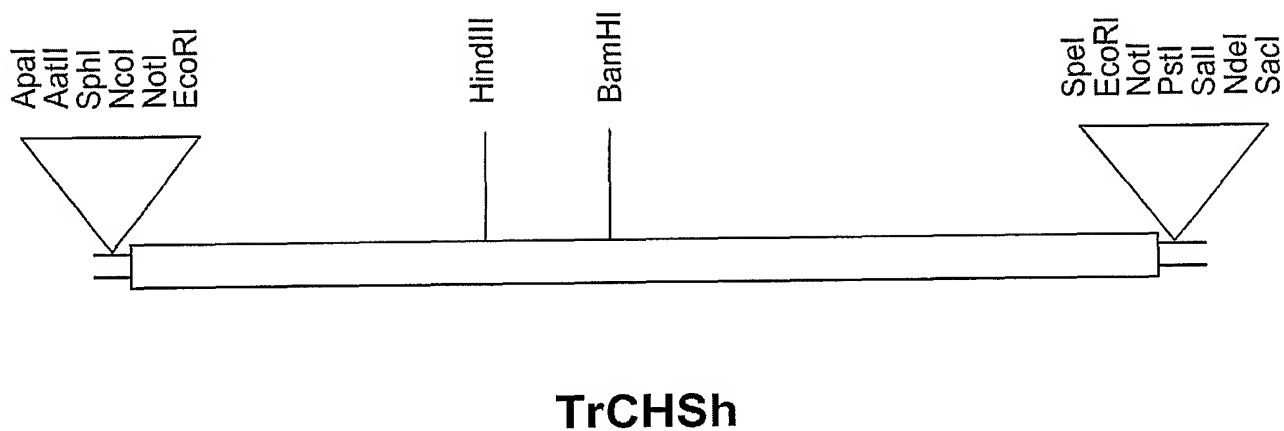


FIGURE 161

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1  GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGGAA
51 TCCACCAAAT CAACACCATT AATAACCTTC CAAATTCTCG TTACCTCACC
101 AAATCTCATT TTTCATTATA TATCTTGGGT ACATCTTTTG TTACCTCCAA
151 CAAAAAATG GTGACCGTAG AAGAGATTCG TAACGCCCAA CGTTCAAATG
201 GCCCTGCCAC TATCTTAGCT TTTGGCACAG CCACTCCTTC TAACTGTGTC
251 ACTCAAGCTG ATTATCCTGA TTACTACTTT CGTATCACCA ACAGCGAACA
301 TATGACTGAT CTTAAGGAAA AATTCAAGCG GATGTGTGAT AGATCAATGA
351 TAAAGAAACG TTACATGCAC CTAACAGAAG ACTTTCTGAA GGAGAATCCA
401 AATATGTGTG AATACATGGC ACCATCACTA GATGTAAGAC GAGACATAGT
451 GGTGTGTGAA GTACCAAAGC TAGGTAAAGA AGCAGCAAAA AAAGCCATAT
501 GTGAATGGGG ACAACCAAAA TCCAAAATCA CACATCTTGT TTTCTGCACC
551 ACTTCCGGTG TTGACATGCC GGGAGCCGAT TACCAACTCA CCAACTTTT
601 AGGCTTAAAA CCTTCTGTCA AGCGTCTCAT GATGTATCAA CAAGGTTGTT
651 TCGCTGGCGG CACAGTTCTC CGCTTAGCAA AAGACCTTGT TGAGAATAAC
701 AAAAATGCAA GAGTTCTTGT TGTTTGTTCT GAAATTACTG CGGTTACTTT
751 TCGTGGAACA TCGGATACTC ATCTTGATTG GCTCGTGGA CAGGCGCTTT
801 TTGGTGATGG AGCCGCAGCA ATGATTATTG GTGCGGATCC TGATTTAACC
851 GTGGAGCGTC CGATTTTCGA GATTGTTTCG GCTGCTCAGA CTATTCTTCC
901 TGATTCTGAT GGC GCAATTG ATGGACATCT TCGTGAAGTG GGGCTCACTT
951 TTCATTTATT GAAAGATGTT CCGGGGATTA TTTCAAAGAA CATTGAAAAA
1001 AGTTTAGTTG AAGCTTTTGC GCCTATTGGG ATTAATGATT GGAAC TCAAT
1051 ATTTTGGGTT GCACATCCAG GTGGACCGGC TATTTTAGAC CAGGTTGAAG
1101 AGAAACTCCA TCTTAAAGAG GAGAAACTCC GGTCCACCCG GCATGTGCTT
1151 AGTGAATATG GAAATATGTC AAGTGCATGT GTTTTATTTA TTTTGGATGA
1201 AATGAGAAAG AGGTCTAAAG AGGAAGGGAT GATTACAAC T GGTGAAGGGT
1251 TGGAATGGGG TGTGTTGTTT GGGTTTGGAC CGGGTTTAAAC TGTTGAAACC
1301 GTTGTGCTTC ATAGTGTTCC GGTTCAGGGT TGAATTTATT ATACATAGAT
1351 TGGAAAATAA AATTTGCCTG CCGAGAGATG TGAAC TAACT TTGTAGGCAA
1401 GCTCAAATTA AAGTTTGAGA TAATATTGTG CTTTAGTTAT TATGGTATGT
1451 AATGTAATGT TTTTACTTTT TTCGAAATTC ATGTAATTTG ATATGTAAAG
1501 TAATATGTTT GGGTTGGAAT ATAATTATTT GTTAACTAAA AAAAAAAAAA
1551 AAAAAAAAAA AAAAAGTACT CTGCGTTGTT ACCACTGCTT AATCGAATTC

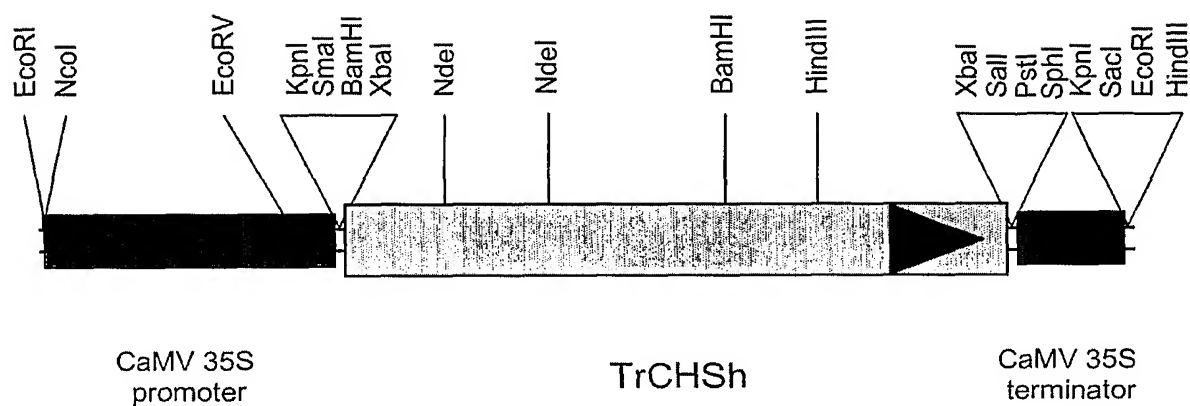
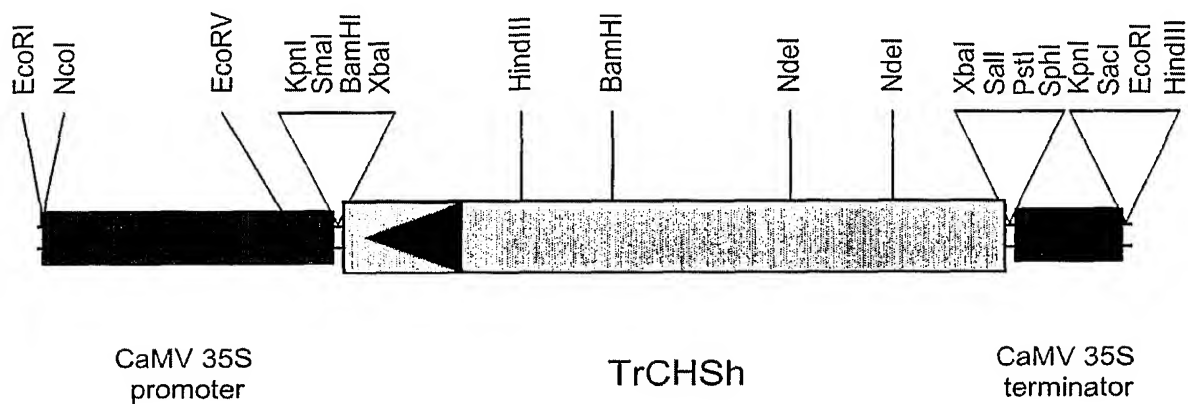
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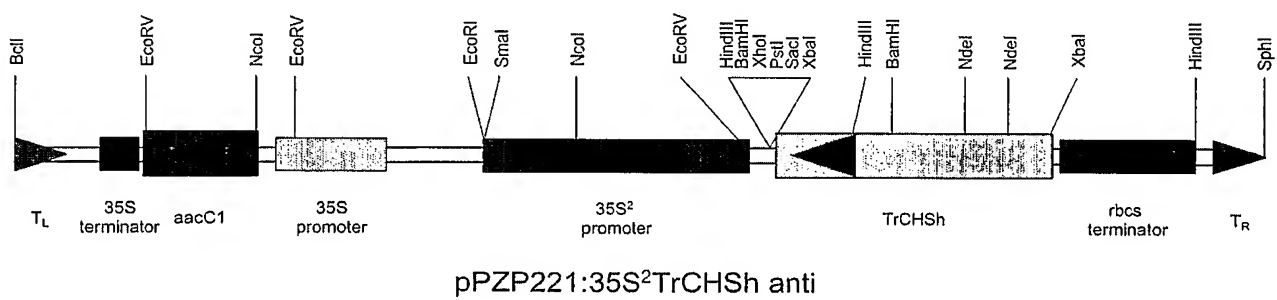
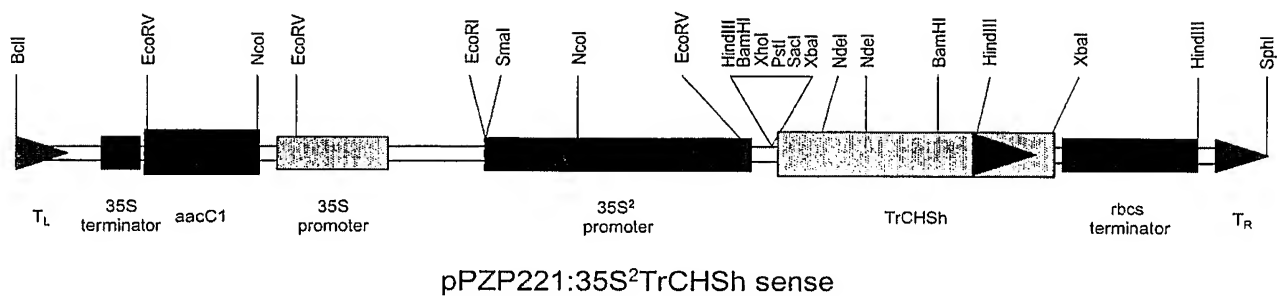
FIGURE 162

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1  MVTVEEIRNA QRSNGPATIL AFGTATPSNC VTQADYPDYY FRITNSEHMT
51 DLKEKFKRMC DRSMIKKRYM HLTEDFLKEN PNMCEYMAPS LDVRRDIVVV
101 EVPKLGKEAA KKAICEWGQP KSKITHLVFC TTSGVDMPGA DYQLTKLLGL
151 KPSVKRLMMY QQGCFAGGTV LRLAKDLVEN NKNARVLVVC SEITAVTFRG
201 PSDTHLDSLV GQALFGDGAA AMIIGADPDL TVERPIFEIV SAAQTILPDS
251 DGAIDGHLRE VGLTFHLLKD VPGIISKNIE KSLVEAFAPI GINDWNSIFW
301 VAHPGGPAIL DQVEEKLHLK EEKLRSTRHV LSEYGNMSSA CVLFILDEMR
351 KRSKEEGMIT TGEGLEWGV LFGFGPGLTVE TVVLHSVPVQ G
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FIGURE 163

237/271**pDH51TrCHSh sense****pDH51TrCHSh anti****FIGURE 164**

238/271**FIGURE 165**

239/271**TrDFRd****FIGURE 166**

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1  GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGGTG
51 ACTTGATCTA GCAGTTATCA AACACAACAG TCTTCCACTT GAGCTCTGTT
101 TCTCCACATG TCGAAGCTAG TTTGCGTCAC CGGCGGCAGC GGATGCATCG
151 GTTCATGGCT AGTCCATCTC CTTCTCCTCC GCGGCTACAC TGTTACAGCC
201 ACCGTCCAAA ATCTCAATGA TGAGAACGAA ACGAAGCATC TAGAAGCTCT
251 CGAAGGAGCA CAAACTAATC TCCGTCTCTT CCAGATCGAT CTCTTAACCT
301 ACGACACAAT CCTCGCTGCT GTCCGCGGTT GCGTCGGAAT TTTCCACCTC
351 GCTTCACCTT GCACTGTAGA CAAAGTTCAT GATCCTCAGA AGGAGCTTTT
401 GGATCCTGCA ATTAAAGGGA CTTTGAATGT GCTTACTGCA GCTAAGGAAG
451 TAGGGGTGAA GCGTGTGGTT GTTACCTCGT CTGTCTCGGC GATTACTCCT
501 AGTCCTGATT GGCCTTCTGA TGTGTGTTAA AGAGAGGATT GTTGGACTGA
551 TGTGGAATAT TGCAAGAAAA AAGAGTTGTG GTATCCGTTG TCCAAACAT
601 TGGCTGAGAA AGCTGCGTGG GATTTTTCCA AAGAAAATGG TTTGGATGTT
651 GTTGTGGTGA ATCCCGGTAC TGTGATGGGT CCTGTTATTC CACCACGGCA
701 TAATGCAAGC ATGCTCATGC TTGTGAGACT TCTTGAAGGC TGCCTGAAA
751 CATTTGAAGA CTATTTTATG GGATTGGTCC ACTTCAAAGA TGAGCATTG
801 GCGCATATTT TGGTGTATGA GAACAAAGAA GCATCTGGTA GACATGTGTG
851 TGTGAAACT ATCTCTCACT ACGGTGATTT TGTGGCAAAA GTTGCTGAAC
901 TTTATCCAGA ATATAGTGTT CCTAGGATGC AGCGAGATAC GCAACCTGGA
951 TTGTTGAGAG CGAATGATGG ATCAAAGAAG CTCATAGATT TGGGTTTGGA
1001 ATTCATTCCA ATGGAGCAAA TTATCAAGGA TGCTGTAGAG AGTTTGAAGA
1051 ACAAAGGATT CATTTCTTGA ATGATGTTAC TGTTCTTTGG AGAACCTAT
1101 AGTTACCAGA GTATAGACTA AATAATATAT AGGTGATGGG TCAGAGAATG
1151 AGTACTTATG TCATGAGTTG TGTCTGTATA ATATGTTTTT TCAATTCTTA
1201 TATGTTAAAT TGCTAATGTT AACTTCAATA TTTATCAGCC AGTATTGTTT
1251 TTTTAATAAA ATATTGAAGC AAAAAAAAAA AAAAAAAAAA AAAAAAAGT
1301 ACTCTGCGTT GTTACCACTG CTTAATCGAA TTC

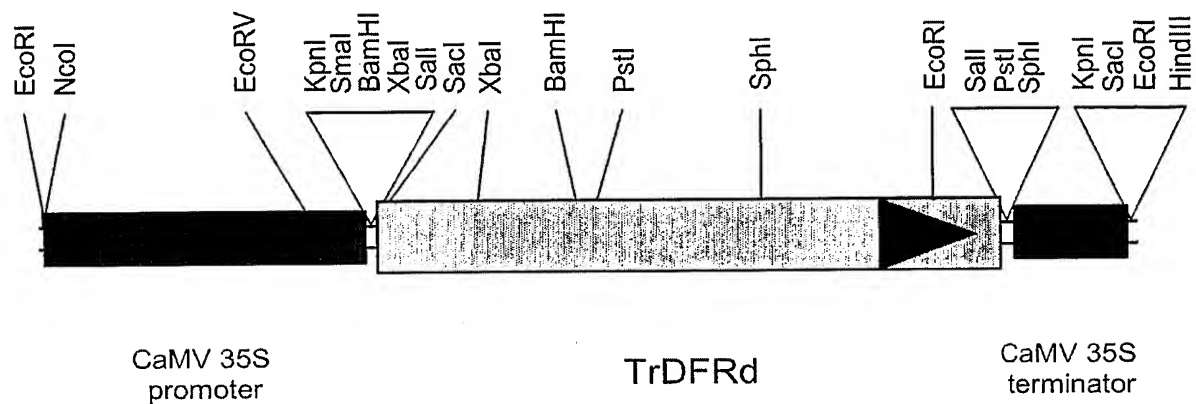
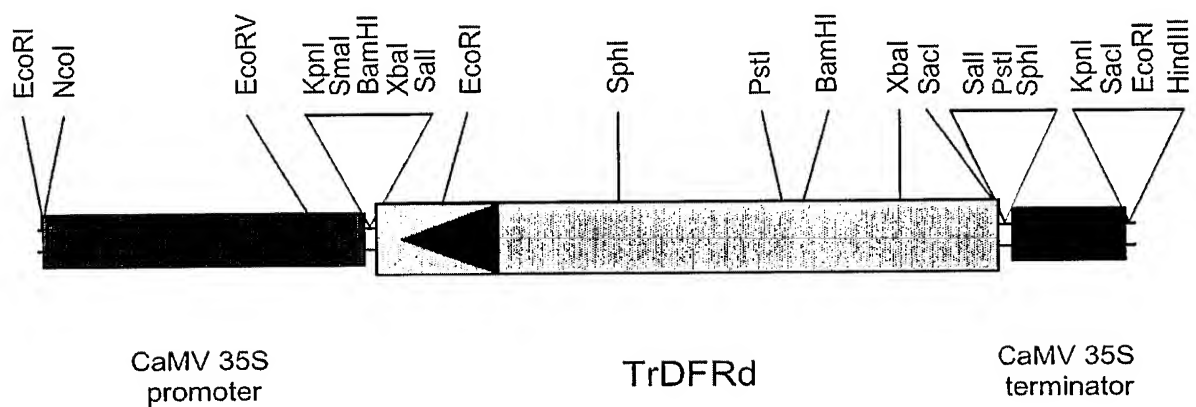
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FIGURE 167

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```
1  MSKLVCVTGG  SGCIGSWLVH  LLLLRGYTVH  ATVQNLNDEN  ETKHLEALEG
51  AQTNLRLFQI  DLLNYDTILA  AVRGCVGIFH  LASPCTVDKV  HDPQKELLD
101  AIKGTNLNLT  AAKEVGVKRV  VVTSSVSAIT  PSPDWPSDVV  KREDCWTDVE
151  YCKKKELWYP  LSKTLAEKAA  WDFSKENGLD  VVVVNP GTVM  GPVIPPRHNA
201  SMLMLVRLLE  GCAETFEDYF  MGLVHFKDVA  LAHILVYENK  EASGRHVCVE
251  TISHYGDFVA  KVAELYPEYS  VPRMQRDTQP  GLLRANDGSK  KLIDLGLEFI
301  PMEQIIKDAV  ESLKNKGFIS
```

FIGURE 168

242/271**pDH51TrDFRd sense****pDH51TrDFRd anti****FIGURE 169**

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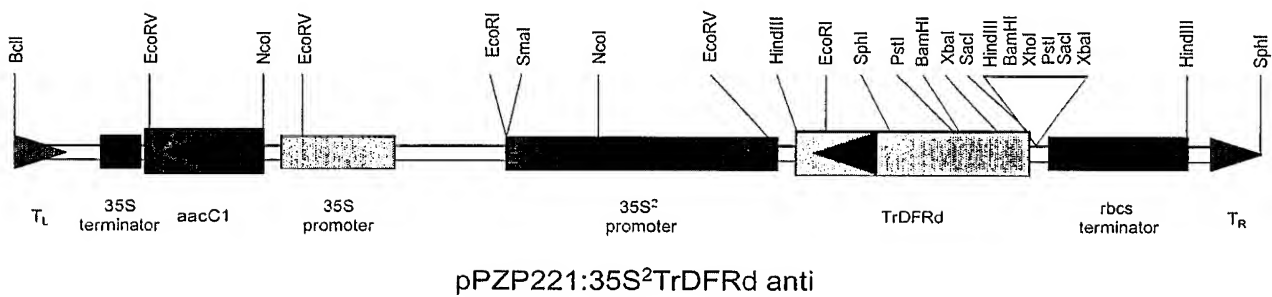
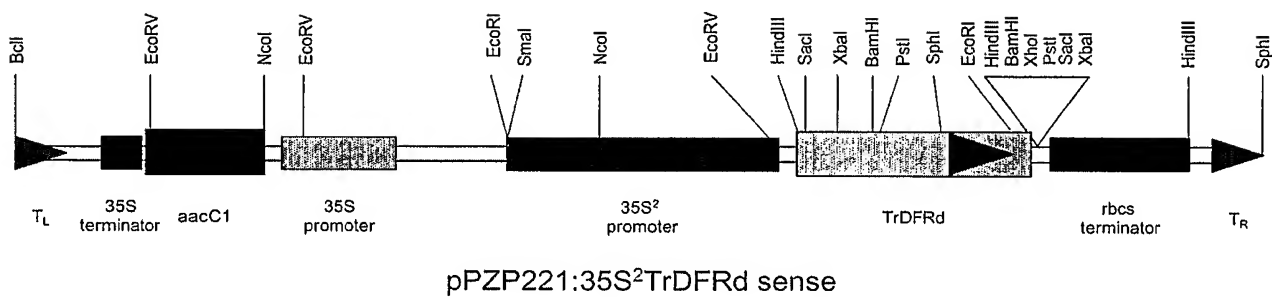


FIGURE 170

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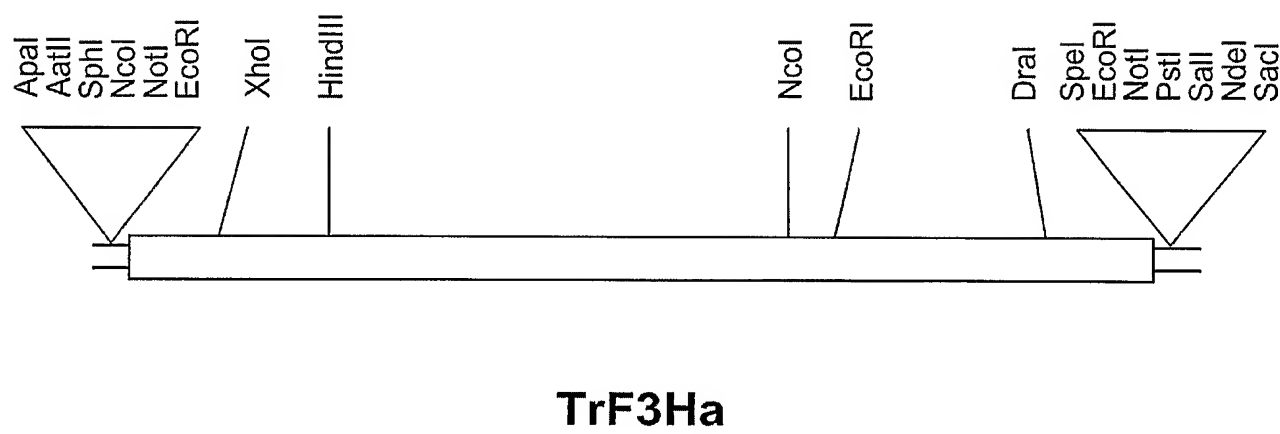


FIGURE 171

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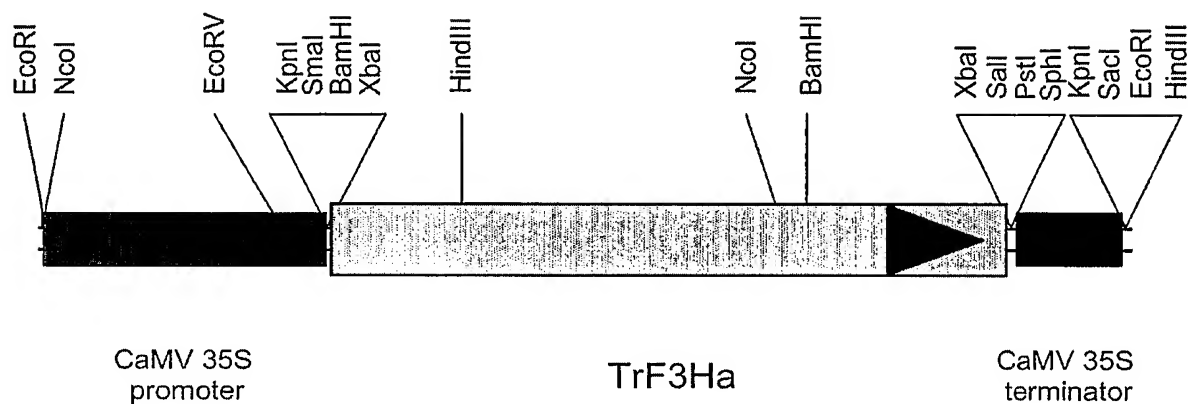
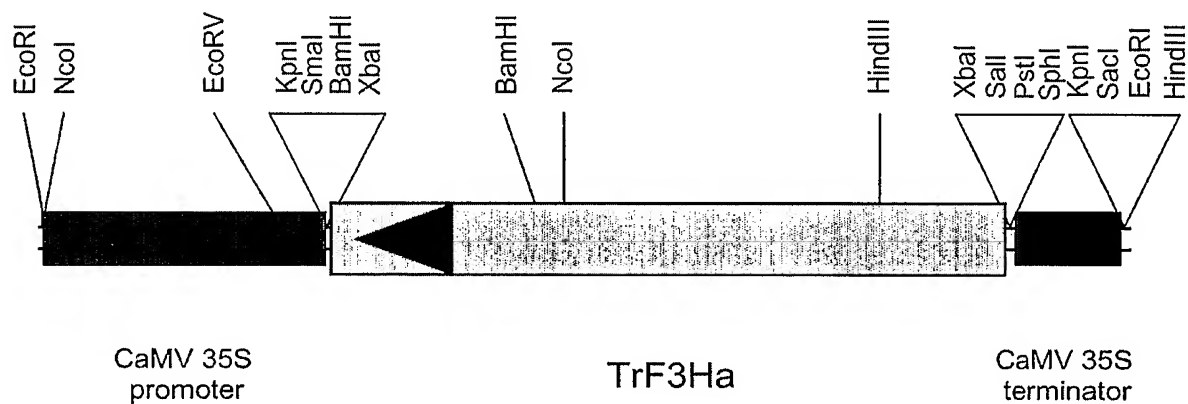
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51  TTTATTTCTA CTTAAACCTC ACAAAAAATA AACCACACAA CACACAAACA
101 CCAAAAACAG AGCACCGTTT CCATCATCAA ACAATGGCAC CAGCCAAAAC
151 TCTAAGTTAT CTCTCACAAC AAAACACTCT CGAGTCAAGT TTCGTTAGGG
201 AAGAAGATGA GCGTCCAAAA GTTGCTTACA ATAACTTCAG CAACGAGATT
251 CCAATCATTT CTCTTGCTGG AATTGATGAG GTTGATGGTC GTAGAACAGA
301 GATATGTAAC AAGATTGTTG AAGCTTGTGA GAATTGGGGT ATTTTTCAGG
351 TTGTTGATCA TGGTGTTGAT ACAAACCTTG TTTCTGAGAT GACCCGTTTT
401 GCTAGAGAGT TTTTGTGCTT GCCACCGGAA GAGAAGCTCC GGTTCGACAT
451 GTCCGGTGGT AAAAAGGGTG GTTTCATTGT CTCTAGTCAT CTCAAGGAG
501 AAGCAGTGAA GGATTGGAGA GAGCTAGTGA CATATTTTTC ATACCCAATT
551 AAACAAAGAG ATTATTCAGG GTGGCCAGAC AAGCCAGAAG GATGGAAAGA
601 GGTAACAGAA AAATACAGTG AAAACCTAAT GAATTTAGCT TGCAAGCTAT
651 TGGAAGTTTT ATCAGAAGCA ATGGGTTTAG AAAAGAAGC TCTAACAAAA
701 GCATGTGTTG ATATGGATCA AAAAGTTGTT ATAAATTATT ACCCAAAATG
751 CCCTGAACCT GACCTCACAC TTGGCCTTAA ACGTCACACT GACCCTGGCA
801 CAATTACTCT TTTGCTTCAA GATCAAGTTG GTGGTCTTCA AGCTACCAAA
851 GATAATGGTA AGACGTGGAT TACAGTTCAA CCAGTTGAAG GTGCTTTTGT
901 TGTTAATCTT GGAGACCATG GTCACATCTT AAGTAATGGA CGGTTCAAAA
951 ATGCTGACCA TCAAGCAGTG GTGAATTCTG ACTACAGCCG TTTATCAATA
1001 GCAACATTTT AAAATCCAGC TCCAGATGCA ACTGTGTACC CTTTGAAGAT
1051 TAGAGATGGT GAAAAATCTG TGTTGGAAGA ACCAATCACT TTTGCTGAAA
1101 TGTATAGAAG GAAGATGACC AAAGACCTTG AAATTGCTAG GATGAAGAAG
1151 TTGGCTAAGG AACAACAAC TTAGGGACTTG GAGGAGAACA AGACTAAATA
1201 TGAGGCCAAA CCTTTGAATG AGATCTTTGC TTAATTAAAT AGTCTTAATT
1251 TAAATAATAA ATTTTAGACT TAATTTACAT ATAATAATTT TAATTTTTTG
1301 TTCAATTAAT CTATGTTTAA TTTGTCTGTA TTGTCCACGT GTATTAAGCT
1351 GCTTGGTTGT GTGTGCCTTG GAGAATAATC AATAATATTA CATCTATGTT
1401 TAATTATAAA AAAAAAAAAA AAAAAAAAAA GTATCTGCGT TGTTACCACT
1451 GCTTAATCAC TAGTGAATTC
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FIGURE 172

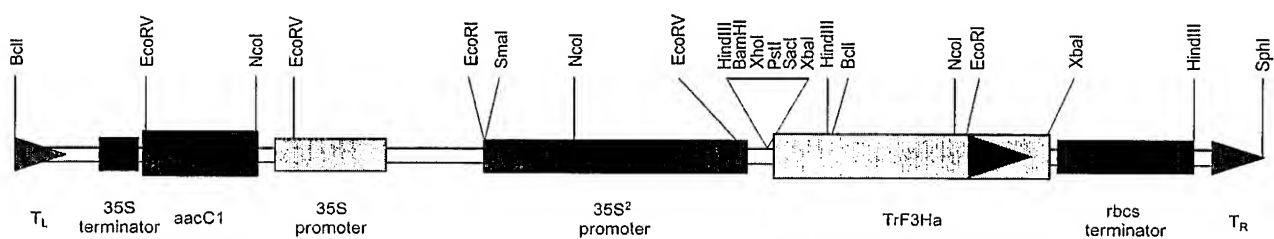
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1 MAPAKTLSYL SQQNTLESSF VREEDERPKV AYN NFSNEIP IISLAGIDEV
51 DGR RTEICNK IVEACENWGI FQVVDHGVD T KLVSEMTRFA REFFALPPEE
101 KLRFDMSGGK KGGFIVSSHL QGEAVKDWRE LV TYFSYPIK QRDYSRW PDK
151 PEGWKEVTEK YSENLMNLAC KLLEVLSEAM GLEKEALTKA CVDMDQKVVI
201 NYYPKCPEPD LTLGLKRHTD PGTITLLLQD QVGGLQATKD NGKTWITVQP
251 VEGAFVVNLG DHGHYLSNGR FKNADHQAVV NSNYSRLSIA TFQNPAPDAT
301 VYPLKIRDGE KSVLEEPITF AEMYRRKMTK DLEIARMKKL AKEQQLRDLE
351 ENKTKYEAKP LNEIFA

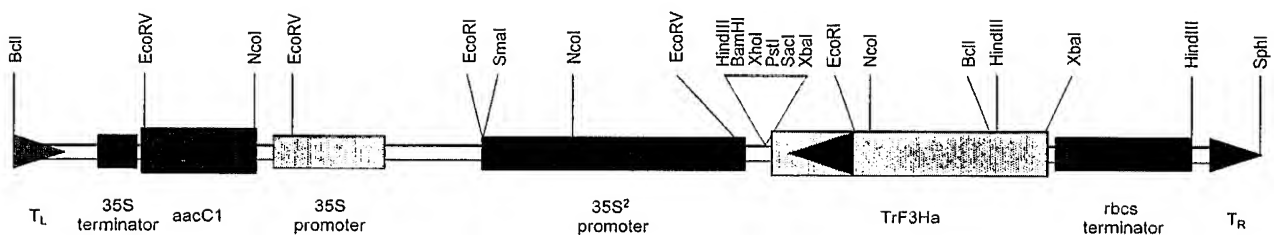
FIGURE 173

247/271**pDH51TrF3Ha sense****pDH51TrF3Ha anti****FIGURE 174**

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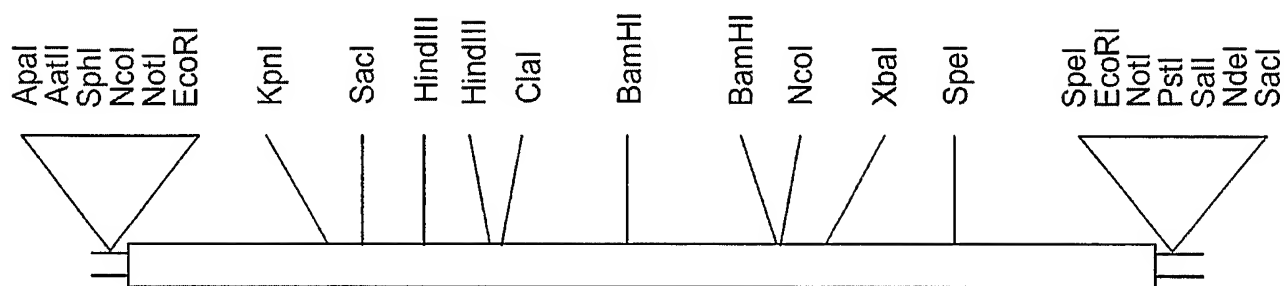


pPZP221:35S²TrF3Ha sense



pPZP221:35S²TrF3Ha anti

FIGURE 175

249/271**TrPALa****FIGURE 176**

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```

1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GAGGAAATTC
51 ACAACTCAAA TATTCCTTTA ATTCTTTTCAT ATAATCATTT GAATTTCCAT
101 TCTCCCTAAA AATTCCTATAG CTACCACATC ACACAACATA ACAAATTAAG
151 AAATATTTTAT TACTATATTA AGATATGGAA GTAGTAGCAG CAGCAATCAC
201 AAAAAACAAT GGCAAGATTG ATTCATTTTG CTTGAATCAT GCTAATGCTA
251 ATAACATGAA AGTGAATGGT GCTGATCCTT TGAATTGGGG TGTGGCTGCT
301 GAGGCAATGA AGGGAAGTCA CTTGGATGAG GTGAAGCGTA TGGTGGAGGA
351 ATACCGGAAA CCGGTTGTCC GTCTTGGTGG CGAGACACTA ACCATTTCTC
401 AGGTGGCTGC CATTGCTGCA CACGATGGTG CAACGGTGGA GCTATCGGAA
451 TCTGCTAGAG CCGGCGTTAA GGCAAGCAGT GACTGGGTTA TGGAGAGTAT
501 GAACAAAGGT ACCGACAGCT ACGGTGTCCC AACAGGGTTC GGCCTACCT
551 CGCACCGCCG AACCAAACAA GGTGGTGCTT TGCAGAAAGA GCTCATAAGG
601 TTTTTGAATG CTGGAATATT TGGAAATGGA ACTGAGTCAA GCCACACACT
651 ACCACACACA GCCACAAGAG CTGCCATGCT AGTGAGAATC AACACACTTC
701 TCCAAGGCTA TTCAGGAATT AGATTTGAAA TCTTAGAAGC TATCACCAG
751 CTTCTTAACA ACAATGTCAC CCCATGTTTA CCGCTTCGCG GTACAATCAC
801 AGCTTCAGGA GATTTAGTCC CTCTTCTTCA CATTGCTGGT TTACTAACCG
851 GACGACCAA TTCCAAGGCT CATGGACCTT CTGGAGAAGT ACTTAATGCA
901 AAACAAGCTT TTCAATCAGC TGGAATCGAT GCCGAGTTCT TTGAATTACA
951 ACCAAAAGAA GGCCTTGCCC TTGTTAACGG AACCGCTGTT GGTTCCTGGT
1001 TAGCTTCTAT TGTTCTTTTT GAGGCTAATA TATTGGCGGT GTTGTCTGAA
1051 GTTCTATCTG CAATTTTCGC TGAAGTTATG CAAGGGAAGC CCGAATTTAC
1101 CGATCATTTG ACACATAAGT TGAACATCA CCCTGGTCAA ATTGAGGCTG
1151 CTGCTATTAT GGAACACATT TTGGATGGGA GTGCTTATGT TAAAGACGCT
1201 AAGAAGTTGC ATGAGATGGA TCCTTTACAG AAGCCAAAC AAGATAGATA
1251 TGCACTTAGG ACTTCGCCAC AATGGCTTGG TCCTTTGATT CAAGTGATTA
1301 GATTCTCTAC CAAGTCAATT GAGAGAGAGA TCAACTCTGT CAATGACAAT
1351 CTTTTGATTG ATGTTTCAAG GAACAAGGCT TTGCATGGTG GAAATTTTCA
1401 AGGAACACCT ATCGGAGTAT CCATGGATAA TACACGTTTG GCTCTTGCAT
1451 CAATTGGCAA ACTTATGTTT GCTCAATTCT CTGAGCTTGT CAATGATTTT
1501 TACAACAATG GATTGCCATC AAATCTCTCT GCTAGTAGAA ATCCGAGCTT
1551 GGATTATGGG TTCAAGGGAT CCGAAATTGC CATGGCTTCT TATTGTTCCG
1601 AGTTGCAATA TCTTGCAAAT CCGGTTACAA CTCATGTCCA AAGTGC GGAA
1651 CAACACAACC AAGATGTCAA CTCTTTGGGT TTGATTTCTT CTAGAAAAAC
1701 TTATGAAGCA ATTGAGATCC TTCAATTGAT GTCTTCCACA TTCTTGATTG
1751 CACTTTGTCA AGCAATTGAT TTAAGACATT TGGAGGAGAA TTTGAAAAAC
1801 TCGGTCAAAA ATACCGTAAG CCAAGTGGCC AAAAAGACAC TAACCATAGG
1851 TGTCAATGGA GAACTTCATC CTTCAAGATT TTGTGAAAAA GACTTATTGA
1901 AAGTGGTTGA TAGGGAACAT GTCTTTGCCT ACATTGATGA TCCTTGTAGT
1951 GCTACATACC CATTGATGCA AAAACTCAGG CAAGTACTAG TGGATCATGC
2001 ATTAGTTAAT GGAGAAAGTG AGAAGAATTT GAACACATCA ATCTTCCAAA
2051 AGATTGCAAC TTTTGAGGAA GAGTTGAAAA ACCTTTGCCA AAAGAGGTTG
2101 AAAGTGCAAG GATTGCATAT GAAAGTGGA AATCAACAAT TCCAAACAAG
2151 ATCAATGGAT GCAGATCTTA TCCACTCTAC AATTTTGTGA GAAAGGAGTT
2201 GGGAACTGGT TTGCTAACTG GAGAAAATGT CATTTCACCG GGTGAAGAGT
2251 GTGACAACT ATTCACAGCT ATGTGTCAAG GAAAAATCAT TGATCCTCTT
2301 CTTGAATGCT TGGGAGAGTG GAACGGTGCT CCTCTTCCAA TTTGTTAACT
2351 TTGATTGTTA GTTCATAAAA TGTTTTATTT GTATTTATCA TTTGTATTTA
2401 TGCGAGTGTA GTAATAATGA TTAGGTGTTT TGTGCCTTTA ATGAAAAAAA
2451 AAAAAAAAAA AAAAAAAAAA AAAAGTACTC TCGGTTGTTA CCACTGCTTA
2501 ATCACTAGTG AATTC

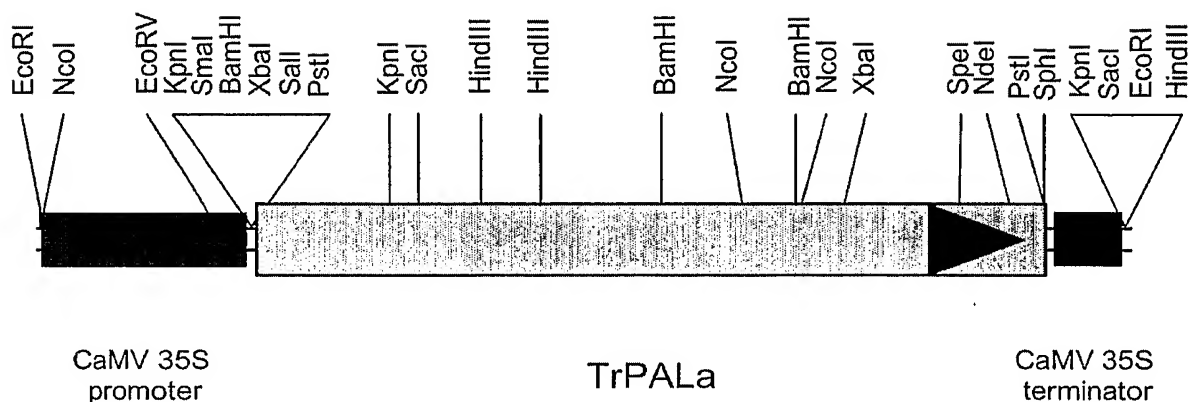
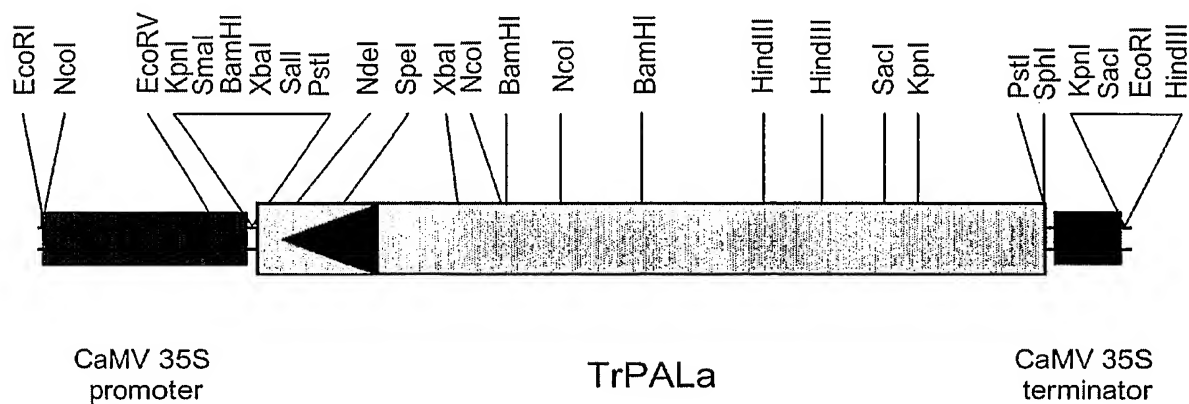
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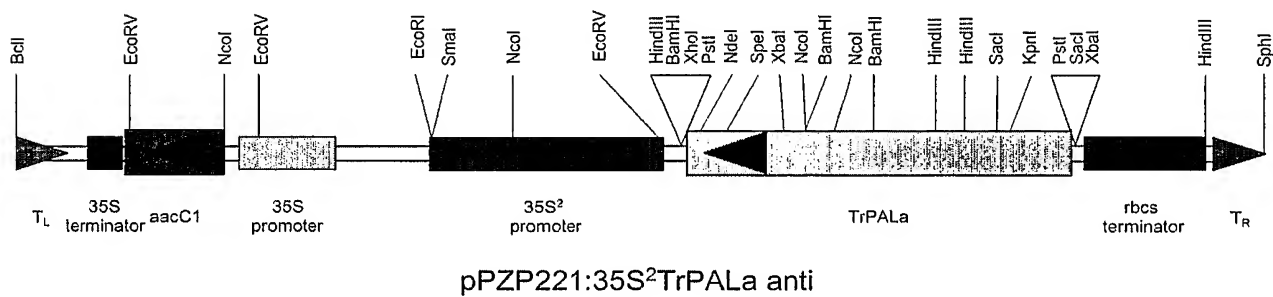
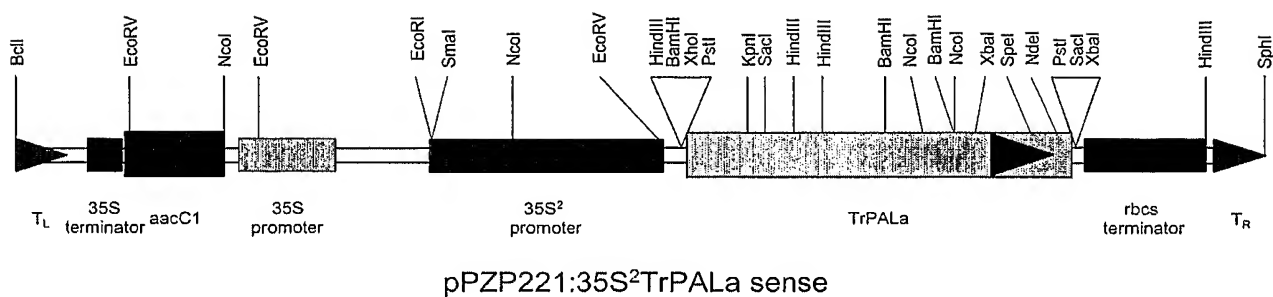
FIGURE 177

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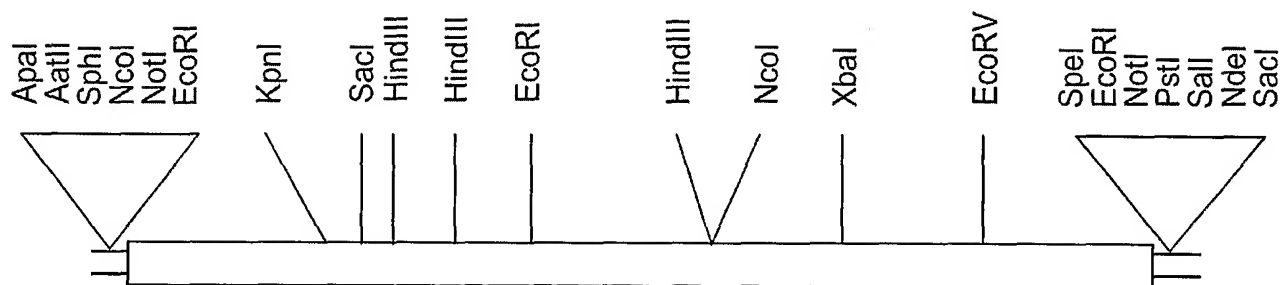
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51 DEVKRMVEEY RKPVVRLGGE TLTISQVAAI AAHDGATVEL SESARAGVKA
101 SSDWVMESMN KGTD SYGVPT GFGATSHRRT KQGGALQKEL IRFLNAGIFG
151 NGTESSHTLP HTATRAAMLV RINTLLQGYS GIRFEILEAI TKLLNNNVTP
201 CLPLRG TITA SGDLVPLSYI AGLLTGRPNS KAHGPSGEVL NAKQAFQSAG
251 IDAEFFELQP KEGLALVNGT AVGSGLASIV LFEANILAVL SEVLSAIFAE
301 VMQ GKPEFTD HLTHKLK HHP GQIEAAAIME HILDGSAYVK DAKKLHEMDP
351 LQKPKQDRYA LRTSPQWLGP LIEVIRFSTK SIEREINSVN DNPLIDVSRN
401 KALHGGNFQG TPIGVSM DNT RLALASIGKL MFAQFSELVN DFYNNGLPSN
451 LSASRNPSLD YGFKGSEIAM ASYCSELQYL ANPVTTHVQS AEQHNQDVNS
501 LGLISSRKTY EAIEILQLMS STFLIALCQA IDLRHLEENL KNSVKNTVSQ
551 VAKKTLTIGV NGELHPSRFC EKDLLKVVD R EHV FAYIDDP CSATYPLMQK
601 LRQVLVDHAL VNGESEKNLN TSIFQKIATF EEELKNLCQK RLKVQGLHMK
651 VEIQQFQTRS MDADLIHSTI L

FIGURE 178

252/271**pDH51TrPALa sense****pDH51TrPALa anti****FIGURE 179**

253/271**FIGURE 180**

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TrpPALb

FIGURE 181

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```

1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG AGGAAATAAA
51  TTCATCATTG TTCCTTATTT CCCACCCAAC ACAACATAAC AAATACATTT
101 CCTCTCCTCT CATCACAATT ATTACTTTCT ACACCCCCC CTCTCAACTA
151 TTATTAACTA ACATAATGGA GGAATTACC AATGGCCATG CTGAAGCAAC
201 TTTTTCGCTG ACCAAAAGTG TTGGTGATCC ACTCAACTGG GGTGCAGCCG
251 CGGAGTCGTT GATGGGGAGT CATTGATG AGGTGAAGCG TATGGTGGAG
301 GAATACCGTA ATCCATTGGT TAAAATTGGC GGCGAGACGC TTACCATTCG
351 TCAGGTGGCT GGAATTGCTT CTCATGATAG TGGTGTGAGG GTGGAGCTGT
401 CTGAGTCCGC CAGGGCCGGC GTTAAGGCGA GTAGTGGTTG GGTGATGGAC
451 AGCATGAACA ATGGGACTGA TAGTTATGGT GTTACCACTG GTTTCGGCGC
501 CACCTCTCAC CGGAGAACCA AGCAGGGTGG TGCCTTGCAG AAGGAGCTAA
551 TTAGGTTTTT GAATGCCGGA ATATTTGGCA ATGGTACAGA ATCTAACTGT
601 ACACACTACC ACACAGCAAC CAGAGCTGCA ATGCTTGTGA GAATCAACAC
651 TCTTCTTCAA GGATATTCTG GAATTAGATT TGAAATTTTG TGAAATTTCA
701 CAAAGCTTCT AAACAACAAC ATTACCCCAT GTTTACCACT TCGTGGTACA
751 ATCACGGCTT CCGGTGATCT CGTTCGCTT TCCTACATTG CCGGTTTGTT
801 AACC GGTTAG CCGAACTCCA AAGCCGTTGG ACCCTCCGGA GAAATTCCTCA
851 ATGCAAAAGA AGCTTTTCAA CTTGCCGGCA TTGGTTCTGA GTTTTTTGAA
901 TTGCAGCCAA AAGAAGGTCT TGCTCTTGTT AATGGTACTG CTGTTGGTTC
951 TGGTTTAGCT TCTATTGTTT TGTGTTGAAG AAATGTACTA GCTGTTTTGT
1001 CTGAAGTTAT GTCGGCGATT TTCGTTGAAG TTATGCAAGG GAAACCAAGG
1051 TTCACCTGATC ATTTGACTCA TAAGTTGAAA CATCACCTG GTCAAAATTGA
1101 AGCTGCTGCA ATTATGGAAC ATATTTTGGA TGGAAGTGCT TATGTTAAAG
1151 CAGCTAAGAA ATTACACGAA ACCGATCCTT TACAAAAGCC GAAACAAGAT
1201 CGTTATGCAC TTAGAACTTC ACCTCAATGG CTTGGTCCTT TGATTGAAGT
1251 GATAAGATTT TCAACTAAGT CAATTGAGAG AGAAATTAAC TCTGTCAATG
1301 ATAACCCTTT GATTGATGTT TCAAGGAACA AGGCCATTCA CCGTGGTAAT
1351 TTTCAAGGAA CACCTATTGG AGTTTCAATG GATAACACAC GTTTAGCTCT
1401 TGTCTCAATT GGTAAACTCA TGTTTGCTCA ATTCTCTGAA CTTGTAATG
1451 ATTTTACAA CAACGGGTTA CCTTCGAATC TTAGTGCTAG TAGGAACCCA
1501 AGCTTGGAAT ACGGTTTCAA GGGATCGGAA ATTGCCATGG CTTCTTATTG
1551 TTCTGAGTTA CAATATCTTG CTAATCCTGT CACCACCCAT GTCCAAAGTG
1601 CGGAGCAACA CAATCAAGAT GTTAACCTCT TGGGTTTGAT TTCTTCAAGA
1651 AAAACAAATG AAGCTATTGA GATCCTAAAG CTCATGTCTT CGACATTTCT
1701 GATTGCACTT TGTCAAGCAA TTGATTTAAG GCATTTGGAG GAAAATCTGA
1751 GGAACACTGT CAAGAACACG GTAAGCCAAG TAGCGAAGAG AACACTCACC
1801 ACCGGTGTTA ATGGAGAACT TCATCCTTCT AGATTTTGTTG AGAAAGATTT
1851 GCTCAAAGTT GTTGATAGGG AGTATGTATT TGCCTATGTC GACGATCCTT
1901 GTCTAGCTAC ATACCCTTTG ATGCAAAAGT TGAGACAAGT GCTTGTGGAT
1951 CATGCATTGG TAAATGCTGA TGGAGAGAAG AATTTGAACA CATCAATCTT
2001 TCAAAAGATT GCAACTTTTG AGGATGAATT GAAAGCTATC TTGCCAAAGG
2051 AAGTTGAAAG TACAAGAACT GCATATGAAA ATGGACAATG TGGAATTTCA
2101 AACAAGATTA AGGAATGCAG GTCTTATCCA TTGTACAAGT TTGTTAGAGA
2151 GGAGTTAGGA ACCGCGTTGC TAACCGGAGA AAAAACGATA TCGCTGGGCG
2201 AAGAGTGTGA CAAATTGTTT ACAGCTATGT GCCAAGGTAA AATTGTTGAT
2251 CCTCTTTTGG AATGCCCTTG AGAGTGGAAT GGTGCTCCTC TACCAATATG
2301 TTAATTAGCA GAATTAATAT GTTCTTTTGA GAAGTGATTT CTTTATATAT
2351 TTGTAGTATA CTATAGTAGT TGCATTGAGA AGCAATTGGT TTGTCTATAA
2401 GCCTATGGAA AATGGCAAAA CAATTTTCTG CTCAAAGCAT CGTTTATTAA
2451 GTTTTCCTTA AAGTGTTAAG GAACTTTTAA TTGTTTTTGT AATAGAATTT
2501 CATTTGTTTG CCACAACCTT GGGTGCAAAT ATCACGTGAT ACATGAGTTG
2551 TTTGATGTAA ATGGTGTTTT CTCAAATTAAT AAATAGTGTT TCAGCCATGA
2601 AAAAAAAAAA AAAAAAAAAA AAAAAAGTAC TCTGCGTTGT TACCACTGCT
2651 TAATCACTAG TGAATTC

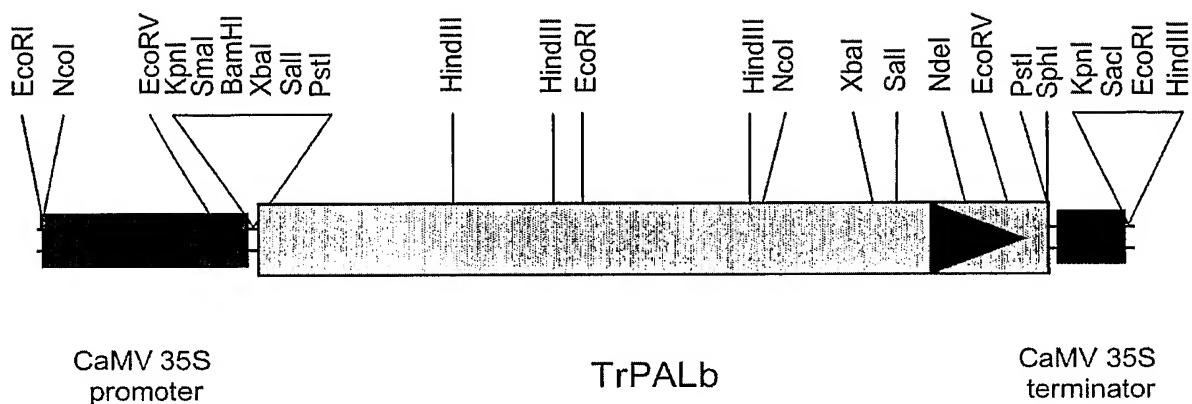
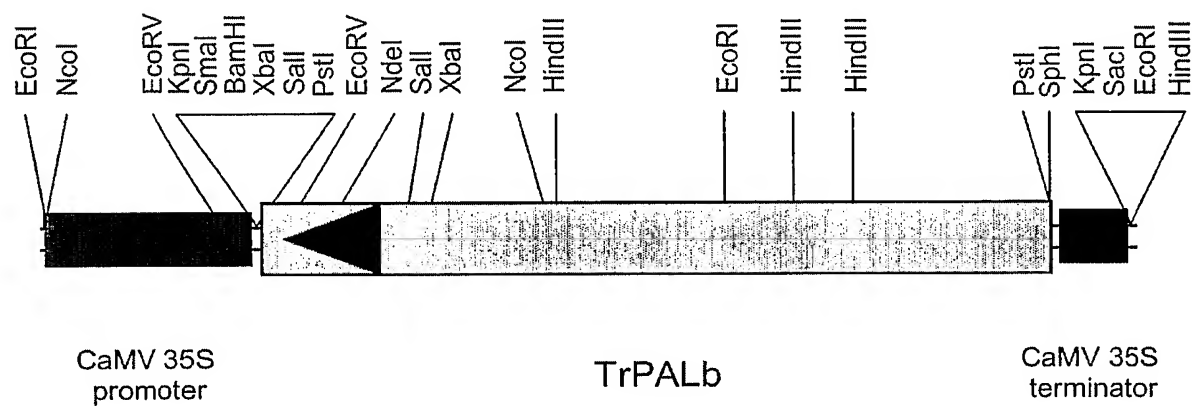
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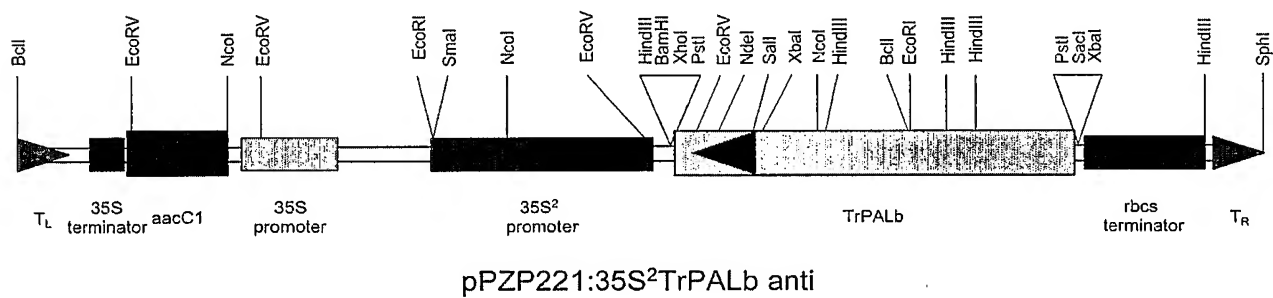
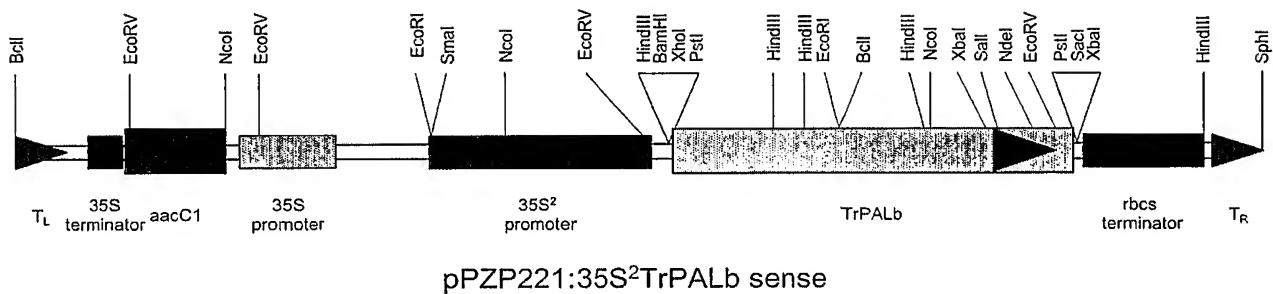
FIGURE 182

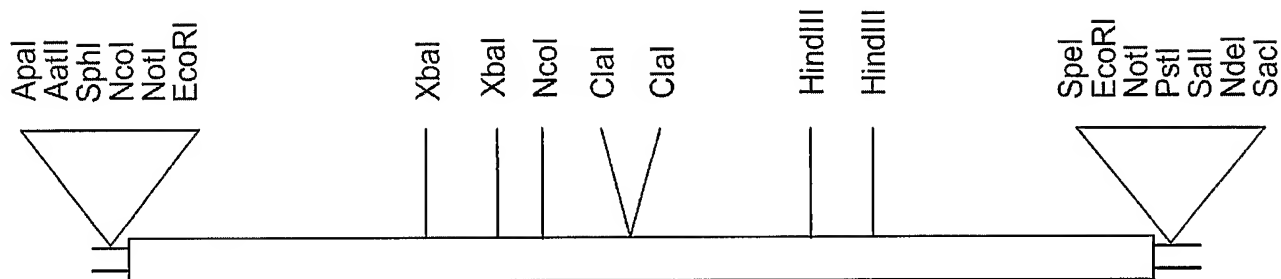
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51 LVKIGGETLT IAQVAGIASH DSGVRVELSE SARAGVKASS GWVMDSMNNG
101 TDSYGVTTGF GATSHRRTKQ GGALQKELIR FLNAGIFGNG TESNCTLPHT
151 ATRAAMLVRI NTLLQGYSGI RFEILEAITK LLNNNITPCL PLRGTITASG
201 DLVPLSYIAG LLTGRPNKA VGPSGEILNA KEAFQLAGIG SEFFELQPKE
251 GLALVNGTAV GSGLASIVLF EANVLAVLSE VMSAIFAEVM QGKPEFTDHL
301 THKLKHHPGQ IEAAAIMEHI LDGSAYVKAA KKLHETDPLQ KPKQDRYALR
351 TSPQWLGPLI EVIRFSTKSI EREINSVNDN PLIDVSRNKA IHGGNFQGTP
401 IGVSMNTRL ALASIGKLMF AQFSELVNDF YNNGLP SNLT ASRNPSLDYG
451 FKGSEIAMAS YCSELQYLAN PVTTHVQSAE QHNQDVNSLG LISSRKTNEA
501 IEILKLSST FLIALCQAID LRHLEENLRN TVKNTVSQVA KRTLTTGVNG
551 ELHPSRFCEK DLLKVVDREY VFAYVDDPCL ATYPLMQKLR QVLVDHALVN
601 ADGEKNLNTS IFQKIATFED ELKAILPKEV ESTRTAYENG QCGISNKIKE
651 CRSYPLYKFV REELGTALLT GEKTISLGEE CDKLFTAMCQ GKIVDPLEC
701 LGEWNGAPLP IC

FIGURE 183

257/271**pDH51TrPALb sense****pDH51TrPALb anti****FIGURE 184**

258/271**FIGURE 185**

259/271**TrPALf****FIGURE 186**

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1  GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGAGG
51 AAATAAATTC ATCATTGTTC ATTATTTCCC ACCCAACACA ACATAACAAA
101 TACATTATTC TCTCCTCTGA TCACAATTAT TACTTTCTAC ACCCTCCTCT
151 CAACTATTAT TAACTAGCAT AATGGAGGGA ATTACCAATG GCCATGCTGA
201 AACAACTTTT TGCGTGACCA AAAGTGTGGG TGATCCACTC AACTGGGGTG
251 CAGCCGCGGA GTCGTTGACG GGGAGTCATT TGGATGAGGT GAAGCGTATG
301 GTGGAGGAGT ACCGTAATCC GTTGGCTAAA ATTGGCGGCG AGACGCTTAC
351 CATTGCTCAG GTGGCTGGAA TTGCTTCTCA TGATAGTGGT GTGAGGGTGG
401 AGCTGTCCGA GTCCGCAAGG GCCGGCGTTA AGGCGAGTAG TGATTGGGTG
451 ATGGATAGCA TGAACAATGG GACTGATAGT TACGGTGTTA CCACCGGTTT
501 TGGTGCCACC TCTCACC GGAACCAAGCA GGGTGGTGGT TTGCAGAAAG
551 AGCTAATTAG GTTTTTGAAT GCTGGAATAT TTGGCAATGG TACAGAATCT
601 AACTGTACAC TACCACACAC AGCAACTAGA GCTGCAATGC TTGTGAGAAAT
651 CAACACTCTT CTTCAAGGGT ACTCTGGTAT TAGATTTGAA ATTTTGGAAG
701 CTATCACAAA GCTTCCAAAC AACAACATTA CCCCATGTTT ACCACTTCGT
751 GGTACAATCA CGGCTTCCGG TGATCTTGTT CCGCTTTCCT ACATTGCCGG
801 TTTGTTAACC GGAAGACCCA ACTCCAAAGC AGTTGGACCT TCCGGAGAAA
851 TTTTGAGTGC TAAAGAAGCT TTTCAACTCG CCGGCATGGG TTCTGAGTTT
901 TTTGAATTGC AACCAAAAAGA AGTCTTGCT CTTGTTAATG GTACTGCTGT
951 TGGCTCTGGT TTAGCTTCTA TTGTTCTGTT TGAAGCAAAT GTACTAGCTG
1001 TTTTATCCGA AGTTATGTCG GCGATTTTCG CTGAAGTTAT GCAAGGGAAA
1051 CCGGAATTTA CCGATCATTT GACTCATAAG TTGAAACATC ACCCTGGTCA
1101 AATTGAAGCT GCTGCAATTA TGAACATAT TTTGGATGGA AGTGCTTATG
1151 TTAAAGCAGC TAAGAAGTTA CACGAAACCG ATCCTTTACA AAAACCGAAA
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1751 ATCTCAGGAA CACCGTCAAG AACACGGTAA GCCAAGTAGC GAAGAGAACA
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1901 ATCCTTGCTT AGCTACATAC CCTTTGATGC AAAAGTTGAG ACAAGTGCTT
1951 GTGGATCATG CATTGGTAA TGTGTATGGA GAGAAGAATT TGAACACATC
2001 AATCTTTCAA AAGATTGCAA CTTTTGAGGA TGAGTTGAAA GCTATTTTGC
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2151 TAGAGAGGAG TTAGGAACCG CGTTGCTAAC CGGAGAAAAA ACTATATCGC
2201 CGGGCGAAGA GTGCGATAAA TTGTTTACAG CTATGTGCCA AGGTAAAATT
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2551 GTGTTTGATG TAAATGGTGT TTTTTCAATA AATAAATAGT GTTTCAACTA
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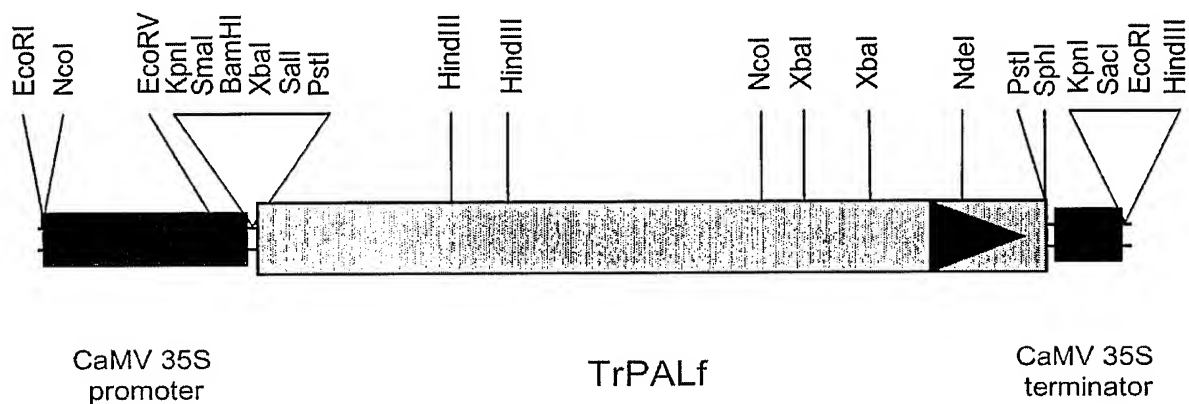
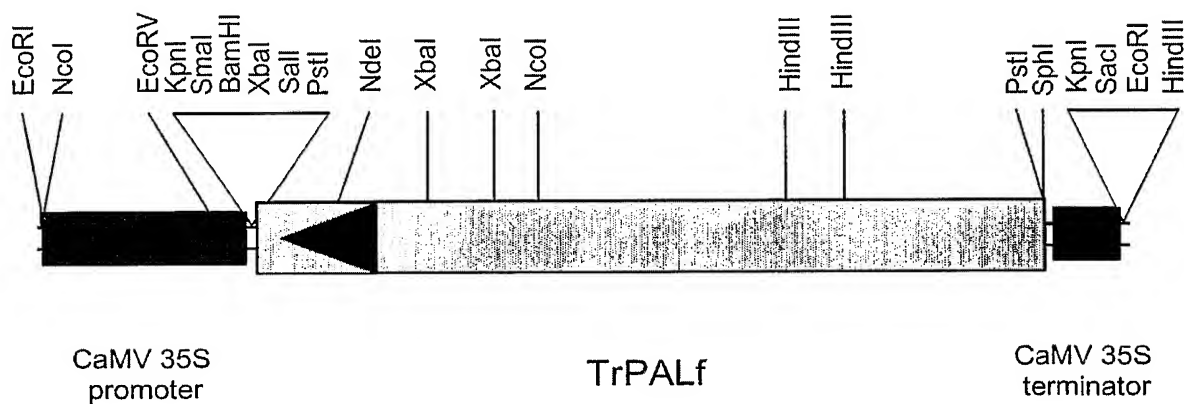
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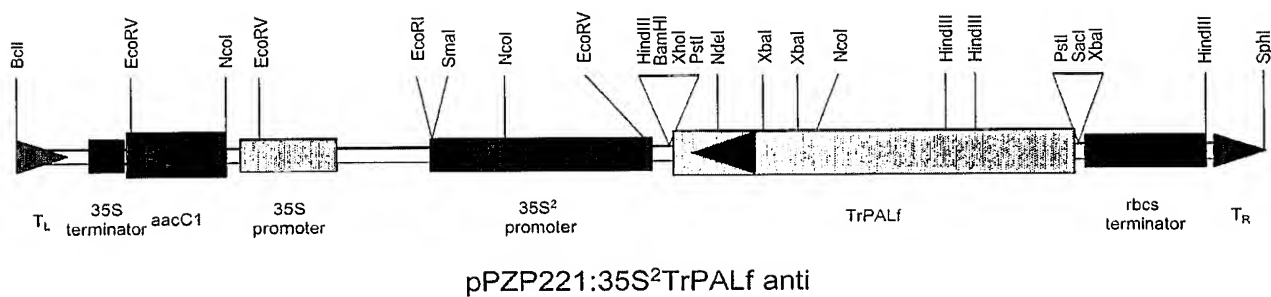
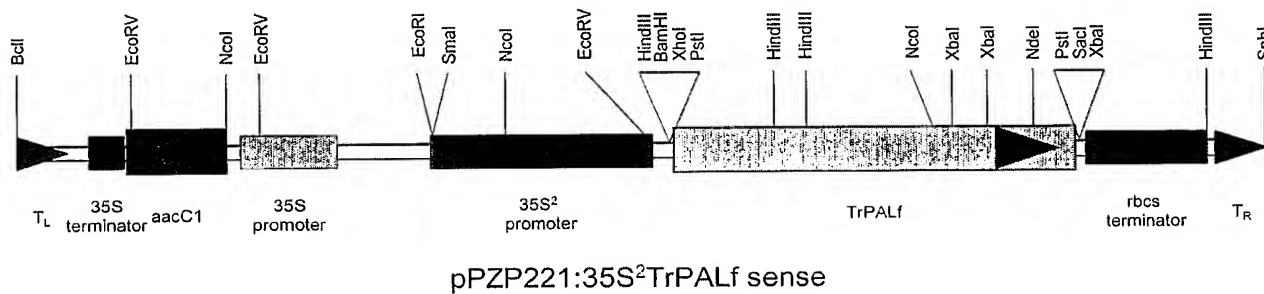
FIGURE 187

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151 ATRAAMLVRI  NTLLQGYSGI  RFEILEAITK  LPNNNITPCL  PLRGTITASG
201 DLVPLSYIAG  LLTGRPNska  VGPSGEILSA  KEAFQLAGIG  SEFFELQPKE
251 GLALVNGTAV  GSGLASIVLF  EANVLAVLSE  VMSAIFAEVM  QGKPEFTDHL
301 THKLKHHPGQ  IEAAAIMEHI  LDGSAYVkaa  KKLHETDPLQ  KPKQDRYALR
351 TSPQWLGPLI  EVIRFSTKSI  EREINSVNDN  PLIDVSRNKA  IHGGNFQGTP
401 IGVSM DNTRL  ALASIGKLMF  AQFSELVNDf  YNNGLPsYLT  ASRNPSLDYG
451 FKGSEIAMAS  YCSELQYLAN  PVTTHVQSAE  QHNQDVNSLG  LISSRKTNEA
501 IEILKLMSST  FLIALCQAID  LRHLEENLRN  TVKNTVSQVA  KRTLTTGVNG
551 ELHSSRFCEK  DLLKVVDREY  VFAYADDPCL  ATYPLMQKLR  QVLVDHALVN
601 VDGEKNLNTS  IFQKIATFED  ELKAILPKEV  ESTRTAYENG  QCGISNKIKE
651 CRSYPLYKfV  REELGTALLT  GEKTISPGEe  CDKLFTAMCQ  GKIVDPLMEC
701 LGEWNGAPLP  IC
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FIGURE 188

262/271**pDH51TrPALf sense****pDH51TrPALf anti****FIGURE 189**

263/271**FIGURE 190**

264/271

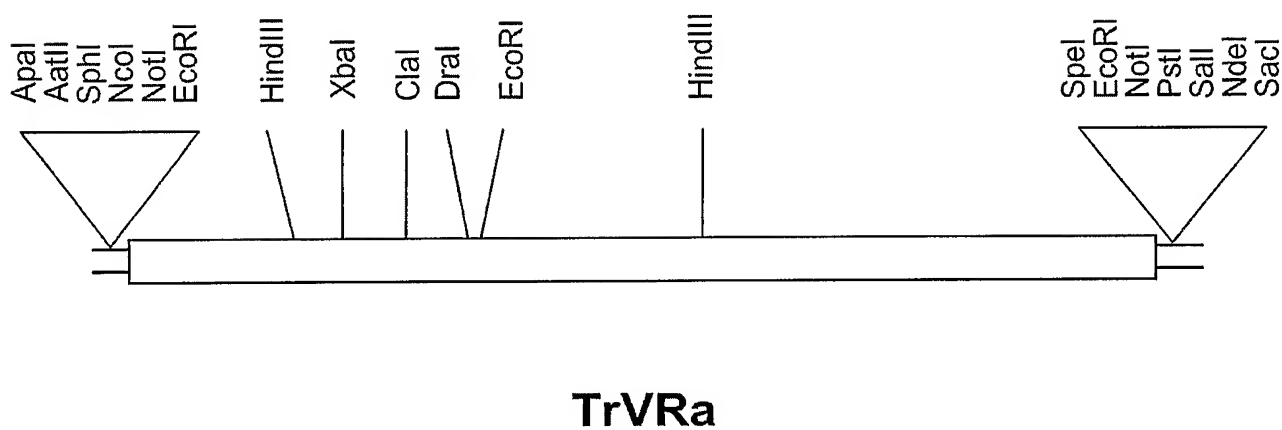


FIGURE 191

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201 ATACCACTAT TAGAGCTGAT CCAGAACGTA AGAGGGATGT AAGCTTCCTA
251 ACAAATCTAC CCGGCGCATC CGAAAGGCTA CATTTCTTCA ACGCCGATCT
301 AGACGACCCA GAGAGTTTCA ACGAAGCAAT TGAAGGTTGT GTCGGGATAT
351 TCCACACCGC TTCACCAATC GATTTCGCCG TGAGTGAGCC AGAAGAAATA
401 GTGACAAAAA GAACAGTGGA TGGAGCATTA GGAATTTTAA AAGCATGTGT
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501 TTTCATTCAA TGGAAAAAAC AAAGATGTTT TGGATGAGAG TGATTGGAGT
551 GATGTTGATT TGCTTAGAAG TGTAAACCA TTTGGTTGGA GTTATGGTGT
601 TTCAAAGACT TTGGCTGAGA AAGCAGTGCT TGAATTTGGT CAACAAAATG
651 GGATTGATGT TGTTACTTTG ATTCTTCCTT TTATTGTTGG AAGTTTTGTT
701 TGTCCTAAGC TTCCTGATTC TGTTGAGAAA GCTCTTGTTT TGGTACTAGG
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1001 GACGCTGGTT TTGAGTTTAA GTATAGTGTC GGTGATATGT TCGATGATGC
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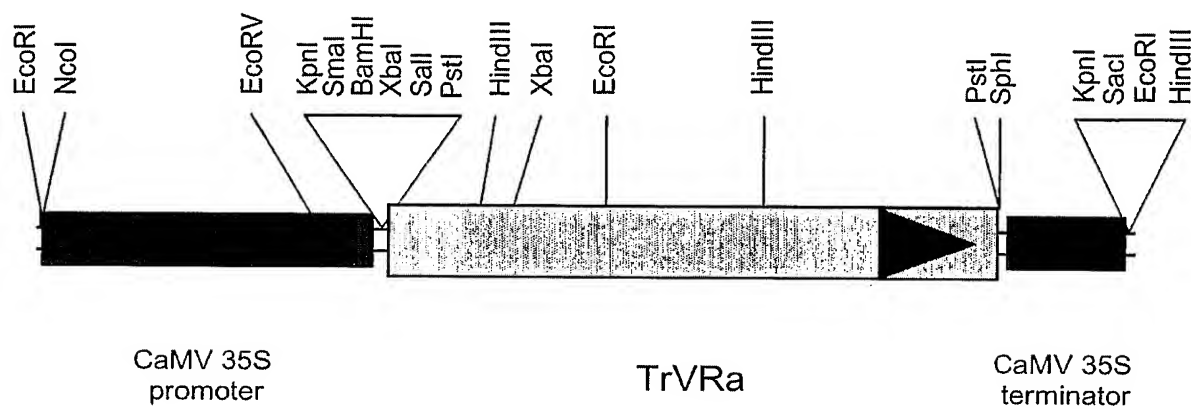
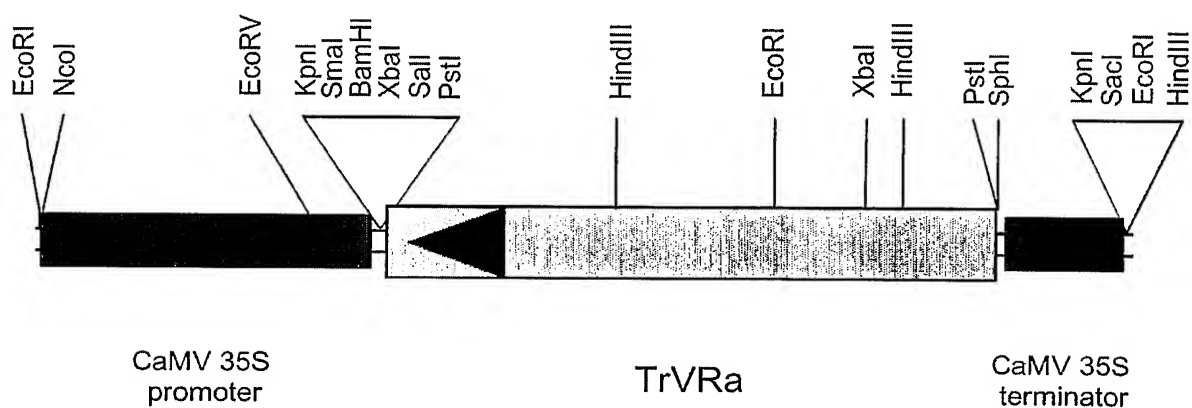
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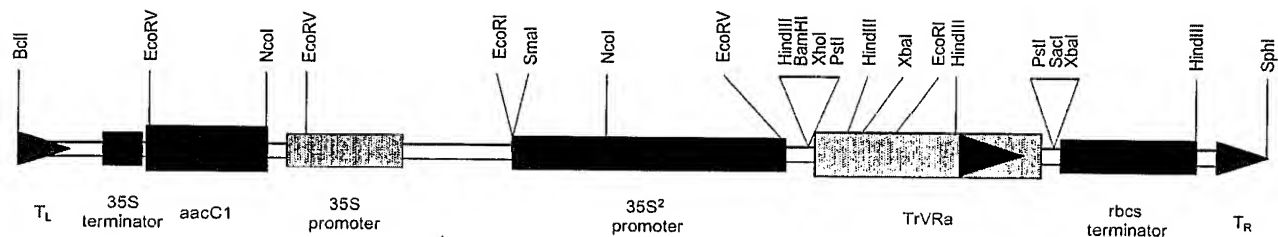
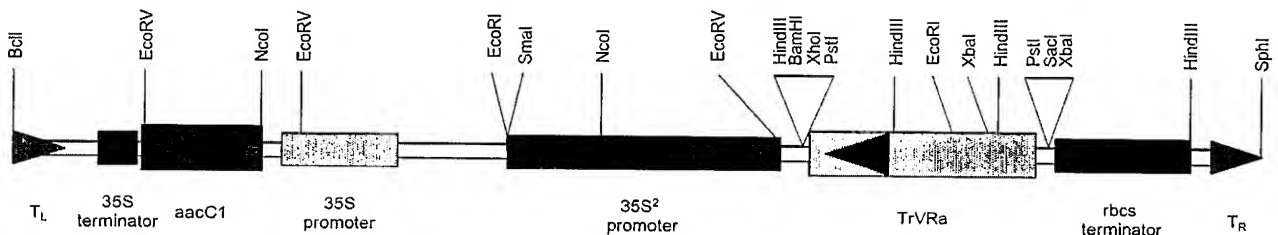
FIGURE 192

266/271

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101 TKRTVDGALG ILKACVNSKT VKRFIYTSSG SAVSFNGKNK DVLDESDWSD
151 VDLLRSVKPF GWSYGVSKTL AEKAVLEFGQ QNGIDVVTLI LPFIVGSFVC
201 PKLPDSVEKA LVLVLGKKEQ IGIISFHMVH VDDVARAHY LLENPVPGGR
251 YNCSPFFVSI EEMSQLLSAK YPEYQILSVD ELKEIKGARL PDLNSKKLVD
301 AGFEFKYSVG DMFDDAIQCC KEGGYL

FIGURE 193

267/271**pDH51TrVRa sense****pDH51TrVRa anti****FIGURE 194**

268/271**pPZP221:35S²TrVRa sense****pPZP221:35S²TrVRa anti****FIGURE 195**

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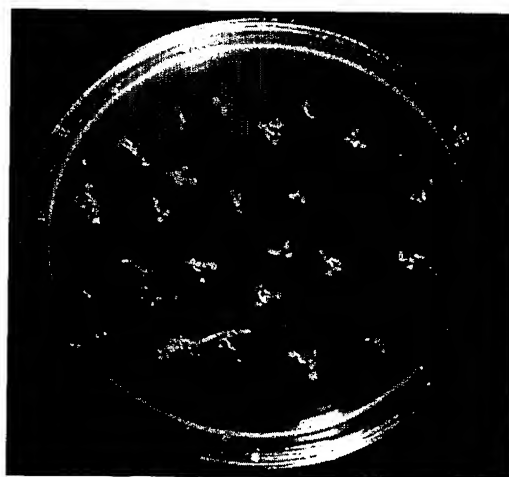
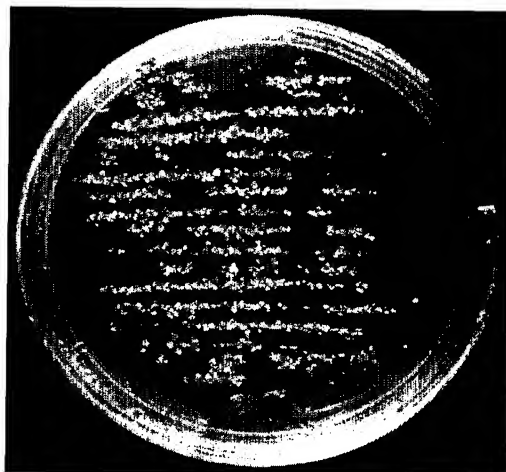
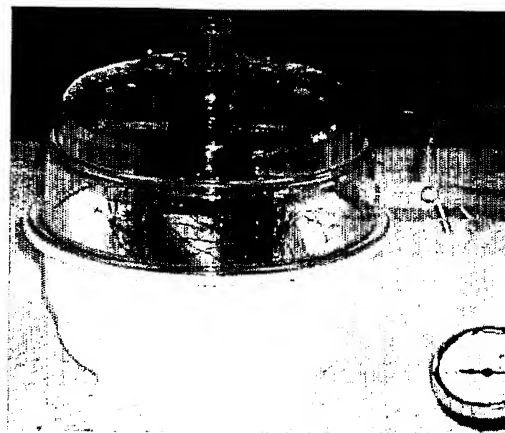
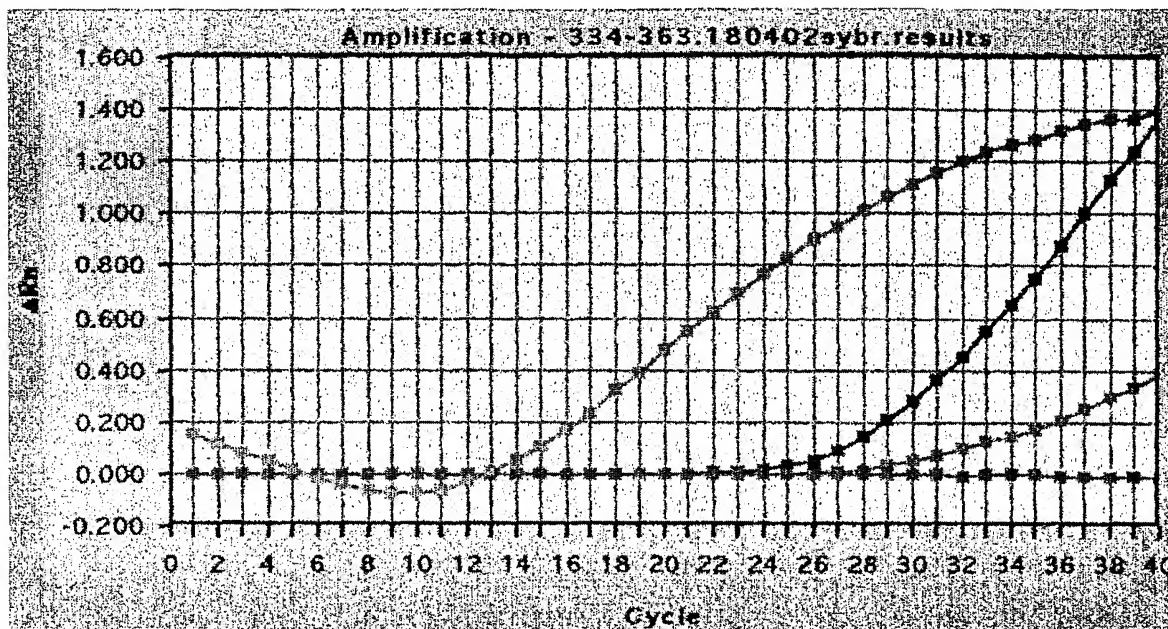
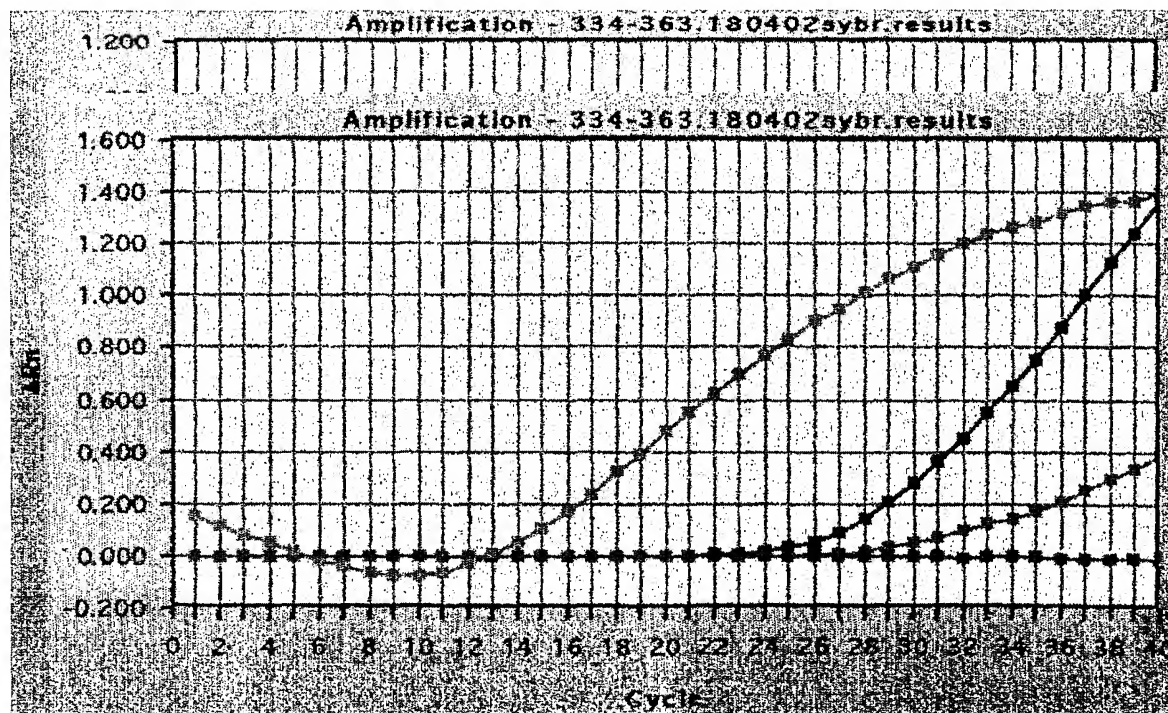
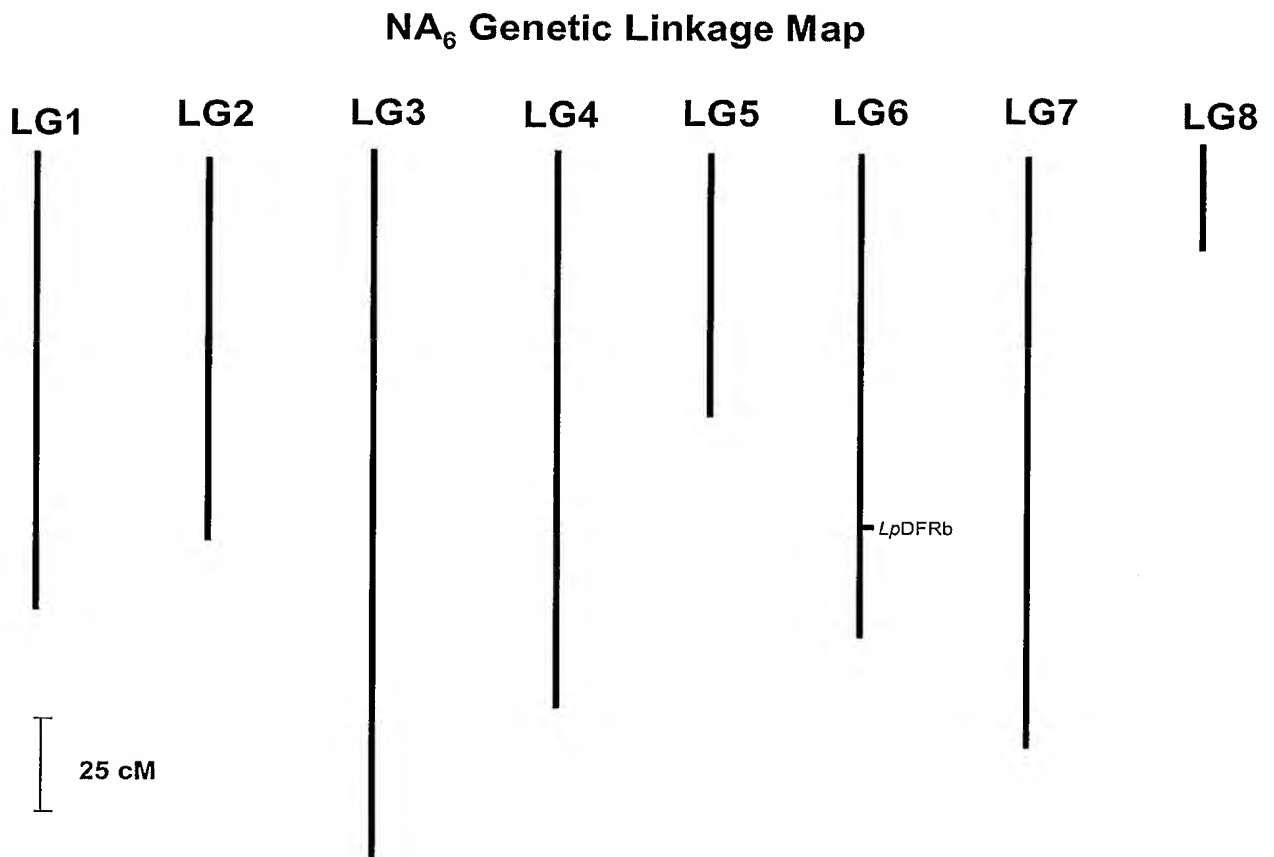


FIGURE 196

270/271**D****E****FIGURE 196 (cont)**

271/271**FIGURE 197**

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AgResearch Limited

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<130> M80393510

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 35 40 45

Ile Gly Val Tyr Leu Glu Asp Val Ala Val Ala Ser Leu Ala Thr Lys
 50 55 60

Trp Lys Gly Lys Ser Ser Glu Glu Leu Leu Glu Thr Leu Asp Phe Tyr
 65 70 75 80

Arg Asp Ile Ile Ser Gly Pro Phe Glu Lys Leu Ile Arg Gly Ser Lys
 85 90 95

Ile Arg Glu Leu Ser Gly Pro Glu Tyr Ser Arg Lys Val Asn Glu Asn
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Cys Val Ala His Leu Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu Val
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Glu Ala Met Gln Lys Phe Val Glu Ala Phe Lys Pro Ile Asn Phe Pro
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Pro Gly Ala Ser Val Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu Gly
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ccggctgtgg ttactttctcc ggccaccggt aagtcataatt ttcttggtgg tgcaggggag
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gtcgagaacc ttgaattccc ggcggtgatt acttctccgg tcaacggtaa gtcatatattt
180

cttggtggtg caggggagag aggtttgact attgaaggaa acttcatcaa gttcactgcc
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tcgagaacct tgaattcccg gcggtgatta cttctccggt caacggtaag tcatattttc
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ttggtggtgc aggggagaga ggttngacta ttgaaggaaa cttcatcaag ttcactgcca
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tgttgggact tatggagatg cagaagctga agctatgcaa aaatttggtg aagccttcaa
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35 40 45

Phe Val Glu Ala Phe Lys Pro Ile Asn Phe Pro Pro Gly Ala Ser Val
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Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu Gly Val Ser Ile Ala Asn
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120

tggtgggact tatggagatg cagaagctga agctatgcaa aaatttggtg aagccttcaa
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gcctattaat tttccacctg gtgcctctgt tttttacagg caatcacctg atggaatatt

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120

tatggagatg cagaagctga agctatgcaa aaatttggtg aagccttcaa gcctattaat
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attgccaatt catttttttt aact
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180
gcaggagagc ggggtcttca aattcaagac aaatttgtca aattcacgcg tattggtggt
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tatctacagg acattgctgt tccttacctc gccactaaat ggaagggtaa gactgctcaa
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Gly Ala Gly Glu Arg Gly Leu Gln Ile Gln Asp Lys Phe Val Lys Phe
 35 40 45

Thr Ala Ile Gly Val Tyr Leu Gln Asp Ile Ala Val Pro Tyr Leu Ala
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Thr Lys Trp Lys Gly Lys Thr Ala Gln Glu Leu Thr Glu Thr Val Pro
 65 70 75 80

Phe Phe Arg Asp Ile Val Thr Gly Pro Phe Glu Lys Phe Met Gln Val
 85 90 95

Thr Met Ile Leu Pro Leu Thr Gly Gln Gln Tyr Ser Glu Lys Val Ser
 100 105 110

Glu Asn Cys Val Ala Ile Trp Lys Ser Leu Gly Ile Tyr Thr Asp Glu
 115 120 125

Glu Ala Lys Ala Ile Glu Lys Val Ser Val Phe Lys Glu Thr Phe Pro
 130 135 140

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Pro Gly Ser Ser Ile Leu Phe Thr Leu Pro Lys Gly Leu Gly Ser Leu
145 150 155 160

Thr Ile Xaa Phe Ser Lys Asp Gly Ser Ile Pro Glu Thr Glu Ser Ala
165 170 175

Val Ile Glu Asn Lys Leu Leu Ser Gln Ala Val Xaa Glu Ser Met Ile
180 185 190

Gly Ala His Gly Val Ser Pro Ala Ala Lys Gln Ser Phe Gly His Gln
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300
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420
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120

tcacaccacc gggatccacc aacaatttct tcctcggcggg tgcaggagag cggggctcttc
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tcaagacaaa tttgtcaa
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attgactggg caacaatact cagagaaagt gtcagaaaat tgtgtagcta tttggaagtc
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tcttgggatt tataccgacg aagaagccaa agcaattgag aagtttggtt ctgtcttcaa
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atcactaacg ataagtttct ctaaagatgg atccattcca gagaccgagt ctgcagttat
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atcggttacag gtccatttga gaaatttatg cagggtgacaa tgatcttgcc attgactggg
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caacaatact cagagaaagt gtcagaaaat tgtgtagcta tttggaagtc tcttgggata
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120

acaacaacct ataactanac atattatttt tatntattta gtatataatt gaaataaact
180

gctaaagata nttattaaga tatggtgagt gtagctgaaa ttcgcaaggc tcagagggct
240

gaaggccctg caaccatttt ggccattggc actgcaaadc cagcaaaccg tgttgagcag
300

agcacatatc ctgatttcta cttcaaaatc acaaacagtg agcacaagac tgagctcaaa
360

gagaaattcc agcgcatgtg tgacaaatct atgatcaaga gcagatacat gatatctaaca
420

gaagagattt tgaaagaaaa tcctagtctt tgtgaatata tggcaccttc attggatgct
480

aggcaagaca tgggtggtggt tgaggtacct agacttggga aggaggctgc agtgaaggct
540

attaaagaat ggggtcaacc aaagtcaaag attactcact taatcttttg caccacaagt
600

ggtgtagaca tgccctggtgc tgattaccaa ctcacaaaac tcttaggtct tcgcccataat
660

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720

gcaaaagatt tggccgagaa caacaaaggt gctcgtgtgt tggttgtttg ttctgaagta
780

accgcagtca cattccgcgg ccccgatgac actcaattgg acagtcttgt tggacaagca
840

ctatttggag atggagctgc tgcactcatt gttggctcag acccagtacc agaaattgag
900

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960

attgatggtc accttcgtga agctggacta acatttcata ttcttaaaga tgttcctggg
1020

attgtatcaa agaacattaa taaagcattg gtcgaggctt tccaaccatt aggaatttct
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35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
 85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys
 100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
 115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
 130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr
 145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
 165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
 180 185 190

Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
 195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
 210 215 220

Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
 225 230 235 240

Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
 245 250 255

His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
 260 265 270

Gly Ile Val Ser Lys Asn Ile Asn Lys Ala Leu Val Glu Ala Phe Gln
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gcggaacata ctaaatacaa catggttagt gtttctgaaa ttcgcaaggc tcaaagggct
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gaaggcctg caactatttt ggccattggt actgcaaatc cagcaaatcg tgttgaccag
300
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420
gaagagatth tgaaagaaaa tcctagtctt tgtgaatata tggcaccttc attggatgct
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180
caaaccgtgt tgatcagagt acatatcctg atttctactt caaaatcact aacagtgagc
240
ataaagttga gctcaaagag aaattccagc gcatgtgtga taaatctatg atcaagagca
300
gatacatgta tctaacagaa gagattttga aagaaaatcc tagtccttgt gaatacatgg
360
caccttcatt ggatgctagg caagatatgg tgggtggtga ggtacctaga cttggaaagg
420
aggctgcagt gaaggctatt aaagaatggg gtcaacaaaa atctaagatt acacatttga
480
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120

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180

atccagcaaa ccgtgttgat cagagcacat atcctgattt ctacttcaaa atcactaaca
240

gtgaacataa agttgagctc aaagagaaat tccagcgcat gtgtgataaa tctatgatca
300

agagcagata catgtatcta acagaagaga ttttgaaaga aaatcctagt ctttgtgagc
360

acatggcacc ttcattggat gctaggcaag acatgggtgg gggtgaggta cctagacttg
420

ggaaggaggc tgcagtgaaa gctataaaaag aatgggggtca accaaagtca aagattactc
480

acttaatctt ttgcaccaca agtgggtgttg acatgcctgg tgctgattac caactcacia
540

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<210> 28
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aaagggcaga aggccctgca acaatcttgg ccattggcac tgcaaataca gcaaaccgtg
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ttgatcagag cacatatact gatttctact tcaaaatcac taacagtga cataaagttg
240

agctcaaaga gaaattccag cgcattgtgt ataaatctat gatcaagagc agatacatgt
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atctaacaga agagattttg aaagaaaatc ctagtctttg tgagcacatg gcaccttcat

360

tggatgctag gcaagacatg gtggtggttg aggtacctag acttggaag gaggtgcag
420

tgaaagctat aaaagaatgg ggtcaaccaa agtcaaagat tactcactta atcttttgca
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ccacaagtgg tgttgacatg cctggtgctg attaccaact cacaaaactc ttaggtcttc
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120

caaagggcag aaggccctgc aaccatttta gccattggta ctgcaaattcc agcaaaccgt
180

gtagaccaga gcacatatcc tgattttctac ttcaaaatca ctaacagtga gcataagggtt
240

gagcttaaag agaaattcca gcgcatgtgt gataaatcta tgatcaagag cagatacatg
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tatctaacag aagagatttt gaaagaaaat cctagtcttt gtgaatacat ggcaccttca
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ttggatgcta ggcaagacat ggtgggtggt gaggtacctt gactaggaaa ggaggctgca
420

gtcaaggcca ttaaagaatg ggtcaacca aagtcaaaga ttactcactt aatcttttgc
480

accacaagtg gtgtagacat gcctgggtgct gattaccaac tcacaaaact cttgggactt
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120

gccctgcaac cattttggcc attggcactg caaatccacc aaaccgtggt gagcagagca
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catatcctga tttctacttc aaaattacaa acagtgcagca caagactgag ctcaaagaga
240

agttccaacg catgtgtgac aaatccatga tcaagagcag atacatgtat ctaacagaag
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agattttgaa agaaaatcct agtctttgtg aatacatggc accttcattg gatgctaggg
360

aagacatggt ggtggttgag gtacctagac ttgggaagga ggctgcagtc aaggccatta
420

aagaatgggg tcaaccaaag tcaaagatta ctacttaat cttttgcacc acaagtgggtg
480

ttgacatgcc tgggtgctgat taccaactca caaaactctt aggtcttcgc ccatatgtga
540

aaaggtatat gatgtaccaa caagggtgtt ttgcaggagg cacgggtgctt cgtttggcaa
600

aaagatttggc cgagaacaac aaagggtgctc gtgtgctagt tgtttgttct gaagtcaccg
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ctgaaggccc tgcaaccatt ttggccattg gcaactgcaaa tccaccaaac cgtgttgagc
180

agagcacata tcctgatttc tacttcaaaa ttacaaacag tgagcacaag actgagctca
240

aagagaagtt ccaacgcatg tgtgacaaat ccatgatcaa gagcagatac atgtatctaa
300

cagaagagat ttgaaagaa aatcctagnc tttgtgaata catgncacct tcattggatg
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240
agttccaacg catgtgtgac aaatccatga tcaagagcag atacatgtat ctaacagaag
300
agattttgaa agaaaatcct agtctttgtg aatacatggc accttcattg gatgctaggc
360
aagacatggg ggtgggttgag gtacctanac ttgggaagga ggctgcannc aaggccatta
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483

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120

ctgaaggccc tgcaaccatt ttggccattg gactgcaaa tccaccaaac cgtgttgagc
180

agagcacata tcctgatttc tacttcaaaa ttacaaacag tgagcacaag actgagctca
240

aagagaagtt ccaacgcatg tgtgacaaat ccatgatcaa gagcagatac atgtatctaa
300

cagaagagat tttgaaagaa aatcctagtc tttgtgaata catggcacct tcattggatg
360

ctagacaaga catggtgggtg gttgaggtac ctagacttgg gaaggaggct gcagtcaagg
420

ctatcaaaga atgggggtcaa ccaaaatcta agattacaca tttgatcttt tgcaccacaa
480

gtggtgtaga catgcctggt gctgattacc aactcacaaa actcttagga cttcgtccat
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<210> 34

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<212> DNA

<213> *Trifolium repens*

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120

gaaggccctg caactatttt ggccattggc actgcaaatc cagcaaaccg tgttgatcag
180

agcacatatc ctgattttta cttcaaaatc actaacagtg agcataaggt tgagcttaaa
240

gagaaatttc agcgcatgtg tgataaatct atgatcaaga gcagatacat gtatctaaca
300

gaagagattt tgaaagaaaa tcctagtctt tgtgaatata tggcaccttc attggatgct
360

aggcaagaca tgggtgggtggt tgagggtacct agacttggga aggaggctgc agtgaaagct
420

atcaaagaat ggggtcaacc aaagtcaaag attactcact taatcttttg caccacaagt
480

ggtgtagaca tgcctgggagc tgattaccaa ctcacaaaac tcttaggtct tcgccccatat

540

gtgaagaggt acatgatgta ccaacaaggg tgct
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120

gcaaccatct tggccattgg tactgcaaat ccaccaaacc gtgttgagcg gagcacatat
180

cctgatttct acttcaaat tacaaacagt gagcacaaga ctgagctcaa agagaagttc
240

caacgcatgt gtgacaaatc catgatcaag agcagatata tgtatctaac agaagagatt
300

ttgaaagaaa atcctagtct ttgtgaatac atggcacctt cattggatgc taggcaagac
360

atggtggtgg ttgaggtacc tagacttggg aaggaggctg cagtgaaagc tatcaaagaa
420

tgggggtcaac caaagtcaaa gattactcac ttaatctttt gcaccacaag tgggtgtagac
480

atgcctggag ctgattacca actcacaaaa ctcttaggtc ttcgcccata tgtgaaaagg
540

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120

caactatfff ggccattggg actgcaaadc agcaaadc tgttgaccag agtacatadc
180

ctgatttcta cttcaaaadc actaacagtg agcataaggg tgagcttaaa gagaaatttc
240

agcgcacgtg tgataaatct atgatcaaga gcagatacat gtatctaaca gaagagattt
300

tgaaagaaaa tcctagtctt tgtgaataca tggcaccttc attggatgct aggcaagaca
360

tggtggtggg tgaggtagct agacttggga aggaggctgc agtgaaagct atcaaagaat
420

gggggtcaacc aaagtcaaag attactcact taatcttttg caccacaagt ggtgttgaca
480

tgccctggtgc cgattaccaa ctcacaaaac tcttaggtct tcgcccatac gtgaagaggg
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120
aaggccctgc aactattttg gccattggta ctgcaaatac agcaaatacg gttgaccaga
180
gtacatatcc tgatttctac ttcaaaatca ctaacagtga gcataagggt gagcttaaag
240
agaaatttca gcgcattgtg gataaatcta tgatcaagag cagatacatg tatctaacag
300
aagagatttt gaaagaaaat cctagtcttt gtgaatacat ggcaccttca ttggatgcta
360
ggcaagacat ggtggtggtt gaggtaccta gacttgggaa ggaggctgca gtgaaagcta
420
tcaaagaatg ggggtcaacca aagtcaaaga ttactcactt aatcttttgc accacaagtg
480
gtgtagacat gcctggagct gattaccaac tcacaaaact cttagggtctt cgcccatatg
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tgaagaggta catgatgtac caacaagggt gctttgcagg tgggacggtt cttcgttt
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ggccctgcaa ccattttggc cattggcact gcaaattcac caaacctgtg tgagcagagc
180
acatatcctg atttctactt caaaattaca aacagtgagc acaagactga gctcaaagag
240
aagttccaac gcatgtgtga caaatccatg atcaagagca gatacatgta tctaacagaa
300
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360
caagacatgg tgggtggtga ggtacctaga cttgggaagg aggctgcagt caaggccatt
420
aaagaatggg gtcaaccaa gtcaaagatt actcacttaa tcttttgcac cacaagtggg
480
gttgacatgc ctggtgctga ttaccaactc acaaaactct taggtcttcg cccatatgtg
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120

caactatttt ggccatttgt actgcaaata cagcaaatcg tgttgaccag agtacatata
180

ctgatttcta cttcaaaaata actaacagtg agcataaggt tgagcttaaa gagaaatttc
240

agcgcatgtg tgataaatct atgatcaaga gcagatacat gtatctaaca gaagagattt
300

tgaagaaaaa tcctagtcct tgtgaatata tggnaacctt attgnatgnt agncaagaca
360

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<210> 40

<211> 561

<212> DNA

<213> Trifolium repens

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taaagatant tattaagata tgggtgagtgt agctgaaatt cgcaaggctc agaggggctga
120

aggccctgca accatttttgg ccattggcac tgcaaattcca ccaaaccgtg ttgagcagag
180

cacatatcct gatttctact tcaaaattac aaacagtgag cacaagactg agctcaaaga
240

gaagttccaa cgcattgtgtg acaaattccat gatcaagagc agatacatgt atctaacaga
300

agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcat tggatgctag
360

acaagacatg gtgggtggtg aggtacctag acttggaag gaggctgcag tcaaggctat
420

caaagaatgg ggtcaaccaa aatctaagat tacacatttg atcttttgca ccacaagtgg

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tgtanacatg cctgggtgctg attaccnact ngcaaaaactn ttaggacttn gcccatatgt
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gangaggcgc gtgntgnncc n
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120
ggccctgcaa ctattttggc cattggtact gcaaatccag caaatcgtgt tgaccagagt
180
acatatcctg atttctactt caaaatcact aacagtgagc ataagggtga gcttaaagag
240
aaatttcagc gcatgtgtga taaatctatg atcaagagca gatacatgta tctaacagaa
300
gagattttga aagaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg
360
caagacatgg tgggtggtga ggtacctaga cttgggaagg aggctgcagt gaaagctatc
420
aaagaatggg gtcaaccaa gtcaaagatt actcacttaa tcttttgcac cacaagtggg
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120

gccctgcaac tattttggcc attggtactg caaatccagc aaaccgtgtt gatcagagta
180

catatcctga tttctacttc aaaatcacta acagtggagca taaagttgag ctcaaagaga
240

aattccagcg catgtgtgat aaatctatga tcaagagcag atacatgtat ctaacagaag
300

agattttgaa agaaaatcct agtctttgtg aatacatggc accttcattg gatgctaggc
360

aagatatggt ggncgttgag gtacctanac ttgnaaagga ggctgcnntg aaggctatta
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<210> 43

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<212> DNA

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120
ccctgcaacc attttggcca ttggcactgc aaatccacca aaccgtgttg agcagagcac
180
atatcctgat ttctacttca aaattacaaa cagtgagcac aagactgagc tcaaagagaa
240
gttccaacgc atgtgtgaca aatccatgat caagagcaga tacatgtatc taacagaaga
300
gattttgaaa gaaaatccta gtctttgtga atacatggca ccttcattgg atgctaggca
360
agacatgggtg gtggttgagg tacctagact tgggaaggag gctgcagtga aagctatcaa
420
agaatgggggt caaccaaagt caaagattac tcacttaatc ttttgcacca caagtgggtg
480
agacatgcct ggagctgatt accaactcac aaaactctta ggtcttcgcc catatgtgaa
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agatttg
607

<210> 44
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120
ctgcaaccat tttggccatt ggсactgcaa atccaccaaa ccgtgttgag cagagcacat
180
atcctgattt ctacttcaaa attacaaaca gtgagcacia gactgagctc aaagagaagt
240
tccaacgcat gtgtgacaaa tccatgatca agagcagata catgtatcta acagaagaga
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ttttgaaaga aaatcctagt ctttgtgaat acatggcacc ttcattggat gctaggcaag
360
acatggтggt ggттgaggta cctagacttg ggaaggaggc tgcagtcaag gccattaaag
420
aatggggтca accaaagtca aagattactc acttaatctt ttgcaccaca agтggtgttg
480
acatgcctgg тgctgattac caactcacia aactcttagg tcttcgcccc tatgtgaaaa
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120

tgcaaccatt ttggccattg gcaactgcaaa tccaccaaac cgcgttgagc agagcacata
180

tcctgatttc tacttcaaaa ttacaaacag tgagcacaag actgagctca aagagaagtt
240

ccaacgcattg tgtgacaaat ccatgatcaa gagcagatac atgtatctaa cagaagagat
300

tttgaaagaa aatcctagtc tttgtgaata catggcacct tcattggatg ctaggcaaga
360

catgggtggtg gttgaggtac ctagacttgg gaaggaggct gcagtcaagg ctatcaaaga
420

atgggggtcaa ccaaaatcta agattacaca tttgatcttt tgcaccacaa gtggtgtaga
480

catgcctggt gctgattacc aactcacaaa actcctggga cttcgtccat atgtgaagag
540

attcatgatg taccaacaag gctgctttgc aggtgggacg gttcttcg
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<211> 613

<212> DNA

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120

aaccattttg gccattggca ctgcaaatcc accaaaccgt gttgagcaga gcacatatcc

180

tgattttctac ttcaaaatta caaacagtga gcacaagact gagctcaaag agaagttcca
240

acgcatgtgt gacaaatcca tgatcaagag cagatacatg tatctaacag aagagatttt
300

gaaagaaaat cctagtcttt gtgaatacat ggcaccttca ttggatgcta ggcaagacat
360

ggtgggtggt gaggtaccta gacttgggaa ggaagctgca gtcaaggcca ttaaagaatg
420

gggtcagcca aagtcaaaga ttactcactt aatcttttgc accacaagtg gtgttgacat
480

gcctggagct gattaccaac tcacaaaact cttaggtctt cgcccatatg tgaaaaggta
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tatgatgtac caacaagggt gttttgcagg aggcacggtg cttcgtttgg caaaagattt
600

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613

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120

tttggccatt ggtactgcaa atccagcaaa ccgtgttgat cagagtacat atcctgattt
180

ctacttcaaa atcactaaca gtgagcataa ggttgagctc aaggagaaat tccagcgcac
240

gtgtgacaaa tctatgatca agagcagata catgtatcta acagaagaga ttttgaaaga
300

aaatcctagt ctttgtgaat acatggcacc ttcattggat gctaggcaag atatggtggt
360

cgttgaggta cctagactgg gaaaggaagc tgcagtgaag gctattaaag aatgggggtca
420

accaaagtca aagattactc acttaatctt ttgcactaca agtggtgtag acatgcctgg
480

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gtat
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<210> 48
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120

ccattttggc cattggtact gcaaattccag caaacctgtg tgatcagagt acatatcctg
180

atttctactt caaaatcact aacagtgagc ataagggtga gctcaaggag aaattccagc
240

gcatgtgtga taaatctatg atcaagagca gatacatgta tctaacagaa gagattttga
300

aagaaaatcc tagtctgtgt gagtacatgg caccttcatt ggatgctagg caagacatgg
360

ttgtgggtga ggtacctaga cttggaaagg aggctgcagt caaggccatt aaagaatggg
420

gtcaacaaaa gtcaaagatt actcacttaa tcttttgcac cacaagtggg gtagacatgc
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ctgggtgctga ttaccaactc acaaaaactct tangtcttcg tccatacgtg aagagggaca
540

tgatgtacca acaag
555

<210> 49
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<212> DNA
<213> *Trifolium repens*

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<222> (5)..(5)
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<222> (13)..(13)
<223> Any nucleotide

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<222> (25)..(25)
<223> Any nucleotide

<220>
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<222> (58)..(58)
<223> Any nucleotide

<400> 49
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attaagatat ggtgagtga gctgaaattc gcaaggctca gagggtgaa ggccctgcaa
120

ccattttggc cattggcact gcaaattcac caaacctgtg tgagcagagc acatatcctg
180

atttctactt caaaattaca aacagtgagc acaagactga gctcaaagag aagttccaac
240

gcatgtgtga caaatccatg atcaagagca gatacatgta tctaacagaa gagattttga

300

aagaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg caagacatgg
360

tggtgggtga ggtacctaga cttgggaagg aggctgcagt caaggccatt aaagaatggg
420

gtcaaccaa gtcaaagatt actcacttaa tcttttgcac cacaagtggg gttgacatgc
480

ctgggtgctga ttaccaactc acaaaactct taggtcttcg cccatattgtg aaaaggtata
540

tgatgtacca acaaggttgt tttgcaggag
570

<210> 50

<211> 546

<212> DNA

<213> *Trifolium repens*

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<223> Any nucleotide

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<221> misc_feature

<222> (49)..(49)

<223> Any nucleotide

<400> 50

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tggttactgt ttctgaaatt cgcaaggctc aaagggctga aggccttgca accatttttg
120

ccattggtac tgcaaatcca gcaaaccgtg ttgatcagag tacatatacct gattttctact
180

tcaaaatcac taacagtgag cataaggttg agctcaagga gaaattccag cgcattgtgtg
240

ataaatctat gatcaagagc agatacatgt atctaacaga agagattttg aaagaaaatc
300

ctagtctgtg tgagtacatg gcaccttcac tggatgctag gcaagacatg gttgtgggtg
360

aggtagcctag acttggaaag gaggtgtcag tcaaggccat taaagaatgg ggtcaaccaa
420

agtcaaagat tactcactta atcttttgca ccacaagtgg ttagacatg cctggtgctg
480

attaccaact cacaaaactc ttaggtcttc gtccatacgt gaagaggtag atgatgtacc
540

aacaag
546

<210> 51
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<400> 51
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120

ttggtactgc aaatccagca aaccgtgttg atcaaagtag atactctgat ttctacttca
180

aaatcactaa cagtgagcat aagggtgagc tcaaagagaa attccagcgc atgtgtgata
240

aatctatgat caagagcaga tacatgtatc caacagaaga gatattgaaa gaaaatccta
300

gtctttgtga atacatggca ccttcattgg atgctagaca agacatggtg gtggttgagg
360

tacctagact tggaaaggag gctgcagtga aggccattaa agaatggggg caacaaaaat
420

ctaagattac acatttgatc ttttgcacca caagtgggtg agacatgcct ggtgctgatt
480

accagctcac aaaactctta ggtcttcgtc catatgtgaa aaggatatatg atgtaccaac
540

aagggtgctt tgcagggtggg acggtgcttc gtttggccaa gg
582

<210> 52
<211> 649
<212> DNA
<213> Trifolium repens

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120

ttggccattg gtactgcaaa tccagcaaac cgtgttgatc aaagtacata tcctgatttc
180

tacttcaaaa tctaatacag tgagcataag gttgagctca aagagaaatt ccagcgcnnng
240

tgtgataaat ctatgatcaa gagcagatac atgtatctaa cagaagagat tttgaaagaa
300

aatcctagtc tttgtgaata catggcacct tcattggatg ctagacaaga catggtggtg
360

gttgaggtag ctagacttgg aaaggaggct gcagtgaagg ccattaaaga atgggggtcaa
420

ccaaaatcta agattacaca tttgatcttt tgcaccacaa gtggtgtana catgcctggt
480

gctgattacc agctcacaaa actcttaggt cttcgtccat atgtgaaaag ggatatgatg
540

taccaacaag ggtgctttgc aggtgggacc gtgcttcntt tggccaanga tttggcccan
600

aacaacaaan gngctcgngn gttggntggt tggctctnaan tcaccgcan
649

<210> 53
<211> 521
<212> DNA
<213> *Trifolium repens*

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<222> (4)..(4)
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gcaaggctca gagggctgaa ggccctgcaa ccattttggc cattggcact gcaaattccac
120

caaaccgtgt tgagcagagc acatatcctg atttctactt caaaattaca aacagtgagc
180

acaagactga gctcaaagag aagttccaac gcatgtgtga caaatccatg atcaagagca
240

67/390

gatacatgta tctaacagaa gagattttga aagaaaatcc tagtctttgt gaatacatgg
300
caccttcatt ggatgctagg caagacatgg tgggtggttga ggtacctaga cttgggaagg
360
aggctgcagt gaaagctatc aaagaatggg gtcaacaaaa gtcaaagatt actcacttaa
420
tcttttgcac cacaagtggg gtagacatgc ctggagctga ttaccaactc acaaaactct
480
taggtcttcg cccatatgtg aaaaggtata tgatgtacca a
521

<210> 54
<211> 506
<212> DNA
<213> *Trifolium repens*

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<223> Any nucleotide

<220>
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<222> (354)..(354)
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<222> (506)..(506)

<223> Any nucleotide

<400> 54

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tgaaggccct gcaaccattt tggccattgg cactgcaaatt ccaccaaacc gtgttgagca
120

gagcacatat cctgatttct acttcaaaat tacaacagc gagcacaaga ctgagctcaa
180

agagaagttc caacgcatgt gtgacaaatc catgatcaag agcagatata tgtatctaac
240

agaagagatt ttgaaagaaa atcctagtct ttgtgaatac atggcacctt cattgggatgc
300

taggcaagac atggtggtgg ttgaggtacc tagacttggg aaggaggctg cagncnaggc
360

cattaaanaa tggggncnac caaagncaaa gattactcac ttaatctttt gcaccacaag
420

tggtgctgac atgnctggtg ctgattacca actcacaaaa ctcttaggnc ttcccccata
480

tgtnaaaagg natatgatgc ccncan
506

<210> 55

<211> 504

<212> DNA

<213> Trifolium repens

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<222> (466)..(467)
<223> Any nucleotides

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<222> (473)..(473)
<223> Any nucleotide

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<222> (504)..(504)
<223> Any nucleotide

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120
cacatatcct gattttctact tcaaaattac aaacagtga cacaagactg agctcaaaga
180
gaagttccaa cgcattgtgtg acaaataccat gatcaagagc agatacatgt atctaacaga
240
agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcat tggatgctag
300
gcaagacatg gtgggtggtg aggtacctag acttggaag gaggtgcag tcaaggccat
360
taaagaatgg ggtnaaccaa agtgaaagat tactnactta atcttttgca ccacaagtgg
420
tgttgacatg nctgggtgctg attaccaact cacaaaactc ttaggnnttg gcncatatgt
480
gaaaaggtct atgatgcacc aacn
504

<210> 56
<211> 782
<212> DNA
<213> *Trifolium repens*

<400> 56
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aggccctgca accatthtttg ccattggcac tgcaaatacca ccaaaccgtg ttgagcagag
120
cacatatcct gattttctact tcaaaattac aaacagtga cacaagactg agctcaaaga
180
gaagttccaa cgcattgtgtg acaaataccat gatcaagagc agatacatgt atctaacaga
240
agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcat tggatgctag
300
gcaagacatg gtgggtggtg aggtacctag acttggaag gaggtgcag tgaaagctat
360
caaagaatgg ggtcaaccaa agtcaaagat tactcaactta atcttttgca ccacaagtgg
420
tgtagacatg cctggagctg attaccaact cacaaaactc ttaggtcttc gccatatgt
480
gaaaaggtat atgatgtacc aacaagggtg ttttgcagga ggcacgggtg ttcgthttggc
540
aaaagatttg gccgagaaca acaaagggtg tcgtgtggtg gttgthttgt ctgaagtcac
600

tgcagttaca ttccgtggcc cgagtgcacac tcacttggac agtcttggtg gacaagcatt
660

gtttggagat ggagcagctg cacttatcgt tggttctgat ccagtgccag aaattgagaa
720

accaatattt gagatgggtt ggactgcaca aacaattgct ccagacagtg aaggtgccat
780

tg
782

<210> 57
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<212> DNA
<213> *Trifolium repens*

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<222> (9)..(10)
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<222> (12)..(13)
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<222> (15)..(15)
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<222> (19)..(20)
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aggccctgca accatttttg ccattggcac tgcaaattcca ccaaaccgtg ttgagcagag
120

cacatatcct gatttctact tcaaaattac aaacagtgag cacaagactg agtcaaaga
180

gaagttccaa cgcattgtgtg acaaattccat gatcaagagc agatacatgt atctaacaga
240

agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcat tggatgctag
300

acaagacatg gtgggtggtt aggtacctag acttgggaag gaggctgcag tcaaggctat
360

caaagaatgg ggtcaaccaa aatctaagat tacacatttg atcttttgca ccacaagtgg
420

tgtagacatg cctggtgctg attaccaact cacaaaactc ttaggacttc gtccatatgt
480

gaagaggtac atgatgtacc aacaagggtg ctttgcaggt ggggcggttc ttcgtttggc
540

taaagatttg gccgagaaca acaaagggtgc tcgtgtgttg gttgtttggt ctgaagt
597

<210> 58
<211> 590
<212> DNA
<213> *Trifolium repens*

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<222> (7)..(7)
<223> Any nucleotide

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gtgttgagca gagcacatat cctgatttct acttcaaaat taaaaacagt gagcacaaga
120

ctgagctcaa agagaagttc caacgcatgt gtgacaaatc catgatcaag agcagatata
180

tgtatctaac agaagagatt ttgaaagaaa atcctagtct ttgtgaatac atggcacctt
240

cattggatgc tagacaagac atggtggttg ttgaggtacc tagacttggg aaggaggccg
300

cagtcaaggc tatcaaagaa tgggggtcaac caaaatctaa gattacacat ttgatctttt
360

gcaccacaag tgggtgtagac atgcctggtg ctgattacca actcacaaaa ctcttaggac
420

ttcgtccata tgtgaagagg tacatgatgt accaacaagg gtgctttgca ggtgggacgg
480

ttcttcgttt ggctaaagat ttggccgaga acaacaaagg tgctcgtgtg ttggttgttt
540

gttctgaagt aactgcagtc acattccgtg gcccgagtga cactcattg
590

<210> 59
<211> 618
<212> DNA

<213> Trifolium repens

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<222> (15)..(15)

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<222> (41)..(41)

<223> Any nucleotide

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<222> (58)..(58)

<223> Any nucleotide

<400> 59

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gtacatatcc tgatttctac ttcaaaatca ctaacagtga gcataagatt gagcttaaag
120

agaaatttca gcgcatgtgt gataaatcta tgatcaagag cagatacatg tatctaacag
180

aagagatttt gaaagaaaat cctagtcttt gtgaatacat ggcaccttca ttggatgcta
240

ggcaagacat ggtggtggtt gaggtaccta gacttgggaa ggaggctgca gtgaaagcta
300

tcaaagaatg ggggtcaacca aagtcaaaga ttactcactt aatcttttgc accacaagtg
360

gtgttgacat gcctggtgct gattaccaac tcacaaaact cttaggtctt cgcccatatg
420

tgaagaggta catgatgtac caacaagggt gctttgcagg tgggacgggt cttcgtttgg
480

ccaaggattt ggccgagaac aacaaagggtg ctctgtgtgtt gggttgtttgc tctgaagtaa
540

ccgcagtcac attccgcggc ccagtgaca ctcatattgga cagccttggt ggacaagcac
600

tatttggaga tggagctg
618

<210> 60

<211> 619

<212> DNA

<213> Trifolium repens

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120
aaatttcagc gcatgtgtga taaatctatg atcaagagca gatacatgta tctaacagaa
180
gagattttga aagaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg
240
caagacatgg tgggtggttga ggtacctaga cttgggaagg aggctgcagt gaaagctatc
300
aaagaatggg gtcaacccaa gtcaaagatt actcacttaa tcttttgcac cacaagtggg
360
gttgacatgc ctggtgctga ttaccaactc aaaaactct taggtcttcg cccatatgtg
420
aagaggtaca tgatgtacca acaagggtgc tttgcagggtg ggacggttct tcgtttggcc
480
aaggatttgg ccgagaacaa caaagggtgct cgtgtgttgg ttgtttgctc tgaagtaacc
540
gcagtcacat tccgcggccc cagtgacact catttggaca gccttggttg acaagcacta
600
tttggagatg gagctgctg
619

<210> 61
<211> 559
<212> DNA
<213> *Trifolium repens*

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<222> (27)..(28)
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<220>
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<222> (559)..(559)
<223> Any nucleotide

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120

caccttcatt ggatgctagg caagacatgg tgggtggtga ggtacctaga cttgggaagg
180

aggctgcagt gaaagctatc aaagaatggg gtcaaccaa gtcaaagatt actcacttaa
240

tcttttgcac cacaagtggg gtagacatgc ctggagctga ttaccaactc acaaaactct
300

taggtcttcg cccatatgtg aagaggtaca tgatgtacca acaagggtgc tttgcagggtg
360

ggacgggttct tcgtttggcc aaggatttgg ccgagaacaa caaagggtgct cgtgtgttgg
420

ttgtttgttc tgaagtaacc gcagtcacat tccgtggccc cagtgcact catttgaca
480

gtcttggttg acaagcacta ttcggagatg gagctgctgc actcattgtt ggctcagacc
540

cagtaccaga aattgagan
559

<210> 62

<211> 553

<212> DNA

<213> *Trifolium repens*

<400> 62

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gagtacatgg caccttcatt ggatgctagg caagacatgg ttgtggttga ggtacctaga
120

cttggaagg aggctgcagt caaggccatt aaagaatggg gtcaaccaa gtcaaagatt
180

actcacttaa tcttttgcac cacaagtggg gtagacatgc ctggtgctga ttaccaactc
240

acaaaactct taggtcttcg tccatacgtg aagaggtaca tgatgtacca acaagggtgc
300

tttgcagggtg ggacgggtgct tcgtttggcc aaggatttgg ccgagaacaa caaagggtgct
360

cgtgtgttgg ttgtttgttc tgaagtcacc gcagtcacat tccgtggccc tagtgacact
420

catttgaca gtcttggttg acaagcacta tttggagatg gagctgctgc tctcattgtt
480

ggttctgatc cagtaccaga aattgagaag ccaatatattg agatggatatg gaccgcacag
540

acaattgctc cag
553

<210> 63
<211> 591
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (18)..(18)
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<222> (33)..(33)
<223> Any nucleotide

<220>
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<222> (35)..(35)
<223> Any nucleotide

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120
tgtgaagagg tatatgatgt atcaacaagg ttgctttgca ggaggcacgg tgcttcgttt
180
ggctaaagat ttggccgaga acaacaaagg tgctcgtgtg ctagttgttt gttctgaagt
240
aacagcagtc acattccgcg gtccaagtga cactcacttg gacagtcttg ttggacaagc
300
actattcgga gatggagctg ctgctctcat tgttgggtca gaccctgtac cagaaatcga
360
gaaacctata tttgagatgg tatggaccgc acagacaatt gtcccggaca gtgaagggtgc
420
cattgatggt caccttcgtg aagctggact aacatttcat cttcttaaag atgttcctgg
480
gattgtatca aagaacatta ataaagcatt ggtcgaggct ttccaaccat taggaatttc
540
tgattacaac tcaatctttt ggattgcaca cccgggtgga cctgcaattc t
591

<210> 64
<211> 634
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (7)..(7)
<223> Any nucleotide

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<222> (9)..(9)
<223> Any nucleotide

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<222> (18)..(18)
<223> Any nucleotide

<220>
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<222> (26)..(26)
<223> Any nucleotide

<400> 64
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gaacattgat aaggcattgg ttgaggcatt ccaaccatta aacatctctg attacaattc
120
aatcttttgg attgctcatc caggtgggtcc tgcaattcta gaccaagttg agataaagtt
180
gggcttaaaa cctgaaaaaa tgaaggccac cagagatgta cttagtgaat atggtaacat
240
gtcaagtgca tgtgtattgt tcattcttaga tgagatgcaa aagaaatcgg ctgaaaatgg
300
actgaaaacc acaggagaag gacttgactg ggggtgtggtg tttggatttg gaccaggact
360
taccattgaa actgttgttc tacatagtgt ggctatatga gaatgcgaga cttgattggt
420
ttgtattgta ttgtattgta ttgtattact tttaatcttg cttgaatttc catttaacaa
480
taaatatgga gttcaataag taccatcagt gttaaaataa tatatcggtta atagctatta
540
ttttagtgtc tgtttctttt tactaaacta tattttatct tagtatttgc tattgatttg
600
aaataaatat tgtcctctta actgaaaaaa aaaa
634

<210> 65
<211> 132
<212> PRT
<213> Trifolium repens

<220>
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<223> Any amino acid

<220>
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<222> (6)..(6)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Any amino acid

<400> 65

Leu Arg Xaa Ala Gly Xaa Thr Phe Xaa Leu Leu Lys Asp Val Pro Glu
1 5 10 15

Ile Val Ser Lys Asn Ile Asp Lys Ala Leu Val Glu Ala Phe Gln Pro
20 25 30

Leu Asn Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro Gly
35 40 45

Gly Pro Ala Ile Leu Asp Gln Val Glu Ile Lys Leu Gly Leu Lys Pro
50 55 60

Glu Lys Met Lys Ala Thr Arg Asp Val Leu Ser Glu Tyr Gly Asn Met
65 70 75 80

Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Gln Lys Lys Ser
85 90 95

Ala Glu Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly Val
100 105 110

Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu His
115 120 125

Ser Val Ala Ile
130

<210> 66
<211> 491
<212> DNA
<213> Trifolium repens

<220>
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<223> Any nucleotide

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<222> (9)..(9)
<223> Any nucleotide

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<222> (18)..(18)
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<222> (486)..(486)
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<222> (488)..(488)
<223> Any nucleotide

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<222> (491)..(491)
<223> Any nucleotide

<400> 66
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gaacattgat aaggcattgg ttgaggcatt ccaaccatta aacatctctg attacaattc
120
aatcttttgg attgctcatc cagggtggcc tgcaattcta gaccaagttg agataaagtt
180
gggcttaaaa cctgaaaaaa tgaaggccac cagagatgta cttagtgaat atggtaacat
240
gtcaagtgca tgtgtattgt tcactcttaga tgagatgaga aagaaatcgg ctgaaaatgg
300
acttaaaacc acaggagaag gacttgactg ggggtgtgttg tttggatttg ggcccggact
360
taccattgaa actgttggtc tacatagtgt ggctatatga gaatgagaga cttgatttgt
420
ttttattgna ttgtattact ttaaactctg gntgaacttc catttaanaa taagtatggn
480
gntcantntg n
491

<210> 67
<211> 363
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (22)..(22)
<223> Any nucleotide

<400> 67
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gggtgtgtgt ttggatttgg accaggactt accattgaaa ctgttggtct acatagtgtg
120
gctatatgag aatgcgagac ttgattgttt tgtattgtat tgtattgtat tgtattactt
180
ttaatcttgc ttgaatttcc atttaacaat aaatatggag ttcaataagt accatcagtg
240
ttaaataaat atatcgtaa tagctattat tttagtgtct gtttcttttt actaaactat
300
attttatttt agtatttgct attgatttga aataaatatt gtctctttaa ctgaaaaaaa
360
aaa

363

<210> 68
<211> 363
<212> DNA
<213> *Trifolium repens*

<400> 68
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60

ggtgtgttgt ttggatttgg accaggactt accattgaaa ctggtgttct acatagtgtg
120

gctatatgag aatgcgagac ttgattgttt tgtattgtat tgtattgtat tgtattactt
180

ttaatcttgc ttgaatttcc atttaacaat aaatatggag ttcaataagt accatcagtg
240

ttaaaataat atatcgtaa tagctattat tttagtgtct gtttcttttt actaaactat
300

attttatttt agtatttggc attgatttga aataaatatt gtcctcttaa ctgaaaaaaaa
360

aaa
363

<210> 69
<211> 897
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (2)..(2)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (26)..(26)
<223> Any nucleotide

<220>
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<222> (33)..(33)
<223> Any nucleotide

<400> 69
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60

caaagaagaa atatgggaga cgaagggtata gtgagagggtg tcacaaagca gacaaccctt
120

gggaaggcta ctatattggc tcttggcaag gcattccctc accaacttgt gatgcaagag
180

tatttagttg atgggttatt tagggacact aattgtgaca atcctgaact taagcagaaa
240

cttgctagac tttgtaagac aaccacggta aaaacaaggt atgttggttat gaatgaggag
 300
 atactaaaga aatatccaga acttggtgtc gaaggcgcct caactgtaaa acaacgttta
 360
 gagatatgta atgaggcagt aacacaaatg gcaattgaag cttcccaagt ttgcctaaag
 420
 aattggggta gatccttata ggacataact catgtgggtt atgtttcatc tagtgaagct
 480
 agattacccg gtggtgacct atacttgtca aaaggactag gactaaaccc taaaattcaa
 540
 agaaccatgc tctattttctc tggatgctcg ggaggcgtag ccggccttcg cgttgcgaaa
 600
 gacatagctg agaacaaccc tggaagtaga gttttgcttg ctacttctga aactacaatt
 660
 attggattca agccaccaag tgttgataga cttatgatac ttgttggtgt ggcactcttt
 720
 ggagatgggtg ctggtgctat gataattggc tcagacccaa tacttgaaac tgagactcca
 780
 ttgtttgagc ttcatacttc agctcaggag tttataccag acacagagaa gaaaatagat
 840
 gggcggctga cggaggaggg cataagtttc acgctagcga gggaactgcc gcagata
 897

<210> 70
 <211> 275
 <212> PRT
 <213> *Trifolium repens*

<400> 70

Met Gly Asp Glu Gly Ile Val Arg Gly Val Thr Lys Gln Thr Thr Pro
 1 5 10 15

Gly Lys Ala Thr Ile Leu Ala Leu Gly Lys Ala Phe Pro His Gln Leu
 20 25 30

Val Met Gln Glu Tyr Leu Val Asp Gly Tyr Phe Arg Asp Thr Asn Cys
 35 40 45

Asp Asn Pro Glu Leu Lys Gln Lys Leu Ala Arg Leu Cys Lys Thr Thr
 50 55 60

Thr Val Lys Thr Arg Tyr Val Val Met Asn Glu Glu Ile Leu Lys Lys
 65 70 75 80

Tyr Pro Glu Leu Val Val Glu Gly Ala Ser Thr Val Lys Gln Arg Leu
 85 90 95

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Glu Ile Cys Asn Glu Ala Val Thr Gln Met Ala Ile Glu Ala Ser Gln
 100 105 110
 Val Cys Leu Lys Asn Trp Gly Arg Ser Leu Ser Asp Ile Thr His Val
 115 120 125
 Val Tyr Val Ser Ser Ser Glu Ala Arg Leu Pro Gly Gly Asp Leu Tyr
 130 135 140
 Leu Ser Lys Gly Leu Gly Leu Asn Pro Lys Ile Gln Arg Thr Met Leu
 145 150 155 160
 Tyr Phe Ser Gly Cys Ser Gly Gly Val Ala Gly Leu Arg Val Ala Lys
 165 170 175
 Asp Ile Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Leu Ala Thr Ser
 180 185 190
 Glu Thr Thr Ile Ile Gly Phe Lys Pro Pro Ser Val Asp Arg Pro Tyr
 195 200 205
 Asp Leu Val Gly Val Ala Leu Phe Gly Asp Gly Ala Gly Ala Met Ile
 210 215 220
 Ile Gly Ser Asp Pro Ile Leu Glu Thr Glu Thr Pro Leu Phe Glu Leu
 225 230 235 240
 His Thr Ser Ala Gln Glu Phe Ile Pro Asp Thr Glu Lys Lys Ile Asp
 245 250 255
 Gly Arg Leu Thr Glu Glu Gly Ile Ser Phe Thr Leu Ala Arg Glu Leu
 260 265 270
 Pro Gln Ile
 275

<210> 71
 <211> 577
 <212> DNA
 <213> Trifolium repens

<220>
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 <222> (2)..(2)
 <223> Any nucleotide

<220>
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 <222> (26)..(26)
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<221> misc_feature
<222> (33)..(33)
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120
gggaaggcta ctatattggc tcttggcaag gcattccctc accaacttgt gatgcaagag
180
tgtttagttg atggttattt tagggacact aattgtgaca atcctgaact taagcagaaa
240
cttgctagac tttgtaagac aaccacggta aaaacaaggt atgttggttat gaatgaggag
300
atactaaaga aatatccaga acttggtgtc gaaggcgcct caactgtaaa acaacgttta
360
gagatatgta atgaggcagt aacacaaatg gcaattgaag cttcccaagt ttgcctaaag
420
aattggggta gatccttata ggacataact catgtgggtt atgtttcatc tagtgaagct
480
agattacccg gtggtgacct atacttgtca aaaggactag gactaaaccc taaaattcaa
540
agaaccatgc tctatttctc tggatgctcg ggaggcg
577

<210> 72
<211> 599
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (12)..(12)
<223> Any nucleotide

<220>
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<222> (20)..(20)
<223> Any nucleotide

<220>
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<222> (23)..(23)
<223> Any nucleotide

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<222> (30)..(30)
<223> Any nucleotide

<400> 72
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agaagaaata tgggagacga aggtatagtg agagggtgtca caaagcagac aacccttggg
120
aaggctacta tattggctct tggcaaggca ttccctcacc aacttgtgat gcaagagtgt
180
ttagttgatg gttatttttag ggacactaat tgtgacaatc ctgaacttaa gcagaaactt
240
gctagacttt gtaagacaac cacggtaaaa acaagggtatg ttgttatgaa tgaggagata
300
ctaaagaaat atccagaact tgttgtcgaa ggcgctcaa ctgtaaaaca acgtttagag
360
atatgtaatg aggcagtaac acaaattggca attgaagctt cccaagtttg cctaaagaat
420
tggggtagat ccttatcgga cataactcat gtggtttatg tttcatctag tgaagctaga
480
ttacccggtg gtgacctata cttgtcaaaa ggactaggac taaaccctaa aattcaaaga
540
accatgctct atttctctgg atgctcgga ggcgtagccg gccttcgcgt tgcgaaaga
599

<210> 73
<211> 581
<212> DNA
<213> Trifolium repens

<220>
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<222> (10)..(11)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (19)..(19)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (26)..(26)
<223> Any nucleotide

<400> 73
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gaaatatggg agacgaaggt atagtgagag gtgtcacaaa gcagacaacc cctgggaagg

120

ctactatatt ggctcttggc aaggcattcc ctcaccaact tgtgatgcaa gagtatttag
180

ttgatggtta ttttagggac actaattgtg acaatcctga acttaagcag aaacttgcta
240

gactttgtaa gacaaccacg gtaaaaacaa ggtatgttgt tatgaatgag gagatactaa
300

agaaatatcc agaacttggt gtcgaaggcg cctcaactgt aaaacaacgt ttagagatat
360

gtaatgaggc agtaacacaa atggcaattg aagcttccca agtttgcta aagaattggg
420

gtagatcctt atcggacata actcatgtgg tttatgtttc atctagttaa gctagattac
480

ccggtgggtga cctatacttg tcaaaaggac taggactaaa ccctaaaatt caaagaacca
540

tgctctatct ctctggatgc tcgggaggcg tagccggcct t
581

<210> 74

<211> 588

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (11)..(11)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (13)..(13)

<223> Any nucleotide

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<222> (25)..(27)

<223> Any nucleotides

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<221> misc_feature

<222> (36)..(36)

<223> Any nucleotide

<400> 74

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gaaatatggg agacgaagg atagtgaag gtgtcacaaa gcagacaacc cctgggaagg
120

ctactatatt ggctcttggc aaggcattcc ctcaccaact tgtgatgcaa gagtggttag
180

ttgatggtta ttttagggac actaattgtg acaatcctga acttaagcag aaacttgcta
240

gactttgtaa gacaaccacg gtaaaaacaa ggtatgttgt tatgaatgag gagatactaa
300

agaaatatcc agaacttggt gtcgaaggcg cctcaactgt aaaacaacgt ttagagatat
360

gtaatgaggc agtaacacaa atggcaattg aagcttccca agtttgccta aagaattggg
420

gtagatcctt atcggacata actcatgtgg tttatgtttc atctagttaa gctagattac
480

ccggtggtga cctatacttg tcaaaaggac taggactaaa ccctaaaatt caaagaacca
540

tgctctatct ctctggatgc tcgggaggcg tagccggcct tcgcgttg
588

<210> 75

<211> 563

<212> DNA

<213> *Trifolium repens*

<400> 75

ttaacatctt tttattgtag aaaatatata tttgatctag caaagaagaa atatgggaga
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cgaaggtata gtgagagggtg tcacaaggca gccaacccct gggaaggcta ctatattggc
120

tcttggcaag gcattccctc accaacttgt gatgcaagag tatttagttg atgggtatct
180

tagggacact aattgtgaca atcctaagct taagcagaaa cttgctagac ttgcaagac
240

aaccacagtg aaaacaaggt atgttggttat gaatgaagag atactaaaga aatatccaga
300

acttactatc ggaggcacct cgacggtaaa acaacattta gagatatgta atgaggcagt
360

aacacaaatg gcaattgaag cttcccaagt ttgcctaaag aattggggta gacccatctc
420

agacataact catgtgggtt atgtttcatc tagtgaagct agattacctg gtggtgacct
480

atacttgtca aaaggactag gactaaacct taaaattcaa agaaccatgc tctattttctc
540

gggatgctcg ggaggcgtag ccg
563

<210> 76

<211> 603

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (4)..(4)
<223> Any nucleotide

<400> 76
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gtgagagggtg tcacaaagca gacaaccctt gggaaggcta ctatattggc tcttggcaag
120
gcattccctc accaacttgt gatgcaagag tatttagttg atgggtatatt tagggacact
180
aattgtgaca atcctgacct taagcagaaa cttgctagac tttgtaagac aaccacggtg
240
aaaacaaggt atgttggttat gaatgaggag atactaaaga aatatccaga acttgttgct
300
gaaggcgctt caactgtaaa acaacgttta gagatatgta atgaggcagt aacacaaatg
360
gcaattgaag cttcccaagt ttgcctaaag aattggggta gatccttatc ggacataact
420
catgtgggtt atgtttcatc tagtgaagct agattaccgc gtggtgacct atacttgtca
480
aaaggactag gactaaacc taaaattcaa agaaccatgc tctattttctc tggatgctcg
540
ggaggcgtag ccggccttcg cgttgcgaaa gacatagctg agaacaaccc tggaagtaga
600
gtt
603

<210> 77
<211> 584
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (1)..(1)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (5)..(5)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (40)..(40)
<223> Any nucleotide

<400> 77
ntccngaact tactgtggaa ggcgccctga ctgtaaaacn acgtttagag atatgtaatg
60

aggcagtaac acaaattggca attgaagctt cccaagtttg cctaaagaat tggggtagac
120

ccttatcaga cataactcat gtgggtttatg tttcctctag tgaagctaga ttacccggtg
180

gtgacctata tttgtcaaaa ggactaggac taaatcctaa aattcaaaga accatgctct
240

atttctctgg atgctcagga ggcgtagccg gccttcgcgt tgcgaaagac atagctgaga
300

acaaccttg aagtagagtt ttgcttgcta cttctgaaac tacaattatt ggattcaagc
360

caccaagtgt tgatagacct tatgatcttg ttgggtgtggc actctttgga gatggtgctg
420

gtgctatgat aattggctca gacccaatac ttgaaactga gactccattg tttgagcttc
480

atacttcagc tcaggagttt ataccagaca cagagaagaa aatagatggg cggctgacgg
540

aggagggcat aagtttcacg ctacgcaggg aactgccgca gata
584

<210> 78
<211> 735
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (47)..(47)
<223> Any nucleotide

<400> 78
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60

ttgctaagtc atcaaccatt ccaattcctt aatataacct atcagtactc accatctttt
120

cttcctccct gctaacttta tacttagaga agatgggtgaa agttaatgag atccgccagg
180

cacagagagc tgaaggccct gccactgtgt tggcaatcgg cactgcaact cctccaaact
240

gtgttgatca gactacatac cccgactact acttccgcat cacaaacagt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcgatgt gtgacaaatc tatgattaag aagagataca
360

tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420

cattggatgc aagacaagac atgggtggttg tggaagtacc aaggctagga aaagaggcag
480

caacaaaggc aatcaaggaa tgggggtcaac ctaagtccaa gattaccac ctcactttt
540

gcaccacaag tgggtgtggac atgcccgggtg ccgactatca gcttacaaag ctttttaggcc
600

ttcgtccgca tgtgaagcgt tacatgatgt accaacaagg ttgttttgct ggtggcacgg
660

tgcttcgttt ggctaaagac ttgggtgaaa acaacaaagg tgcccgtgta ttggtgggtt
720

gttcagagat aactg
735

<210> 79
<211> 194
<212> PRT
<213> *Trifolium repens*

<400> 79

Met Val Lys Val Asn Glu Ile Arg Gln Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Pro Asn Cys Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Thr Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro His Val Lys Arg Tyr Met Met Tyr
145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu

Ile Thr

<210> 80
<211> 574
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (47)..(47)
<223> Any nucleotide

<400> 80
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120
cttcctccct gctaacttta gaatcagaga agatgggtgaa tgttaatgag atccgccagg
180
cacagagagc tgaaggccct gccactgtgt tggcaatcgg cactgcaact cctccaaact
240
gtgtcgatca gagtacatac ccggactact acttccgcat cacaacagc gagcacaaga
300
cagagctcaa agaaaaattc cagcgcgtgt gtgacaaatc tatgattaag aagagatata
360
tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420
cattgggatgc aagacaagac atgggtggttg tggaagtacc aaggctagga aaagaggcag
480
caacaaaggc aattaaggaa tgggggtcaac ctaagtccaa gattaccac ctcacatctttt
540
gcaccaccag tgggtgtcgac atgcccgggtg ccgc
574

<210> 81
<211> 597
<212> DNA
<213> *Trifolium repens*

<400> 81
gtagcaacac acactttgat ttcttttttga gtccttgcta cgtggcttta ccaaaaaacg
60
ttgctaagtc atcaaccatt ccaattcctt aatataacct atcagtactc accatctttt
120
cttcctccct gctaacttta gactcagaga agatgggtgaa tgttaatgag atccgccagg
180
cacagagagc tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact

240

gtgtcgatca gagtacatac ccagactact acttccgcat cacaaacagt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagatata
360

tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420

cattggatgc aagacaagac atggtgggtg tggaagtacc aaggctagga aaagaggctg
480

caacaaaggc tatcaaggaa tgggggtcaac ctaagtccaa gattactcac ctcatctttt
540

gcaccacaag tgggtgtggac atgcctggcg ccgactatca gcttacaag ctttttag
597

<210> 82

<211> 616

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (70)..(70)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (616)..(616)

<223> Any nucleotide

<400> 82

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60

ttgctaagtn atcaaccatt ccaattcctt aatataacct atcagtactc accatctttt
120

cttctctcct gctaacttta gactcagaga agatggtgaa tgtaatgag atccgccagg
180

cacagagagc tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact
240

gtgtcgatca gagtacatac ccagactact acttccgcat cacaaacagt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagatata
360

tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420

cattggatgc aagacaagac atggtgggtg tggaagtacc aaggctagga aaagaggctg
480

caacaaaggc tatcaaggaa tgggggtcaac ctaagtccaa gattactcac ctcatctttt
540

gcaccacaag tgggtgtggac atgcctggcg ccgactatca gcttacaaag ctttttaggcc
600

ttcgtccgca tgtgan
616

<210> 83
<211> 585
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (1)..(3)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (7)..(7)
<223> Any nucleotide

<220>
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<222> (20)..(20)
<223> Any nucleotide

<220>
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<222> (37)..(37)
<223> Any nucleotide

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<222> (61)..(61)
<223> Any nucleotide

<220>
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<222> (451)..(451)
<223> Any nucleotide

<220>
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<222> (507)..(507)
<223> Any nucleotide

<400> 83
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ntcaaccatt ccaattcctt aatataacct atcagtactc accatctttt cttcctccct
120

gctaacttta gactcagaga agatggtgaa tgttaatgag atccgccagg cacagagagc
180

tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact gtgttgatca
240

gagtacatac cccgactact acttccgcat cacaaacagt gagcacaaga cagagctcaa
300

agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagatata tgcatttaac
360

agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt cattggatgc
420

aagacaagac atggtggttg tggaagtacc naggctagga aaagaggcag taacaaaggc
480

aattagggaa tgggggtcaac ctaagtncaa gattaccac ctcattttt gcaccaccag
540

tggtgtggac atgcccgtg ccgactatca gtcacaaag ctctt
585

<210> 84
<211> 596
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (3)..(3)
<223> Any nculeotide

<220>
<221> misc_feature
<222> (14)..(14)
<223> Any nculeotide

<220>
<221> misc_feature
<222> (37)..(37)
<223> Any nculeotide

<400> 84
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60

atccgccagg cacagagagc tgaaggccct gcaactgtgt ttgcaatcgg cactgcaact
120

cctaaaaact gtgttgatca gagtacttac cccgactact atttccgaat cacaaacagc
180

gaacacaaga ctgaactcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag
240

aagagatata tgcatttgac agaagagatt ttgaaggaga attcaagttt atgtgagtac
300

atggcacctt cattggatgc aagacaagac atggtggttg tggaagtacc aaggctagga
360

aaagaggctg caacaaaggc tatcaaggaa tgggggtcaac ctaagtccaa gattactcac
420

ctcatctttt gcaccacaag tggtgtggac atgcctggtg ccgactatca gottacaaag

480

cttttaggcc ttcgccgca tgtgaagcgt tatatgatgt accaacaagg ttgttttgct
540

ggtggcacgg tgcttcgttt ggctaaagac ttggctgaaa acaacaaagg tgcccg
596

<210> 85
<211> 618
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (3)..(3)
<223> Any nucleotide

<220>
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<222> (6)..(6)
<223> Any nucleotide

<220>
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<222> (9)..(9)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (14)..(14)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (37)..(37)
<223> Any nucleotide

<400> 85
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atccgccagg cacagagagc tgaaggccct gcaactgtgt ttgcaatcgg cactgcaact
120

cctaaaaact gtgttgatca gagtacttac cccgactact atttccgaat cacaaacagc
180

gaacacaaga ctgaactcaa agaaaaattc cagcgcacgt gtgacaaatc tatgattaag
240

aagagataca tgcatttgac agaagagatt ttgaaggaga attcaagttt atgtgagtac
300

atggcacctt cattggatgc aagacaagac atgggtggtg tggaagtacc aaggctagga
360

aaagaggctg caacaaaggc tatcaaggaa tgggggtcaac ctaagtccaa gattactcac
420

ctcatctttt gcaccacaag tgggtgtggac atgcctgggtg ccgactatca gcttacaaag
480

cttttaggcc ttctgtccgca tgtgaagcgt tatatgatgt accaacaagg ttgttttgct
540

ggtggcacgg tgcttcgttt ggctaaagac ttggctgaaa acaacaaagg tgcccgtgta
600

ttggtggttt gttcagag
618

<210> 86
<211> 609
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (4)..(4)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (10)..(10)
<223> Any nucleotide

<220>
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<222> (32)..(33)
<223> Any nucleotides

<400> 86
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60

gccaggcaca gagagctgaa ggccctgcaa ctgtgtttgc aatcggcact gcaactccta
120

aaaactgtgt tgatcagagt acttaccocg actactatct ccgaatcaca aacagcgaac
180

acaagactga actcaaagaa aaattccagc gcatgtgtga caaatctatg attaagaaga
240

gatacatgca tttgacagaa gagattttga aggagaattc aagtttatgt gagtacatgg
300

caccttcatt ggatgcaaga caagacatgg tggttgtgga agtaccaagg ctaggaaaag
360

aggctgcaac aaaggctatc aaggaatggg gtcaacctaa gtccaagatt actcacctca
420

tcttttgcac cacaagtggg gtggacatgc ctggtgccga ctatcagctt acaaagcttt
480

taggccttcg tccgcatgtg aagcgttata tgatgtacca acaaggttgt tttgctgggtg
540

gcacgggtgct tcgtttggct aaagacttgg ctgaaaacaa caaagggtgcc cgtgtattgg
600

tggtttggtt
609

<210> 87
<211> 571
<212> DNA
<213> *Trifolium repens*

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<220>
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<222> (14)..(14)
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<222> (91)..(91)
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<222> (247)..(247)
<223> Any nucleotide

<220>
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<222> (571)..(571)
<223> Any nucleotide

<400> 87
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agctgaaggc cctgccactg tgttggnant nggcactgca actcctccaa actgtgtcga
120
tcagagtaca taccgggact actacttccg catcaciaaac agtgagcaca agacagagct
180
caaagaaaaa ttccagcgca tgtgtgacaa atctatgatt aagaagagat acatgcattt
240
gacagangag attttgaagg agaatccaag tttatgtgag tacatggcac cttcattgga
300
tgcaagacaa gacatgggtg ttgtggaagt accaaggcta ggaaaagagg cagcaacaaa
360
ggcaattaag gaatggggcc aacctaagtc caagattacc cacctcatct tttgcaccac
420
cagtgggtgc gacatgcccg gtgccgacta tcagctcaca aagctcttag gcctgcgtcc
480
atatgtgaag cgttacatga tgtatcaaca aggttgtttt gctgggtggca cgggtgcttcg
540
tttggctaaa gacttggctg aaaacaacaa n
571

<210> 88
<211> 603
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (2)..(4)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (9)..(9)
<223> Any nucleotide

<220>
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<222> (13)..(14)
<223> Any nucleotides

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<222> (32)..(32)
<223> Any nucleotide

<220>

<221> misc_feature
<222> (567)..(567)
<223> Any nucleotide

<220>
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<222> (594)..(594)
<223> Any nucleotide

<400> 88
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aaggccctgc cactgtgttg gcaatcggca ctgcaactcc tccaaactgt gtcgatcaga
120
gtacataccc ggactactac ttccgcatca caaacagtga gcacaagaca gagctcaaag
180
aaaaattcca gcgcatgtgt gacaaatcta tgattaagaa gagatacatg catttgacag
240
aagagatttt gaaggagaat ccaagtttat gtgagtacat ggcaccttca ttggatgcaa
300
gacaagacat ggtggttgtg gaagtaccaa ggctaggaaa agaggcagca acaaaggcaa
360
ttaaggaatg gggccaacct aagtccaaga ttaccacact catcttttgc accaccagt
420
gtgtcgacat gcccggtgcc gactatcagc tcacaaagct cttaggcctg cgtccatag
480
tgaagcgta catgatgtat caacaagggt gttttgctgg tggcacggtg cttcgtttgg
540
ctaaagactt ggctgaaaac aacaaangtg cccgtgtgtt ggtgggttgt tcanagataa
600
ctg
603

<210> 89
<211> 588
<212> DNA
<213> Trifolium repens

<220>
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<222> (7)..(7)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (12)..(12)
<223> Any nucleotide

<220>
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<223> Any nucleotide

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<221> misc_feature

<222> (68)..(68)

<223> Any nucleotide

<400> 89

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gccctgcnc tgtgtttgca atcggcactg caactcctaa aaactgtgtt gatcagagta
120

cttaccgccga ctactatttc cgaatcacaa acagcgaaca caagactgag ctcaaagaaa
180

aattccagcg catgtgtgac aaatctatga ttaagaagag atacatgcat ttgacagaag
240

agattttgaa ggagaatcca agtttatgtg agtacatggc accttcattg gatgcaagac
300

aagacatggg gtagtggaa gtaccaaggc taggaaaaga ggcagcaaca aaggcaatta
360

aagaatgggg tcaacctaa tccaagatta cccacctcat cttttgcacc accagtgggtg
420

tggacatgcc cggtgccgac tatcagctca caaagctctt aggcctgcgt ccatatgtga
480

agcgttacat gatgtatcaa caagggtgtt ttgctgggtg cacgggtactt cgtttggtta
540

aagacttggc tgaaaacaac aaagggtgcc gtgtgttggt ggtttggt
588

<210> 90

<211> 250

<212> DNA

<213> Trifolium repens

<220>

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<222> (17)..(17)

<223> Any nucleotide

<220>

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<223> Any nucleotide

<220>

<221> misc_feature

<222> (48)..(49)

<223> Any nucleotides

<220>

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<222> (165)..(165)
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<220>
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<222> (188)..(188)
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<222> (212)..(212)
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<222> (224)..(225)
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<220>
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<222> (247)..(247)
<223> Any nucleotide

<220>
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<222> (250)..(250)
<223> Any nucleotide

<400> 90
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60

cacaagactg agctcaaaga aaaattccag cgcattgtgtg acaaattctat gattaagaag
120

agatacatgc atttgacaga agagattttg aaggagaatc caagnttatg tgagtacatg

180

gcaccttnat tggatgcaag acaagacatg gngggccgccc accnnccntc cncncacacn
240

caacccnccn
250

<210> 91
<211> 583
<212> DNA
<213> Trifolium repens

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<223> Any nucleotide

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<222> (47)..(47)
<223> Any nucleotide

<220>
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<222> (552)..(552)
<223> Any nucleotide

<400> 91
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60

tgctaagtca tcaaccattc caattcctta atataaccta tcagtactca ccatcttttc
120

ttcctccctg ctaacttttag actcagtaga agatgggtgaa tgttaatgag atccgccagg
180

cacagagagc tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact
240

gtgttgatca gagtacatac ccggactact acttccgcat cacaaacagt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcacgt gtaagatatt tatcttatac tccatgcatg
360

tttttttctg ctgactgccg tgtttatata ttgttttggt ttgttcotta aatttggtat
420

gtcactctca catgtacaaa acacttaaga ctaaactgca tatcattttt ttcagggaca
480

aatctatgat taagaagaga tacatgcatt tgacagaaga gattttgaag gagaatccaa
540

gtttatgtga gnacatggca ccttcttggg atgcaagaca agt
583

<210> 92
<211> 95

<212> PRT
<213> Trifolium repens

<220>
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<222> (86)..(86)
<223> Any amino acid

<400> 92

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Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Pro Asn Cys Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Thr Arg Asp Lys Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Xaa Met Ala Pro Ser Trp Asp Ala Arg Gln
85 90 95

<210> 93
<211> 582
<212> DNA
<213> Trifolium repens

<220>
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<223> Any nucleotide

<220>
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<222> (551)..(551)
<223> Any nucleotide

<400> 93

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120

ttcctccctg ctaacttttag actcagagaa gatgggtgaat gttaatgaga tccgccaggc
180

acagagagct gaaggccctg ccaccgtgtt ggcaatcggc actgcaactc ctccaaaactg
240

tgttgatcag agtacatacc cggactacta cttccgcata acaaacagtg agcacaagac

300

agagctcaaa gaaaaattcc agcgcacgtg taagatattt atcttatact ccatgcatgt
360

ctttttctgc tgactgccgt gtttatatat tgttttgttt tgttccttaa atttggtatg
420

tcactctcac atgtacaaaa cacttaagac taaactgcat atcatttttt tcagggacaa
480

atctatgatt aagaagagat acatgcattt gacagaagag attttgaagg agaatccaag
540

tttatgtgag nacatggcac cttcttggga tgcaagacaa gt
582

<210> 94
<211> 167
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (17)..(17)
<223> Any nucleotide

<220>
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<222> (34)..(34)
<223> Any nucleotide

<220>
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<222> (38)..(38)
<223> Any nucleotide

<400> 94
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60

aacctatcag tactcaccat cttttcttcc tccttgctaa ctttagactc agtagaagat
120

ggtgaatgtt aatgagatcc gccaggcaca gagagctgaa ggccctg
167

<210> 95
<211> 613
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (3)..(3)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (16)..(16)

<223> Any nucleotide

<400> 95

gcntaagcct tgattnttgt ttgtttccta acacaagaac tagtgtttgc ttgaatctta
60agaaaaaatg cctcaagggtg atttgaatgg aagttcctcg gtgaatggag cacgtgctag
120acgtgctcct actcagggaa aggcaacgat acttgcatta ggaaaggctt tccccgcccc
180agtcctccct caagagtgcct tgggtggaagg attcattcgc gacactaagt gtgacgatac
240ttatatattg gagaaattgg agcgtctttg caaaaacaca actgtaaaaa caagatacac
300agtaatgtca aaggagatct tagacaacta tccagagcta gccatagatg gaacaccaac
360aataaggcaa aagcttgaaa tagcaaatcc agcagtagtt gaaatggcaa caagagcaag
420caaagattgc atcaaagaat ggggaagggtc acctcaagat atcacacaca tagtctatgt
480ttcctcgagc gaaattcgtc taccggtgg tgacctttat cttgcaaattg aactcggctt
540aaacagcgat gttaatcgcg taatgctcta tttcctcggt tgctacggcg gtgtcactgg
600cttacgtgtc gcc
613

<210> 96

<211> 182

<212> PRT

<213> *Trifolium repens*

<400> 96

Met Pro Gln Gly Asp Leu Asn Gly Ser Ser Ser Val Asn Gly Ala Arg
1 5 10 15Ala Arg Arg Ala Pro Thr Gln Gly Lys Ala Thr Ile Leu Ala Leu Gly
20 25 30Lys Ala Phe Pro Ala Gln Val Leu Pro Gln Glu Cys Leu Val Glu Gly
35 40 45Phe Ile Arg Asp Thr Lys Cys Asp Asp Thr Tyr Ile Lys Glu Lys Leu
50 55 60Glu Arg Leu Cys Lys Asn Thr Thr Val Lys Thr Arg Tyr Thr Val Met
65 70 75 80

Ser Lys Glu Ile Leu Asp Asn Tyr Pro Glu Leu Ala Ile Asp Gly Thr

106/390

85

90

95

Pro Thr Ile Arg Gln Lys Leu Glu Ile Ala Asn Pro Ala Val Val Glu
 100 105 110

Met Ala Thr Arg Ala Ser Lys Asp Cys Ile Lys Glu Trp Gly Arg Ser
 115 120 125

Pro Gln Asp Ile Thr His Ile Val Tyr Val Ser Ser Ser Glu Ile Arg
 130 135 140

Leu Pro Gly Gly Asp Leu Tyr Leu Ala Asn Glu Leu Gly Leu Asn Ser
 145 150 155 160

Asp Val Asn Arg Val Met Leu Tyr Phe Leu Gly Cys Tyr Gly Gly Val
 165 170 175

Thr Gly Leu Arg Val Ala
 180

<210> 97
 <211> 613
 <212> DNA
 <213> Trifolium repens

<220>
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 <222> (3)..(3)
 <223> Any nucleotide

<220>
 <221> misc_feature
 <222> (16)..(16)
 <223> Any nucleotide

<400> 97
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 120

acgtgctcct actcagggaa aggcaacgat acttgcatta ggaaaggctt tccccgccca
 180

agtcctccct caagagtgtg tgggtggaagg attcattcgc gacactaagt gtgacgatac
 240

ttatatattaag gagaaattgg agcgtctttg caaaaacaca actgtaaaaa caagatacac
 300

agtaatgtca aaggagatct tagacaacta tccagagcta gccatagatg gaacaccaac
 360

aataaggcaa aagcttgaaa tagcaaatcc agcagtagtt gaaatggcaa caagagcaag
 420

caaagattgc atcaaagaat ggggaaggtc acctcaagat atcacacaca tagtctatgt
480

ttcctcgagc gaaattcgtc taccgggtgg tgacctttat cttgcaaata aactcggctt
540

aaacagcgat gttaatcgcg taatgctcta ttctcctcggg tgctacggcg gtgtcactgg
600

cttacgtgtc gcc
613

<210> 98
<211> 570
<212> DNA
<213> *Trifolium repens*

<220>
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<223> Any nucleotide

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120

tgctcctact cagggaaagg caacgatact tgcattagga aaggctttcc ccgcccagggt
180

cctccctcaa gagggttggtg tggaaggatt cattcgcgac actaagtgtg acgatactta
240

tattaaggag aaattggagc gtctttgcaa aaacacaact gtgaaaacaa gatacacagt
300

aatgtcaaag gagatcttag acaactatcc agagctagcc atagatggaa caccaacaat
360

aaggcaaaag cttgaaatag caaatccagc agtagttgaa atggcaacaa gagcaagcaa
420

agattgcac aaagaatggg gaaggtcacc tcaagatata acacacatag tctatgtttc
480

ctcgagcgaa attcgtctac ccggtggtga cctttatctt gcaaatgaac tcggcttaaa
540

cagcgatgtt aatcgcgtaa tgcctctatct
570

<210> 99
<211> 575
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (33)..(33)
<223> Any nucleotide

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120
tactcagggg aaggcaacga tacttgcat aggaaaggct ttccccgccc aggtcctccc
180
tcaagagtgc ttggtggaag gattcattcg cgacactaag tgtgacgata cttatattaa
240
ggagaaattg gagcgtcttt gcaaaaacac aactgtgaaa acaagataca cagtaatgtc
300
aaaggagatc ttagacaact atccagagct agccatagat ggaacaccaa caataaggca
360
aaagcttgaa atagcaaata cagcagtagt tgaaatggca acaagagcaa gcaaagattg
420
catcaaagaa tggggaaggt cacctcaaga tatcacacac atagtctatg tttcctcgag
480
cgaaattcgt ctaccgggtg gtgaccttta tcttgcaaat gaactcggct taaacagcga
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tgttaatcgc gtaatgctct atttcctcgg ttgct
575

<210> 100
<211> 573
<212> DNA
<213> *Trifolium repens*

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tgatttgaat ggaagttcct cggatgaatgg agcacgtgct agacgtgctc ctactcaggg
120
aaaggcaacg atacttgcat taggaaaggc tttccccgcc caagtcctcc ctcaagagtg
180
cttggtggaa ggattcattc gcgacactaa gtgtgacgat acttatatta aggagaaatt
240
ggagcgtctt tgcaaaaaca caactgtaaa aacaagatac acagtaatgt caaaggagat
300
cttagacaac tatccagagc tagccataga tggaacacca acaataaggc aaaagcttga
360
aatagcaaata ccagcagtag ttgaaatggc aacaagagca agcaaagatt gcatcaaaga
420
atgggggaagg tcacctcaag atatcacaca catagtctat gtttcctcga gcgaaattcg
480
tctacccggg ggtgaccttt atcttgcaaa tgaactcggc ttaaacagcg atgttaatcg
540

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cgtaatgctc tatttccctcg gttgctacgg cgg
573

<210> 101
<211> 607
<212> DNA
<213> *Trifolium repens*

<400> 101
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aacaacaaag gtgcccgtgt gttgggtgggt tgttcagaga taactgcagt tactttccgt
120

ggacccagtg acactcacct tgatagcctt gtggggcaag cattgtttgg agatgggtgca
180

gcagctgtga ttgttggttc agaccctttg ccagaagttg agaagccttt gtttgaattg
240

gtatggaccg cacaacaat cgctccagat agtgaaggag ccattgatgg tcaccttcgc
300

gaagcagggc tgacattcca tctcctcaag gatgttcta gccttgtctc aaataacatt
360

gagaaagcgc ttgttgatgc ctttcaacct ttgaatattt ctgactacaa ttccatcttt
420

tggattgcac acccaggcgg accagcaatt cttgaccaag ttgaagctaa gttaggctta
480

aagccagaga aaatgcaagc cactcgacat gtacttagcg aatatggtaa catgtcaagt
540

gcgtgtgtgt tatttatctt ggatgagatg aggaggaagt caaaagaaga cggacttgcc
600

acaacag
607

<210> 102
<211> 202
<212> PRT
<213> *Trifolium repens*

<400> 102

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Asp	Leu	Ala	Glu	Asn	Asn	Lys	Gly	Ala	Arg	Val	Leu	Val	Val	Cys	Ser
			20					25					30		

Glu	Ile	Thr	Ala	Val	Thr	Phe	Arg	Gly	Pro	Ser	Asp	Thr	His	Leu	Asp
		35					40					45			

Ser	Leu	Val	Gly	Gln	Ala	Leu	Phe	Gly	Asp	Gly	Ala	Ala	Ala	Val	Ile
	50					55					60				

Val Gly Ser Asp Pro Leu Pro Glu Val Glu Lys Pro Leu Phe Glu Leu
65 70 75 80

Val Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp
85 90 95

Gly His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val
100 105 110

Pro Ser Leu Val Ser Asn Asn Ile Glu Lys Ala Leu Val Asp Ala Phe
115 120 125

Gln Pro Leu Asn Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His
130 135 140

Pro Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Ala Lys Leu Gly Leu
145 150 155 160

Lys Pro Glu Lys Met Gln Ala Thr Arg His Val Leu Ser Glu Tyr Gly
165 170 175

Asn Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Arg
180 185 190

Lys Ser Lys Glu Asp Gly Leu Ala Thr Thr
195 200

<210> 103
<211> 607
<212> DNA
<213> *Trifolium repens*

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<222> (12)..(12)
<223> Any nucleotide

<220>
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<222> (46)..(46)
<223> Any nucleotide

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aacaacaaag gtgcccggtg gttggtggtt tggtcagaga taactgcagt tactttccgt
120

ggaccagtg acactcatct tgatagcctt gtggggcaag cattgtttgg agatggtgca
180

gcagctgtga ttgttggttc agaccctttg ccagaagttg agaagccttt gtttgaattg
240

gtatggaccg cacaaacaat cgctccagat agtgaaggag ccattgatgg tcaccttcgc
300

gaagcagggc tgacattcca tctcctcaag gatgttccta gccttgcttc aaataacatt
360

gagaaagctc ttgttgatgc ctttcaacct ttgaatatct ccgattacaa ttccatcttt
420

tggattgcac acccaggcgg accagcaatt cttgaccaag ttgaagctaa gttaggctta
480

aagccagaga aaatgcaatc cactcgacat gtacttagcg aatatggtaa catgtcgagt
540

gcgtgtgtgt tatttatctt ggatgagatg aggaggaagt caaaagaaga cggacttgcc
600

acaacag
607

<210> 104
<211> 591
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (562)..(562)
<223> Any nucleotide

<220>
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<222> (587)..(587)
<223> Any nucleotide

<220>
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<222> (589)..(589)
<223> Any nucleotide

<400> 104
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caaaggtgcc cgtgtgttgg tggtttggtc agagataact gcagttactt tccgtggacc
120

cagtgcact caccttgata gccttggtgg gcaagcattg tttggagatg gtgcagcagc
180

tgtgattggt ggttcagacc ctttgccaga agttgagaag cttttgtttg aattggatatg
240

gaccgcacaa acaatcgctc cagatagtga aggagccatt gatggtcacc ttgcggaagc
300

agggctgaca ttccatctcc tcaaggatgt tcttagcctt gtctcaaata acattgagaa
360

agcgcttggt gatgccttcc aacctttgaa tatttctgac tacaattcca tcttttggat

420

tgcacaccca ggcggaccag caattcttga ccaagttgaa gctaagttag gcttaaagcc
480

agagaaaatg caagccactc gacatgtact tagcgaatat ggtaacatgt caagtgcgtg
540

tgtgttatatt atcttggatg anatgaggag gaagtcaaaa gaacacngnc t
591

<210> 105

<211> 590

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (55)..(55)

<223> Any nucleotide

<400> 105

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ggtgcccgtg tgttggtggt ttgttcagag ataactgcag ttactttccg tggaccaggt
120

gacactcacc ttgatagcct tgtggggcaa gcattgtttg gagatgggtgc agcagctgtg
180

attgttggtt cagacccttt gccagaagtt gagaagcctt tgtttgaatt ggtatggacc
240

gcacaaacaa tcgctccaga tagtgaagga gccattgatg gtcaccttcg cgaagcaggg
300

ctgacattcc atctcctcaa ggatgttcct agccttgtct caaataacat tgagaaagcg
360

cttgttgatg cctttcaacc tttgaatatt tctgactaca attccatctt ttggattgca
420

caccagggcg gaccagcaat tcttgaccaa gttgaagcta agttaggctt aaagccagag
480

aaaatgcaag ccactcgaca tgtacttagc gaatatggta acatgtcaag tgcgtgtgtg
540

ttatattatct tggatgagat gaggaggaag tcaaaagaag acggacttgc
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<210> 106

<211> 510

<212> DNA

<213> *Trifolium repens*

<220>

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<222> (4)..(4)

<223> Any nucleotide

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<223> Any nucleotide

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<222> (458)..(458)
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<222> (496)..(496)
<223> Any nucleotide

<400> 106
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120
cccaacgttc aaatggccct gccactatct tagcttttgg cacagccact ccttctaact
180
gtgtcactca agctgattat cctgattact actttcgtat caccaacagc gaacatatga
240
ctgatcttaa ggaaaaattc aagcggatgt gtgatagatc aatgataaag aaacggtaca
300
tgcacctaac agaagacttt ctgaaggaga atccaaatat gtgtgaatac atggcaccat
360

cactagatgt aagacgagac atagtgggtg ttgaagnacc aaagctaggt aaagaancac
420

caaaaaaagc catatgngaa tggggacaac caaaatcnaa aatcacacat gcttggtttc
480

tgaccacttc cggtgntgac atgcccgggg
510

<210> 107
<211> 137
<212> PRT
<213> *Trifolium repens*

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<223> Any amino acid

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<222> (121)..(121)
<223> Any amino acid

<400> 107

Met Val Thr Val Glu Glu Ile Arg Asn Ala Gln Arg Ser Asn Gly Pro
1 5 10 15

Ala Thr Ile Leu Ala Phe Gly Thr Ala Thr Pro Ser Asn Cys Val Thr
20 25 30

Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Met Thr Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp Arg Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Asp Phe Leu Lys Glu Asn
65 70 75 80

Pro Asn Met Cys Glu Tyr Met Ala Pro Ser Leu Asp Val Arg Arg Asp
85 90 95

Ile Val Val Val Glu Xaa Pro Lys Leu Gly Lys Glu Pro Lys Lys Ala
100 105 110

Ile Xaa Glu Trp Gly Gln Pro Lys Xaa Lys Ile Thr His Ala Trp Phe
115 120 125

Leu Thr Thr Ser Gly Asp Met Pro Gly
130 135

<210> 108
<211> 240
<212> DNA
<213> *Trifolium repens*

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<222> (162)..(162)
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<222> (217)..(218)
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<222> (231)..(231)
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<400> 108
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aagatgcaat cggtgaagcc atcaaacaag gttatagaca ctttgatact gctgctgctt
120

atgggtcana acaagctctt ggtgaagggt tgaaagaagc anttgaactt ggtcttgtca
180

ctanagaaga gctntttgtt acttctaaac tttgggnnac tgaaaatcat nctaaccttg
240

<210> 109
 <211> 79
 <212> PRT
 <213> Trifolium repens

<220>
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 <223> Any amino acid

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<220>
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 <223> Any amino acid

<400> 109

Gln Met Xaa Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr Cys Lys
 1 5 10 15

Lys Asp Thr Lys Asp Ala Ile Val Glu Ala Ile Lys Gln Gly Tyr Arg
 20 25 30

His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Xaa Gln Ala Leu Gly Glu
 35 40 45

Gly Leu Lys Glu Ala Xaa Glu Leu Gly Leu Val Thr Xaa Glu Glu Xaa
 50 55 60

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Phe Val Thr Ser Lys Leu Trp Xaa Thr Glu Asn His Xaa Asn Leu
 65 70 75

<210> 110
 <211> 604
 <212> DNA
 <213> Trifolium repens

<220>
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 <222> (13)..(13)
 <223> Any nucleotide

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 120
 gtccatcaaa tgatgttctt gcttcaatct ttgttgatgc aattgaagtt gggtatcgcc
 180
 atttcgattc tgcttctgtg tatggaacag aggaagccat aggaattgct ttagcaaaaag
 240
 ctttagaaaa agggcttatt aagagtagag atgaagtttt catcacttca aagccatgga
 300
 atactgatgc agattatgaa cttattgttc cagctctcaa gaccacattg aaaaagctgg
 360
 ggacggagta tgtggatctt tatctgatcc attggccagt gagacttaga catgatcttg
 420
 aaaaccctgt tgttttcacc aaagaagatt tacttccctt tgatatagaa gggacatgga
 480
 aagctatgga agaatgttat aagttaggct tagcaaagtc tattggtata tgcaattatg
 540
 gtacaaaaaa actcaccaaa ctcttggaag cagccaccat taccctgca gtcaatcagg
 600
 tgga
 604

<210> 111
 <211> 189
 <212> PRT
 <213> Trifolium repens

<400> 111

Met Ala Gly Lys Lys Ile Pro Glu Val Leu Leu Asn Ser Gly His Lys
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Met Pro Val Ile Gly Met Gly Thr Ser Val Asp Asn Arg Pro Ser Asn
 20 25 30

Asp Val Leu Ala Ser Ile Phe Val Asp Ala Ile Glu Val Gly Tyr Arg

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35

40

45

His Phe Asp Ser Ala Ser Val Tyr Gly Thr Glu Glu Ala Ile Gly Ile
50 55 60

Ala Leu Ala Lys Ala Leu Glu Lys Gly Leu Ile Lys Ser Arg Asp Glu
65 70 75 80

Val Phe Ile Thr Ser Lys Pro Trp Asn Thr Asp Ala Asp Tyr Glu Leu
85 90 95

Ile Val Pro Ala Leu Lys Thr Thr Leu Lys Lys Leu Gly Thr Glu Tyr
100 105 110

Val Asp Leu Tyr Leu Ile His Trp Pro Val Arg Leu Arg His Asp Leu
115 120 125

Glu Asn Pro Val Val Phe Thr Lys Glu Asp Leu Leu Pro Phe Asp Ile
130 135 140

Glu Gly Thr Trp Lys Ala Met Glu Glu Cys Tyr Lys Leu Gly Leu Ala
145 150 155 160

Lys Ser Ile Gly Ile Cys Asn Tyr Gly Thr Lys Lys Leu Thr Lys Leu
165 170 175

Leu Glu Thr Ala Thr Ile Thr Pro Ala Val Asn Gln Val
180 185

<210> 112
<211> 334
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<223> Any nucleotide

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<222> (328)..(328)
<223> Any nucleotide

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<222> (330)..(330)
<223> Any nucleotide

<220>
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<222> (334)..(334)
<223> Any nucleotide

<400> 112
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tggtattgaa ttcaggacac aaaatgccag tcataggaat gggaacatca gtagacaatc
120

gtccatcaaa tgatgttctt gcttcaatct ttgttgatgc aattgaagtt ggttatcgcc
180

atttcgattc tgcttctgtg tatggaacag aggaagccat aggaattgct ttagcaaaag
240

ctttanaaaa agggccttatt aagagtanag atgaagnttt natcacttgc aagncatgga
300

atactgatgc acattatgaa cttattgntn caan
334

<210> 113
<211> 602

<212> DNA
<213> Trifolium repens

<220>
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<222> (14)..(14)
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<223> Any nucleotide

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<223> Any nucleotide

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<222> (22)..(22)
<223> Any nucleotide

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ttattgaatt caggacacaa aatgccagtc ataggaatgg gaacatcagt agacaatcgt
120
ccatcaaatg atgttcttgc ttcaatcttt gttgatgcaa ttgaagttgg ttatcgccat
180
ttcgattctg cttctgtgta tggaacagag gaagccatag gaattgcttt agcaaaagct
240
ttagaaaaag ggcttattaa gagtagagat gaagttttca tcaattcaaa gccatggaat
300
actgatgcag attatgaact tattgttcca gctctcaaga ccacattgaa aaagctgggg
360
acggagtatg tggatcttta tctgatccat tggccagtga gacttagaca tgatcttgaa
420
aaccctgttg ttttcaccaa agaagattta cttccctttg atatagaagg gacatggaaa
480
gctatggaag aatgttataa gttaggctta gcaaagtcta ttggtatatg caattatggt
540
accaaaaaac tcaccaaact cttggaaaca gccaccatta cccctgcagt caatcaggtg
600
ga
602

<210> 114
<211> 584
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (4)..(5)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (27)..(27)
<223> Any nucleotide

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attcaggaca caaaatgcc a gtcattaggaa tgggaacatc agtagacaat cgtccatcaa
120
atgatgttct tgcttcaatc tttgttgatg caattgaagt tggttatcgc catttcgatt
180
ctgcttctgt gtatggaaca gaggaagcca taggaattgc tttagcaaaa gctttagaaa
240
aagggttat taagagtaga gatgaagttt tcattcattc aaagccatgg aatactgatg
300
cagattatga acttattggt ccagctctca agaccacatt gaaaaagctg gggacggagt
360
atgtggatct ttattctgac cattggccag tgagacttag acatgatctt gaaaaccctg
420
ttgttttcac caaagaagat ttacttccct ttgatataga agggacatgg aaagctatgg
480
aagaatgtta taagttaggc ttagcaaagt ctattggtat atgcaattat ggtacaaaaa
540
aactcaccaa actcttgga acagccacca ttaccctgc agtc
584

<210> 115
<211> 547
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (4)..(5)
<223> Any nucleotides

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<222> (27)..(27)
<223> Any nucleotide

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attcaggaca caaaatgcca gtcataggaa tgggaacatc agtagacaat cgtccatcaa
120
atgatgttct tgcttcaatc tttgttgatg caattgaagt tggttatcgc catttcgatt
180
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240
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300
cagattatga acttattggt ccagctctca agaccacatt gaaaaagctg gggacggagt
360
atgtggatct ttatctgatc cattggccag tgagacttag acatgatctt gaaaaccctg
420
ttgttttcac caaagaagat ttacttcctt ttgatataga agggacatgg aaagctatgg
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120
ttgatgcaat tgaagttggt tatcgtcatt tcgattctgc ttctgtttat ggaacagagg
180
aagctatagg aattgcttta gcaaaagctt tagaaaaagg gcttattaag agtagagatg
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334

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agacaataac atgggtagtg ttgaaattcc aacaaagggtt cttactaaca cttctagtca
 180

agtgaaaatg cctgtgggtg gaatgggatc agctcctgat ttcacatgta agaaagatac
 240

aaaagatgca atcattgaag ccatcaaaca aggttataga cactttgata ctgctgctgc
 300

ttatggctca gaacaagctc ttggtgaagg tttgaaagaa gcaattgaac ttggccttgt
 360

cactagagaa gagctttttg ttacttctaa actttgggtc actgaaaatc atcctcacct
 420

tggtgttctt gctcttcaaa aatctctcaa gactcttcaa ttggagtact tggacttgta
 480

tttgatccat tggccactta gttctcagcc tggaaagttt tcatttccaa ttgatgtggc
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agatctcttg ccatttgatg tgaagggtgt ttgggaatcc atggaagaag gcttgaaact
 600

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Gln Val Lys Met Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr
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Cys Lys Lys Asp Thr Lys Asp Ala Ile Ile Glu Ala Ile Lys Gln Gly
 35 40 45

Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Glu Gln Ala Leu
 50 55 60

Gly Glu Gly Leu Lys Glu Ala Ile Glu Leu Gly Leu Val Thr Arg Glu

125/390																
65				70				75				80				
Glu	Leu	Phe	Val	Thr 85	Ser	Lys	Leu	Trp	Val 90	Thr	Glu	Asn	His	Pro 95	His	
Leu	Val	Val	Pro 100	Ala	Leu	Gln	Lys	Ser 105	Leu	Lys	Thr	Leu	Gln 110	Leu	Glu	
Tyr	Leu	Asp 115	Leu	Tyr	Leu	Ile	His 120	Trp	Pro	Leu	Ser	Ser 125	Gln	Pro	Gly	
Lys	Phe 130	Ser	Phe	Pro	Ile	Asp 135	Val	Ala	Asp	Leu	Leu 140	Pro	Phe	Asp	Val	
Lys 145	Gly	Val	Trp	Glu	Ser 150	Met	Glu	Glu	Gly	Leu 155	Lys	Leu	Gly	Leu	Thr 160	
Lys	Ala	Ile	Gly	Val 165	Ser	Asn	Phe	Ser	Val 170	Lys	Lys	Leu	Gln	Asn 175	Leu	
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180
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240
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300
ttatggctca gaacaagctc ttggtgaagg ttgaaagaa gcaattgaac ttggtcttgt
360
cactagagaa gagctttttg ttgcttctaa actttgggtc actgaaaatc atcctcatct
420
tgttgttcct gctcttcaaa aatctctcaa gactcttcaa ttggagtact tggacttgta
480
tttgattcac tggccactta gttctcagcc cggaaagttt tcatttccaa ttgaggtggc
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gttgaaattc caacaaagggt tcttactaac acttctagtc aagtgaaaat gcctgtgggt
180

ggaatgggat cagctcctga tttcacatgt aagaaagata caaaagatgc aatcattgaa

240

gccatcaaac aagggttatag acactttgat actgctgctg cttatggctc agaacaagct
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cttgggtgaag gtttgaaaga agcaattgaa cttgggtcttg tcactagaga agagcttttt
360

gttgcttcta aactttgggt cactgaaaat catcctcctc ttgttggtcc tgctcttcaa
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120

acacttctag tcaagtgaag atgcctgtgg ttggaatggg atcagctcct gatttcacat
180

gtaagaaaga taaaaaagat gcaatcattg aagccatcaa acaagggttat agacactttg
240

atattgctgc tgcttatggc tcagaacaag ctcttggtga aggtttgaaa gaagcaattg
300

aacttgggtct tgtcactaga gaagacctt ttgttacttc taaactttgg gtcactgaaa
360

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atcatcctca ccttggttatt cctgctcttc aaaaatctct caagactctt caattggagt
420

acttggactt gtatttgatc cactggccac ttagttctca gcccggaag ttttcatttc
480

caattgaggt ggcagatctc ttgccatttg atgtgagggg tgtttggcaa tccatggaag
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120

acttctagtc aagtgaaaat gcctgtgggt ggaatgggat cagctcctga tttcacatgt
180
aagaaagata caaaagatgc aatcattgaa gccatcaaac aaggttatag acactttgat
240
attgctgctg cttatggctc agaacaagct cttgggtgaag gtttgaaaga agcaattgaa
300
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catcctcacc ttgttattcc tgctcttcaa aaatctctca agactcttca attggagtag
420
ttggacttgt atttgatcca ctggccactt agttctcagc cgggaaagtt ttcatttcca
480
attgaggtgg cagatctctt gccatttgat gtgaggggtg tttggcaatc catggaagaa
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120
gttctagtca agtgaaaatg cctgtggttg gaatgggatc agctcctgac ttcacatgta
180
agaaagacac aaaagatgca atcattgaag ccatcaaaca aggntataga cactttgaaa
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cttctagtca agtgaaaatg cctgtgggtg gaatgggato agctcctgat tttacatgta
180
aaaaagacac aaaagatgca atcattgaag ccatcaaaca aggttataga cactttgata
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ctgntgctgc ttatgggtca naacaagctc ttggtgaagg tttgaaagaa gcaattgaac
300
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360
atcctcacct tgttgttcct gctcttcaaa aatctctcaa gactcttcaa ttggagtact
420
tggacttgta tttgatccat tggccactta attctcancc tggaaagttt tcatttccca
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ttgangtggc aaatctcttg ccatttnatg tgaanggtgt ttgggaatcc atggaaaaan
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120

tagtcaagtg aaaatgcctg tgggttggat gggatcagca cctgatttca catgtaagaa
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agacacaaaa gatgcaatca ttgaagccat caaacaaggt tatagacact ttgatactgc
240

tgctgcttat ggctcagaac aagctcttgg tggagggttg aaagaagcaa ttgaacttgg
300

ccttgctcact agagaagagc tttttgttac ttctaaactt tgggtcactg aaaatcatcc
360

tcaccttggt gttcctgctc ttcaaaaatc tctcaagact cttcaattgg agtacttgga
420

cttgatatttg atccattggc cacttagttc tcagcctgga aagttttcat ttccaattga
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tacaaaagat gcaatcattg aagccatcaa acaagggttat agacactttg atactgctgc
240

tgcttatggc tcagaacaag ctcttggtga aggtttgaaa gaagcaattg aacttggcct
300

tgtcactaga gaagagcttt ttgttacttc taaacttttg gtcactgaaa atcatcctca
360

tcttggtggt cctgctcttc aaaaatctct caagactctt caattggagt acttggactt
420

gtatttgatc cattggccac ttagttctca gcctggaaag ttttcatttc caattgatgt
480

ggcagatctc ttgccatttg atgtgaaggg tgtttgggaa tccatggaag aaggcttgaa
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caagtgaaaa tgcctgtggt tggaatggga tcagcacctg atttcacatg taagaaagac
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acaaaagatg caatcattga agccatcaaa caagggtata gacactttga tactgctgct
240
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360
cttggtgttc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420
tatttgatcc attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg
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120

caagtgaata tgctgtggt tggaatggga tcagctctg atttcacatg taagaaagat
180

acaaaagatg caatcattga agccatcaaa caagggtata gacacttga tactgctgnt
240

gcttatggct cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt
300

gtcactagag aagagctttt tggtacttct aaactttggg tcttgaaaa tcctctcac
360

cttggtattc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420

tattgatcc attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg
480

gcagatctct tgccatttga tgtgaagggt gtttgggaat ccatggaaga aggcttgaaa
540

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583

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caagtga aaa tgccgtgtggt tggaatggga tcagcacctg atttcacatg taagaaagac
180
acaaaagatg caatcattga agccatcaaa cagggttata gacactttga tactgctgct
240
gcttatggct cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggctct
300
gtcactagag aagacctttt tgttacttct aaactttggg tcaactgaaaa tcatcctcat
360
cttggtgttc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420
tatttgatcc attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg
480
gcagatctct tgccatttga tgtgaagggt gtttgggaat ccatggaaga aggcttgaaa
540
cttggactca ctaaagctat tgggtgttagt aacttctctg tcaagaaact tcaaaat
597

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120

caagtgaaaa tgcctgtggt tggaatggga tcagcacctg atttcacatg taagaaagac
180

acaaaagatg caatcattga agccatcaaa caaggttata gacactttga tactgctgct
240

gcttatggct cagaacaagc tcttggtgga ggtttgaaag aagcaattga acttggcctt
300

gtcactagag aagagctttt tgttacttct aaactttggg tcactgaaaa tcatocctcac
360

cttggtgttc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420

tatttgatcc attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg
480

gcagatctct tgccatttga tgtgaagggt gtttggcaat ccatggaaga aggcttgaaa
540

cttggactca ctaaagctat tgggtgtagt aacttctctg tcaagaaact tcaaaat
597

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120
tgccctgtggt tggaatggga tcagctcctg atttcacatg taagaaagat acaaaagatg
180
caatcattga agccatcaaa caagggttata gacactttga tactgctgct gcttatggct
240
cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt gtcactagag
300
aagagctttt tggtacttct aaactttggg tcaactgaaaa tcacccctcac cttggtgttc
360
ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg tatttgatcc
420
attggccact tagttctcag cctggaaagt ttccatttcc aattgatgtg gcagatctct
480
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574

<210> 132
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acatgggtag tgttgaaatt ccaacaaagg ttcttactaa cacttctagt caagtgaaaa
120

tgcctgtggt tggaatggga tcagctcctg atttcacatg taagaaagat acaaagatg
180

caatcattga agccatcaaa caagggtata gacactttga tactgctgct gcttatggct
240

cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt gtcactagag
300

aagagctttt tggtacttct aaactttggg tcaactgaaaa tcactcctcac cttggtgttc
360

ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg tatttgatcc
420

attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg gcagatctct
480

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540

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578

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120

tgcctgtggt tggaatggga tcagcacctg atttcacatg taagaaagac acaaaagatg
180

caatcattga agccatcaaa caagggtata gacactttga tactgctgct gcttatggct
240

cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt gtcactagag
300

aagagctttt tgttacttct aaactttggg tcaactgaaaa tcacccctcac cttgttggtc
360

ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg tatttgatcc
420

attggccact tagttctcag cccgaaaagt ttccatttcc aattgatgtg gcagatctct
480

tgccatttga tgtgaagggt gtttggaat ccatggaaga aggcttgaaa cttggactca
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120

atgggatcag ctcttgattt cacatgtaag aaagatacaa aagatgcaat cattgaagcc
180

atcaaacaag gttatagaca ctttgatact gctgctgctt atggctcaga acaagctctt
240

ggtgaagggtt tgaaagaagc aattgaactt ggccttgctca ctagagaaga gctttttgtt
300

acttctaaac tttgggtcac tgaaaatcat cctcaccttg ttgttcctgc tcttcaaaaa
360

tctctcaaga ctcttcaatt ggagtacttg gacttgtatt tgatccattg gccacttagt
420

tctcagcctg gaaagttttc atttccaatt gatgtggcag atctcttgcc atttgatgtg
480

aagggtgttt gggaatccat ggaagaaggc ttgaaacttg gactcactaa agctattggt
540

gttagtaact tctctgtcaa gaaacttcaa aatcttgtct cagttgccac cgttcttcct
600

gcggtcaatc ag
612

<210> 135

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<212> DNA

<213> Trifolium repens

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120
cggctacatt gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt
180
ggaagcaatg gaaggagcaa agggatcatct caaatttttc gaaatggatc ttcttaacag
240
cgactctatt gcggcgcgcg tgaaagggtg tgccggagtt atacatcttg catgtcctaa
300
catcattggt gaagtcaaag accccgagaa gcaaattttg gaaccggcaa ttcaaggaac
360
ggttaatgtg ttgaagggtg caaaggaagc aggggtggag cgtgtggtgg cgacatcgtc
420
gatctccgcc atcataccga gtcctaattg gccagctgat aagattaagg gagaagattg
480
ttggacagac cttgattatt gcaaggaaaa gaagttatac taccaccattg caaagacact
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ccctgggtact
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Trp Val Val Arg Leu Leu Leu Glu Arg Gly Tyr Ile Val His Ala Thr

149/390

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Ile Gln Asp Leu Glu Asp Glu Asn Glu Thr Lys His Leu Glu Ala Met 35 40 45		
Glu Gly Ala Lys Gly His Leu Lys Phe Phe Glu Met Asp Leu Leu Asn 50 55 60		
Ser Asp Ser Ile Ala Ala Ala Val Lys Gly Cys Ala Gly Val Ile His 65 70 75 80		
Leu Ala Cys Pro Asn Ile Ile Gly Glu Val Lys Asp Pro Glu Lys Gln 85 90 95		
Ile Leu Glu Pro Ala Ile Gln Gly Thr Val Asn Val Leu Lys Val Ala 100 105 110		
Lys Glu Ala Gly Val Glu Arg Val Val Ala Thr Ser Ser Ile Ser Ala 115 120 125		
Ile Ile Pro Ser Pro Asn Trp Pro Ala Asp Lys Ile Lys Gly Glu Asp 130 135 140		
Cys Trp Thr Asp Leu Asp Tyr Cys Lys Glu Lys Lys Leu Tyr Tyr Pro 145 150 155 160		
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120

cggctacatt gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt
180

ggaagcaatg gaaggagcaa agggatcatct caaatttttc gaaatggatc ttcttaacag
240

cgactctatt gcggnccgcg tgaaagggtg ngccggagtt atacatnttg nctgtcttac
300

cccccttggg gangagnnng caccenn
327

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cggctacatc gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt
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ggaagcaatg gaaggggcaa agggtcattt taaatttttc gaaatggatc ttcttaacag
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tgactctatt gcggccgccc tgaaagggtg tgccggagtt atacatnttg catgtgctaa
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catcattgct gaangnaaan accncganaa cgngattttg naaccngnn
349

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cggctacatt gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt
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ggaagcaatg gaaggagcaa aggggtcatct caaatttttt gaaatggatc ttcttaacag
240
cgactctatt gcggccgccc tgaaagggtg tgccggagtt atacatcttg catgtcctaa
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catcattggg gaagtcaaag accccgagaa gcaaattttg gaaccggcaa ttcaaggaac
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ggttaatgtg ttgaagggtg caaaggaagc aggggtggag cgtgtgggtg cgacatcgtc
420
gatctccgcc atcataccga gtcctaattg gccagctgat aagattaagg gagaagattg
480
ntggacagac cttgattatt gcaangaaaa gaagttatac taccctattg caaagacatt
540
ancagaaaaa gctgggtggg aatttgctaa agagaccggt tttgatgtg tt
592

<210> 140
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120

cggctacatt gtccacgcca ccatccaaga tctcaggatg gagaacgaga caaacattt
180

ggaagcaatg gaaggagcaa agggatcatct caaatttttc gaaatggatc ttctcaacag
240

cgactctatt gcgccgcgcg tgaaagggtg tgccggaggtt atacatcttg catgtcctag
300

catcattggt gaagtcaaag accccgagaa gcaaattttg gaaccggcaa ttcaaggaaac
360

ggttaatgtg ttgaagggtg caaaggaagc aggggtggag cgtgtggtg cgacatcgtc
420

gatctccgcc atcataccga gtcctaattg gccagctgat aagattaagg gagaagattg
480

ttggacagac cttgattatt gcaaggaaaa gaagttatac taccatttg caaagacact
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agcagaaaaa gctgggtggg aatttgctaa agagaccggt tttgatgttg ttat
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120
gctacattgt ccacgccacc atccaagatc tcgaggatga gaacgagaca aaacatttgg
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aagcaatgga aggagcaaag ggtcatctca aatttttcga aatggatctt cttaacagcg
240
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300
tcattggtga agtcaaagac cccgagaagc aaattttgga accggcaatt caaggaacgg
360
ttaatgtggt gaaggtggca aaggaagcag ggggtggagcg tgtggtggcg acatcgtcga
420
tctctgccat cataccgagt cctaattggc cagctgataa gattaaggga gaagattggt
480
ggacagacct tgattattgc aaggaaaaga agttatacta cccattgca aagacactag
540
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583

<210> 142
<211> 608
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<400> 142
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gtgtnaccgg agccagcgga gccatcggtt catgggtggt tcgcctcctc ctcgaacgcg
120
gctacattgt ccacgccacc atccaagatc tcgaggatga gaacgagaca aaacatttgg
180
aagcaatgga aggagcaaag ggtcatctca aatttttoga aatggatctt ctcaacagcg
240
actctattgc ggccgccgtg aaaggttgtg ccggagttat acatcttgca tgtcctagca
300
tcattggtga agtcaaagac cccgagaagc aaattttgga accggcaatt caaggaacgg
360
ttaatgtggt gaagggtggca aaggaagcag ggggtggagcg tgtggtggcg acatcgtcga
420
tctccgccat cataccgagt cctaattggc cagctgataa gattaagga gaagattggt
480
ggacagacct tgattattgc aaggaaaaga agttatacta cccattgca aagacactag
540
cagaaaaagc tgggtgggaa ttgctaaag agaccggtt tgatgttggt atgattaacc
600
ctggtact
608

<210> 143
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<223> Any nucleotide

<400> 143

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120

acattgtcca cgccaccatc caagatctcg aggatgagaa cgagacaaaa catttggaag
180

caatggaagg agcaaagggt catctcaaatt tttttgaaat ggatcttctt aacagcgact
240

ctattgcggc cgccgtgaaa ggttgtgccg gagttataca tcttgcatgt cctaacaatca
300

ttggtgaagt caaagacccc gagaagcaaa ttttggaacc ggcaattcaa ggaacggtta
360

atgtgttgaa ggtggcaaag gaagcagggg tggagcgtgt ggtggcgaca tcgtcgatct
420

cgcacatcat accgagtcct aattggccag ctgataagat taagggagaa gattgttga
480

cagaccttga ttattgcaag gaaaagaagt tatactaccc cattgcaaag acattancag
540

aaaaagctgg ttgggaattt gctaaagaga c
571

<210> 144
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120

acatcgtcca cgccaccatc caagatctcg aggatgagaa cgagacaaaa catttggaag
180

caatggaagg ggcaaagggt tatcttaaatt ttttcgaaat ggatcttctt aacagtgact
240

ctattgcggc cgccgtgaaa ggttgtgccg gagttataca tcttgcatgt cctaacaatca
300

ttggtgaagt caaagacccc gagaagcaaa ttttggaacc ggcgattcaa ggaacggtta
360

acgtgttgaa ggtggcaaag gaagcagggg tggagcgtgt ggtggcgacg tcatcgatct
420

ccgccatcat accgagtcct aattggccag ctgataagat taaggagaa gattgttgga
480

cggaccttga ttattgcaag gaaaagaagt tacactaccc catcgcaaag aactagcag
540

aaaaagctgg ttgggaattt gctaaagaga ccggttttga tgttgt
586

<210> 145
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naccggagcc ngcggagcca tcggttcacg ggtgggttcgc ctctcctcgc aacgcggcta
120

cattgtccac gccaccatcc aagatctcga ggatgagaac gagacaaaac atttggaagc
180

aatggaagga gcaaagggtc atctcaaatt ttttgaaatg gatcttctta acagcgactc
240

tattgcggnc gccgtgaaag gttgtgccgg agttatacat cttgcatgng ctaacatcat
300

tggggaagcn aaagnactcn ataagnan
328

<210> 146
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120
catttggaag caatggaagg agcaaagggt catntnaaat ttttcgaaat ggatcttntt
180
aacagngact ctattgcggc cgccgtgaaa ggttggtgccg gagttataca tn
232

<210> 147
<211> 623
<212> DNA
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<222> (14)..(14)
<223> Any nucleotide

<400> 147
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120
aaagggtcac acagtaagga ctactgtaag aaaccagat gatttgagaa aggttggtta
180
tctaactgaa ctaagtgaag acaaagagag attgaagatt ttaaaagcag atctattggt
240
ggaagggagt tttgatgagg cagtgagtg tggtgatggt gtgtttcata cagcttcccc
300
tgttcttggt ccacatgatg acaacattca gggtactttg attgatccat gtataaaagg
360
aacacaaaat gtgcttaact catgcatcaa agcaaagggtg aaacgtgtgg tgtaaacatc
420
ttcatgctct tccataagat accgtgacga tgtgcaacaa atttctcttc ttaatgaatc
480
tcattggagt gattctgaat actgcaaacg ctataacctg tggtatgcat atgcaaagac
540
tttaggagaa aaagaagcat ggaggattgc aaaggaaagt ggaattgatc tagttgtagt
600
taaccctct tttggttggtg gtc
623

<210> 148
<211> 190
<212> PRT
<213> Trifolium repens

<400> 148

Met Pro Glu Phe Cys Val Thr Gly Gly Thr Gly Phe Ile Ala Ala Tyr
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20 25 30

Arg Asn Pro Asp Asp Leu Glu Lys Val Gly Tyr Leu Thr Glu Leu Ser
35 40 45

Glu Asp Lys Glu Arg Leu Lys Ile Leu Lys Ala Asp Leu Leu Val Glu
50 55 60

Gly Ser Phe Asp Glu Ala Val Ser Gly Val Asp Gly Val Phe His Thr
65 70 75 80

Ala Ser Pro Val Leu Val Pro His Asp Asp Asn Ile Gln Val Thr Leu
85 90 95

Ile Asp Pro Cys Ile Lys Gly Thr Gln Asn Val Leu Asn Ser Cys Ile
100 105 110

Lys Ala Lys Val Lys Arg Val Val Leu Thr Ser Ser Cys Ser Ser Ile
115 120 125

Arg Tyr Arg Asp Asp Val Gln Gln Ile Ser Pro Leu Asn Glu Ser His
130 135 140

Trp Ser Asp Ser Glu Tyr Cys Lys Arg Tyr Asn Leu Trp Tyr Ala Tyr
145 150 155 160

Ala Lys Thr Leu Gly Glu Lys Glu Ala Trp Arg Ile Ala Lys Glu Ser
165 170 175

Gly Ile Asp Leu Val Val Val Asn Pro Ser Phe Val Gly Gly
180 185 190

<210> 149
<211> 570
<212> DNA
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120
aaaggggtcac acagtaagga ctactgtaag aaaccagat gatttggaga aggttgggta
180
tctaactgaa ctaagtgaag acaaagagag attgaagatt ttaaaagcag atctattggt
240
ggaagggagt tttgatgagg cagtgagtgg tgttgatggt gtgtttcata cagcttcccc
300
tgttcttggt ccacatgatg acaatattca ggttactttg attgatccat gtataaaagg
360
aacacaaaat gtgcttagct catgcatcaa agcaaagggtg aaacgtgtgg tgtaaacatc
420
ttcatgctct tccataagat accgtgacga tgtgcaacaa atttcaccac ttaatgaatc
480
tcattggagt gattctgaat actgcaaacg ctataacctg tggatatgcat atgcaaagac
540
attaggagaa aaagaagcat ggaggattgc
570

<210> 150
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<222> (8)..(9)
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ttcatagcag cctacctagt gaaagcccta ttagaaaagg gtcacacagt aaggactact

120

gtaagaaacc cagatgattt ggagaagggt gggtatctaa ctgaactaag tgaagacaaa
180

gagagattga agatttttaa agcagatcta ttggtggaag ggagttttga tgaggcagtg
240

agtgggtgtg atgggtgtgt tcatacagct tcccctgttc ttgttccaca tgatgacaat
300

attcaggtta ctttgattga tccatgtata aaaggaacac agaatgtgct taactcatgc
360

atcaaagcaa aggtgaaacg tgtgggtgta acatcctcat gctcttccat aagataccgt
420

gacgatgtgc aacaaatttc tcctcttaat gaatctcatt ggagtgttc tgattactgc
480

aaacgctata acctgtggta tgcataatgca aagactttag gagaaaaaga agcatggagg
540

attgcaaagg aaagtgggat taatctagtt gt
572

<210> 151

<211> 572

<212> DNA

<213> *Trifolium repens*

<400> 151

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tgaaagcctt attagaaaag ggtcacacag taaggactac tgtaagaaac ccagatgatt
120

tggagaagggt tgggtatcta actgaactta gtgaagacaa agagagattg aagattttta
180

aagcagatct attggtggaa gggagttttg atgaggcagt gagtgggtgt gatgggtgtgt
240

ttcatacagc tcccctgtt cttgttccac atgatgacaa cattcagggt actttgattg
300

atccatgtat aaaaggaaca caaatgtgc ttaactcatg catcaaagca aaggtgaaac
360

gtgtgggtgtt aacatcttca tgctcttcca taagataccg tgacgatgtg caacaaattt
420

ctcctcttaa tgaatctcat tggagtgtt ctgaatactg caaacgctat aacctgtggt
480

atgcatatgc aaagacttta ggagaaaaag aagcatggag gattgcaaag gaaagtggaa
540

ttgatctagt ttagttaac cctctttttg tt
572

<210> 152

<211> 574

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120
aaggttggtt atctaactga acttagtgaa gacaaagaga gattgaagat tttaaaagca
180
gatctattgg tggaagggag ttttgatgag gcagtgagtg gtgttgatgg tgtgtttcat
240
acagcttccc ctgttcttgt tccacatgat gacaacattc aggttacttt gattgatcca
300
tgtataaaag gaacacaaaa tgtgcttaac tcatgcatca tagcaaaggt gaaacgtgtg
360
gtgttaacat cttcatgctc ttccataaga taccgtgacg atgtgcaaca aatttctcct
420
cttaatgaat ctcatggag tgattctgaa tactgcaaac gctataacct gtggtatgca
480
tatgcaaaga ctttaggaga aaaagaagca tggaggattg caaaggaaag tggaattgat
540
ctagttgtag ttaaccocctc ttttgttggt ggtc
574

<210> 153
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ccctactcca aaaacactac aaaattcacg ccacaatctt cccaattcc aacgcatctc
120

atctcttcac actccaccog gaagctcaat cccggatcac aattttccct gtcgatatcc
180

tcgactccac cgccgtcttc tccgctatca ataactgctc aggtgtcttt catgccgctt
240

ctccatgtac cctcgaagat ccaactgatc cgcaaaaaga gcttctagaa cctgctgtac
300

aaggaaccct aaatgttcta gaagcatcca gcgcgcaggt accaaaccct aattggccgg
360

agaaaaaggc gatcgatgag gcgtcgtgga cggatgttga gtactgtaaa ttgagagggg
420

agtggatatct ggtgtcgaaa acggaggcgg agaaggcggc ttgggatttt cgagagaaaa
480

atgggtggtgt tgatgtgggg gcggnctcatc cggggacttg tttgggagag ttgatacaga

540

aggagttgaa tgcgagttca gcggnntttac agaggttgat gatggggagt gaggatactc
600

aagagtgnta ttggnnngggg ggctgnnnat gntaaagatg n
641

<210> 154
<211> 206
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Leu Val Lys Thr Leu Leu Gln Lys His Tyr Lys Ile His Ala Thr Ile
20 25 30

Phe Pro Asn Ser Asn Ala Ser His Leu Phe Thr Leu His Pro Glu Ala
35 40 45

Gln Ser Arg Ile Thr Ile Phe Pro Val Asp Ile Leu Asp Ser Thr Ala
50 55 60

Val Phe Ser Ala Ile Asn Asn Cys Ser Gly Val Phe His Ala Ala Ser
65 70 75 80

Pro Cys Thr Leu Glu Asp Pro Thr Asp Pro Gln Lys Glu Leu Leu Glu
 85 90 95

Pro Ala Val Gln Gly Thr Leu Asn Val Leu Glu Ala Ser Ser Ala Gln
 100 105 110

Val Pro Asn Pro Asn Trp Pro Glu Lys Lys Ala Ile Asp Glu Ala Ser
 115 120 125

Trp Thr Asp Val Glu Tyr Cys Lys Leu Arg Gly Lys Trp Tyr Leu Val
 130 135 140

Ser Lys Thr Glu Ala Glu Lys Ala Ala Trp Asp Phe Arg Glu Lys Asn
 145 150 155 160

Gly Gly Val Asp Val Gly Ala Xaa His Pro Gly Thr Cys Leu Gly Glu
 165 170 175

Leu Ile Gln Lys Glu Leu Asn Ala Ser Ser Ala Leu Gln Arg Leu Met
 180 185 190

Met Gly Ser Glu Asp Thr Gln Glu Xaa Tyr Trp Xaa Gly Gly
 195 200 205

<210> 155
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120
tcctccgcgg ctacactggt cagccaccg tccaaaatct caatgatgag aacgaaacga
180
agcatctaga agctctcgaa ggagcacaaa ctaatctccg tctcttcag atcgatctcc
240
ttaactacga cacaatcctc gctgctgtcc gcgggtgcgt cggaattttc cacctcgctt
300
caccttgcac tgtagacaaa gttcatgata ctgagaagga gcttttggat cctgcaatta
360
aagggacttt gaatgtgctt actgcagcta aggaagtagg ggtgaagcgt gtgggttgta
420
cctcgctctgt ctggcgatt actcctagtc ctgattggcc ttctgatggt gttaaaagag
480
aggattgttg gactgatggt gaatattgca agaaaaaaga gttgggggat ccgttggtcca
540
aaacattggc tgaaaaagct gcgtgggatt tttncaaaga aaatggtttg gatgttggtg
600
nggtgaatcc cggactgng atgggtcctg tttttccacc acggcataat gcaagcatgc
660
tcatgccttg ggaaactttt ttgaaggctg gnnctgaaac atttgaagac tattttatgg
720
gattggccnn ctttaaagat gtngcattgg cncatnnttt ggggtatgag aacaaanann
780
ctttgggana catngngggg ttgaaactat cnntccttac gg
822

<210> 156
<211> 256
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<213> Trifolium repens

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<400> 156

Met Ser Lys Leu Val Cys Val Thr Gly Gly Ser Gly Cys Ile Gly Ser
 1 5 10 15

Trp Leu Val His Leu Leu Leu Leu Arg Gly Tyr Thr Val His Ala Thr
 20 25 30

Val Gln Asn Leu Asn Asp Glu Asn Glu Thr Lys His Leu Glu Ala Leu
 35 40 45

Glu Gly Ala Gln Thr Asn Leu Arg Leu Phe Gln Ile Asp Leu Leu Asn
 50 55 60

Tyr Asp Thr Ile Leu Ala Ala Val Arg Gly Cys Val Gly Ile Phe His
 65 70 75 80

Leu Ala Ser Pro Cys Thr Val Asp Lys Val His Asp Pro Gln Lys Glu
 85 90 95

Leu Leu Asp Pro Ala Ile Lys Gly Thr Leu Asn Val Leu Thr Ala Ala
 100 105 110

Lys Glu Val Gly Val Lys Arg Val Val Val Thr Ser Ser Val Ser Ala
 115 120 125

Ile Thr Pro Ser Pro Asp Trp Pro Ser Asp Val Val Lys Arg Glu Asp
 130 135 140

Cys Trp Thr Asp Val Glu Tyr Cys Lys Lys Lys Glu Leu Gly Tyr Pro
 145 150 155 160

Leu Ser Lys Thr Leu Ala Glu Lys Ala Ala Trp Asp Phe Xaa Lys Glu
 165 170 175

Asn Gly Leu Asp Val Val Xaa Val Asn Pro Xaa Thr Xaa Met Gly Pro
 180 185 190

Val Phe Pro Pro Arg His Asn Ala Ser Met Leu Met Pro Trp Glu Thr
 195 200 205

Phe Leu Lys Ala Xaa Xaa Glu Thr Phe Glu Asp Tyr Phe Met Gly Leu
 210 215 220

Ala Xaa Phe Lys Asp Xaa Ala Leu Xaa His Xaa Leu Gly Tyr Glu Asn
 225 230 235 240

Lys Xaa Xaa Leu Gly Xaa Xaa Xaa Gly Leu Lys Leu Xaa Xaa Leu Thr
 245 250 255

<210> 157
<211> 535
<212> DNA
<213> *Trifolium repens*

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agctagtgttg cgtcaccggc ggcagcggat gcatcggttc atggctagtc catctccttc
120
tcctccgcgg ctacactggt cacgccaccg tccaaaatct caatgatgag aacgaaacga
180
agcatctaga agctctcgaa ggagcacaaa ctaatctccg tctcttccag atcgatctcc
240
ttaactacga cacaatcctc gctgctgtcc gcggttgctt cggaattttc cacctcgctt
300
caccttgcac tgtagacaaa gttcatgata ctgagaagga gcttttggat cctgcaatta
360
aagggacttt gaatgtgctt actgcagcta aggaagtagg ggtgaagcgt gtgggttgta
420
cctcgtctgt ctgggcgatt actcctagtc ctgattggcc ttctgatggt gttaaaagag
480
aggattgttg gactgatggt gaatattgca agaaaaaaga gttgtggtat ccggt
535

<210> 158
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<213> *Trifolium repens*

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gnggcggatg catcggttca tggctagtcc atctccttct cctccgcggc tacactgttc
120

acgccaccgt ccaaaatctc aatgatgaga acgaaacgaa gcatctagaa gctctcgaag
180

gagcacaaac taatctccgt ctcttcaga tcgatctcct taactacgac acaatcctcg
240

ctgctgtccg oggttgcgtc ggaattttcc acctcgcttc accttgact gtagacaaag
300

ttcatgatcc tcagaaggag cttttggatc ctgcaattac agggactttg aatgtgctta
360

ctgcagctaa ggaagtaggg gtgaagcgtg tggttgttac ctgctctgtc tcggcgatta
420

ctcctagtcc tgattggcct tctgatgttg ttaaaagaga ggattgttgg actgatgttg
480

aatattgcaa gaaaaaagag ttgggggtatc cgttgtccaa aacattggct gaaaaagctg
540

cgtgggattt ttncaaagaa aatgggtttgg atgttggtgn ggtgaatccc ggnactgnga
600

tgggtcctgt ttttccacca cggcataatg caagcatgct catgccttgg gaaacttttt
660

tgaaggctgg nnctgaaaca tttgaagact attttatggg attggccnnc tttaaagatg
720

tngcattggc ncatnntttg gggatatgaga acaaanannc tttggganac atngnggggt
780

tgaaactatc nntccttacg g
801

<210> 159

<211> 582

<212> DNA

<213> *Trifolium repens*

<400> 159

gtcacttatg aaatggaaca caaaggtgga gacaaagtat gtgtgacagg ggcattcaggc
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tttttagcat cttggcttat taagaaactt cttttgtctg gctatcaagt cattggaaca
120

gttagagatt tagggaagaa gaagaaagt gaacatttat ggaaattgga aggagcaaca
180

gaaagactag aactaatcca agctgattta atggaagaaa atagtttcga caaagcgatc
240

atgggatgca aagggtgtctt ccacattgcc tctccagtac tcaatcatat atcagataat
300

cctaaggcgg aaatcttgga accggcagtc caaggtacgc taaatgtggt gcgttcttgt
360

aagaggaacc ccgatcttgt tcgagtgggtg ctagcctcat catcttcggc tgtagagta
420

agagctgatt ttgatccaag cataccaatt gatgaatcat cttggagctc cttggaattg
480

tgcgagaaac tcaaggcatg gtacccaatg tcaaagacaa tggcagaaaa agcagcttgg
540

gaatatagca aagagaatgg aatagactta gtgactatth tc
582

<210> 160

<211> 190

<212> PRT

<213> *Trifolium repens*

<400> 160

Met Glu His Lys Gly Gly Asp Lys Val Cys Val Thr Gly Ala Ser Gly
1 5 10 15

Phe Leu Ala Ser Trp Leu Ile Lys Lys Leu Leu Leu Ser Gly Tyr Gln
20 25 30

Val Ile Gly Thr Val Arg Asp Leu Gly Lys Lys Lys Lys Val Glu His
35 40 45

Leu Trp Lys Leu Glu Gly Ala Thr Glu Arg Leu Glu Leu Ile Gln Ala
50 55 60

Asp Leu Met Glu Glu Asn Ser Phe Asp Lys Ala Ile Met Gly Cys Lys
65 70 75 80

Gly Val Phe His Ile Ala Ser Pro Val Leu Asn His Ile Ser Asp Asn
85 90 95

Pro Lys Ala Glu Ile Leu Glu Pro Ala Val Gln Gly Thr Leu Asn Val
100 105 110

Leu Arg Ser Cys Lys Arg Asn Pro Asp Leu Val Arg Val Val Leu Ala
115 120 125

Ser Ser Ser Ser Ala Val Arg Val Arg Ala Asp Phe Asp Pro Ser Ile
130 135 140

Pro Ile Asp Glu Ser Ser Trp Ser Ser Leu Glu Leu Cys Glu Lys Leu
145 150 155 160

Lys Ala Trp Tyr Pro Met Ser Lys Thr Met Ala Glu Lys Ala Ala Trp
165 170 175

Glu Tyr Ser Lys Glu Asn Gly Ile Asp Leu Val Thr Ile Phe
180 185 190

<210> 161
<211> 572
<212> DNA
<213> Trifolium repens

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<222> (4)..(5)
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<223> Any nucleotide

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120

gtttgtgtca ccggtggtgc tggttatatt ggttctcttt tagtcaaaaa gcttttggaa
180

aagggttaca ccgttcacgc tactcttaga aacttgaagg acgaatccaa agtagatttt
240

ttgagaggct ttccacatgc agatactaga cttatgttat ttgaagctga tatatacaaa
300

tcagatgaat tttggcccgcc aattcaaggc tgtgagtttg tttttcacct tgctactcct
360

tttcaacatc aaactgattc tcagtttaag agcatagagg aagctgcaat agcaggggta
420

aaaagcatag ctgaaaattg cataaaatca ggaacagtga gaaaattgat atacactgga
480

actgtaattg cttcttcttc tctgaaagat gatggaagtg gctacaaaga cttcattgat
540

gaaacttggt ggacacctct ccattcttct ct
572

<210> 162
<211> 156

<212> PRT

<213> Trifolium repens

<400> 162

Met Glu Arg Ser Cys Lys Val Cys Val Thr Gly Gly Ala Gly Tyr Ile
1 5 10 15

Gly Ser Leu Leu Val Lys Lys Leu Leu Glu Lys Gly Tyr Thr Val His
20 25 30

Ala Thr Leu Arg Asn Leu Lys Asp Glu Ser Lys Val Asp Phe Leu Arg
35 40 45

Gly Phe Pro His Ala Asp Thr Arg Leu Met Leu Phe Glu Ala Asp Ile
50 55 60

Tyr Lys Ser Asp Glu Phe Trp Pro Ala Ile Gln Gly Cys Glu Phe Val
65 70 75 80

Phe His Leu Ala Thr Pro Phe Gln His Gln Thr Asp Ser Gln Phe Lys
85 90 95

Ser Ile Glu Glu Ala Ala Ile Ala Gly Val Lys Ser Ile Ala Glu Asn
100 105 110

Cys Ile Lys Ser Gly Thr Val Arg Lys Leu Ile Tyr Thr Gly Thr Val
115 120 125

Ile Ala Ser Ser Ser Leu Lys Asp Asp Gly Ser Gly Tyr Lys Asp Phe
130 135 140

Ile Asp Glu Thr Cys Trp Thr Pro Leu His Leu Pro
145 150 155

<210> 163

<211> 714

<212> DNA

<213> Trifolium repens

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<223> Any nucleotide

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<221> misc_feature

<222> (131)..(131)

<223> Any nucleotide

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<221> misc_feature

<222> (147)..(147)

<223> Any nucleotide

<400> 163
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ttaataattg gaagggagaa taaatagttg aaaaacacac agttggagtg tttttgttgt
120
taaagaagct ngaaaatgga ggaagcnaca aagatggtga aaaagagtgg acaaattgtt
180
cctactgcc aatactgtgt tacaggagca acaggctata ttggttcattg gcttgttgaa
240
gctcttcttc aaagagggtg cactgttcatt gctactgtta gagatcctga aaaatcgta
300
cacctcctgt cgttgttgaa aggtagtgac caattgagaa ttttccgtgc ggatttgcaa
360
gaagaaggaa gtttcgatga tgccgtaaaa ggatgtattg gtgtgttcca tgttcagct
420
tcaatgcaat tcaatattag tgacaaagaa aacactgagg actttgttga agcaaata
480
attgaccctg caatcaaagg aaccataaat cttctcaaat catgcttgaa atcaaattca
540
gtgaaaaggg ttgttttcac atcttcata agtactatta ctgctaaaga caacgacgga
600
aaatggaaac ctattgttga tgaatcttgc caaacaaaaa ctgagattct gtggaataca
660
caaccaagtg gatgggttta tgcactttca aagcttcattg cagaagaagc ggct
714

<210> 164
<211> 187
<212> PRT
<213> *Trifolium repens*

<400> 164

Met Val Lys Lys Ser Gly Gln Ile Val Pro Thr Ala Lys Tyr Cys Val
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Thr Gly Ala Thr Gly Tyr Ile Gly Ser Trp Leu Val Glu Ala Leu Leu
20 25 30

Gln Arg Gly Cys Thr Val His Ala Thr Val Arg Asp Pro Glu Lys Ser
35 40 45

Leu His Leu Leu Ser Leu Trp Lys Gly Ser Asp Gln Leu Arg Ile Phe
50 55 60

Arg Ala Asp Leu Gln Glu Glu Gly Ser Phe Asp Asp Ala Val Lys Gly
65 70 75 80

Cys Ile Gly Val Phe His Val Ala Ala Ser Met Gln Phe Asn Ile Ser
85 90 95

Asp Lys Glu Asn Thr Glu Asp Phe Val Glu Ala Asn Ile Ile Asp Pro
100 105 110

Ala Ile Lys Gly Thr Ile Asn Leu Leu Lys Ser Cys Leu Lys Ser Asn
115 120 125

Ser Val Lys Arg Val Val Phe Thr Ser Ser Ile Ser Thr Ile Thr Ala
130 135 140

Lys Asp Asn Asp Gly Lys Trp Lys Pro Ile Val Asp Glu Ser Cys Gln
145 150 155 160

Thr Lys Thr Glu Ile Leu Trp Asn Thr Gln Pro Ser Gly Trp Val Tyr
165 170 175

Ala Leu Ser Lys Leu His Ala Glu Glu Ala Ala
180 185

<210> 165
<211> 289
<212> DNA
<213> Trifolium repens

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ttaataattg gaagggagaa taaatagttg aaaaacacac agttggagtg tttttgttgt
120

taaagaagct ataaaatgga ggaaacaaca aagatggtga aaaatagtg acaaattgtt
180

cctatagcca aatactgtgt cacaggagcc acaggctata ttggttcatg gcttggtgaa
240

gctcttcttc aaagagggtg cactgttcat gctactgtta gagatcctg
289

<210> 166
<211> 591
<212> DNA
<213> Trifolium repens

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<223> Any nucleotides

<400> 166
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actgccaaat actgtgttac aggagcaaca ggctatatattg gttcatggct tgttgaagct
120
cttcttcaaa gaggttgcaac tggtcatgct actgttagag atcctgaaaa atcgttacac
180
ctcctgtcgt tgtggaaagg tagtgaccaa ttgagaattt tccgtgcgga ttgcaagaa
240
gaaggaagtt tcgatgatgc cgtaaaagga tgtattggtg tgttccatgt tgcagcttca
300
atgcaattca atattagtga caaagaaaac actgaggact ttgttgaagc aaatataatt
360
gaccctgcaa tcaaaggaac cataaatctt ctcaaactcat gcttgaaatc aaattcagt
420
aaaaggggtg ttttcacatc ttccataagt actattactg ctaaagacaa cgacggaaaa
480
tggaaccta ttgttgatga atcttgccaa acaaaaactg agattctgtg gaatacacia
540
ccaagtggat ggggttatgc actttcaaag cttcatgcag aagaagcggc t
591

<210> 167
<211> 572
<212> DNA
<213> *Trifolium repens*

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<222> (19)..(19)
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<400> 167
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caaatactgt gttacaggag caacaggcta tattggttca tggcttggtg aagctcttct
120
tcaaagaggt tgcaactgtc atgctactgt tagagatcct gaaaaatcgt tacacctcct
180

gtcgttgtgg aaaggtagt accaattgag aattttccgt gcggtttgc aagaagaagg
240

aagtttcgat gatgccgtaa aaggatgtat tgggtgtgttc catgttgacag cttcaatgca
300

attcaatatt agtgacaaaag aaaacactga ggactttgtt gaagcaaata taattgaccc
360

tgcaatcaaa ggaaccataa atctttctcaa atcatgcttg aaatcaaatt cagtgaaaag
420

ggttgttttc acatctttcca taagtactat tactgctaaa gacaacgacg gaaaatggaa
480

acctattgtt gatgaatctt gccaaacaaa aactgagatt ctgtggaata cacaaccaag
540

tggatggggt tatgcacttt caaagcttca tg
572

<210> 168
<211> 976
<212> DNA
<213> *Trifolium repens*

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<222> (5)..(5)
<223> Any nucleotide

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<400> 168
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60

agtgaagtga aaacatacat gggttccgaa tcagaaatag tttgtgttac cggagcttca
120

ggtttcatcg gatcgtgggt tggttatgaga cttatagagc gtggctacac gggttcgagcc

180

accgttcgcg acccagataa catgaagaag gtgaagcatt tgggtggaact gccgggtgca
240

aaaagcaaat tgtctctttg gaaggctgat cttgataaag aggggagttt tgatgaagca
300

attaaagggg gcacaggagt ttttcatggt gctacaccaa tggattttga atccaaggac
360

cctgagaatg aagtgataaa gcctacaata aatggattaa tagacatact gaaagcatgc
420

gaaaaggcaa aaacagttag aaaattgggt ttcacatcat cggctggaac tgtggacggt
480

actgaacatc caaagtctat tattgatgaa acatgctgga gtgacgttga cttttgccgt
540

agagtcaaga tgaccgggtg gatgtatttt gtttcaaaga ccctagcaga gcaagaagct
600

tggaagtatt cgaaagagca caacatagac tttgtctcca tcattccacc tcttggtggt
660

ggcccccttc ttatggcctc aatgccacct agtctaata ctgctctttc tcttatcaca
720

ggaaatgagg cccattactc aatcataaag caagggcaat acgtccattt agatgacctt
780

tgtcttgctc atatatttct gtatgagaat ccaaaagctc aaggagata catttgctgt
840

tcacatgaag caaccattca tcaagttgca aaacttatta aagaaaaata cccagagttc
900

aatgtcccaa caaaattcaa tgatatccca gatgaattgg aaattattaa attttctaaa
960

aagaagatca cagact
976

<210> 169

<211> 299

<212> PRT

<213> Trifolium repens

<400> 169

Met Gly Ser Glu Ser Glu Ile Val Cys Val Thr Gly Ala Ser Gly Phe
1 5 10 15

Ile Gly Ser Trp Leu Val Met Arg Leu Ile Glu Arg Gly Tyr Thr Val
20 25 30

Arg Ala Thr Val Arg Asp Pro Asp Asn Met Lys Lys Val Lys His Leu
35 40 45

Val Glu Leu Pro Gly Ala Lys Ser Lys Leu Ser Leu Trp Lys Ala Asp
50 55 60

Leu Asp Lys Glu Gly Ser Phe Asp Glu Ala Ile Lys Gly Cys Thr Gly
 65 70 75 80
 Val Phe His Val Ala Thr Pro Met Asp Phe Glu Ser Lys Asp Pro Glu
 85 90 95
 Asn Glu Val Ile Lys Pro Thr Ile Asn Gly Leu Ile Asp Ile Leu Lys
 100 105 110
 Ala Cys Glu Lys Ala Lys Thr Val Arg Lys Leu Val Phe Thr Ser Ser
 115 120 125
 Ala Gly Thr Val Asp Val Thr Glu His Pro Lys Ser Ile Ile Asp Glu
 130 135 140
 Thr Cys Trp Ser Asp Val Asp Phe Cys Arg Arg Val Lys Met Thr Gly
 145 150 155 160
 Trp Met Tyr Phe Val Ser Lys Thr Leu Ala Glu Gln Glu Ala Trp Lys
 165 170 175
 Tyr Ser Lys Glu His Asn Ile Asp Phe Val Ser Ile Ile Pro Pro Leu
 180 185 190
 Val Val Gly Pro Phe Leu Met Ala Ser Met Pro Pro Ser Leu Ile Thr
 195 200 205
 Ala Leu Ser Leu Ile Thr Gly Asn Glu Ala His Tyr Ser Ile Ile Lys
 210 215 220
 Gln Gly Gln Tyr Val His Leu Asp Asp Leu Cys Leu Ala His Ile Phe
 225 230 235 240
 Leu Tyr Glu Asn Pro Lys Ala Gln Gly Arg Tyr Ile Cys Cys Ser His
 245 250 255
 Glu Ala Thr Ile His Gln Val Ala Lys Leu Ile Lys Glu Lys Tyr Pro
 260 265 270
 Glu Phe Asn Val Pro Thr Lys Phe Asn Asp Ile Pro Asp Glu Leu Glu
 275 280 285
 Ile Ile Lys Phe Ser Lys Lys Lys Ile Thr Asp
 290 295

<210> 170

<211> 586

<212> DNA

<213> Trifolium repens

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<222> (57)..(58)
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60

agtgaagtga aaacatacat gggttccgaa tcagaaatag tttgtgttac cggagcttca
120

tgtttcatcg gatcgtggct tgttatgaga cttatagagc gtggctacac ggttcgagcc
180

accgttcgcg acccagataa catgaagaag gtgaagcatt tgggtggaact gccgggtgca
240

aaaagcaaat tgtctctttg gaaggctgat cttgataaag aggggagttt tgatgaagca
300

attaaagggg gcacaggagt ttttcatggt gctacaccaa tggattttga atccaaggac
360

cctgagaatg aagtgataaa gcctacaata aatggattaa tagacatact gaaagcatgc
420

gaaaaggcaa aaacagttaa aaaattgggt ttcacatcat cggctggaac tgtggacgtt
480

actgaacatc caaagtctat tattgatgaa acatgctgga gtgacgttga cttttgccgt
540

agagtcaaga tgaccggttg gatgtatttt gtttcaaaga ccttag

586

<210> 171
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<220>
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<222> (209)..(209)
<223> Any nucleotide

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120

gtttcatcgg gtcgtggctt gttatgagac ttatggagca tggctacact gttcgagcca
180

cgttcgtga cccagataac atgaagaang tgaagcattt gctggaactg ccaggtgcaa
240

aaagcaaatt gtctcttttg aaggctgatc ttgataaaga ggggagtttt gatgaagcaa
300

ttaaaggggtg cacaggagtt ttcatgttg ctacaccaat ggattttgag tccaaggacc
360

ctgagaatga agtgataaag cctacaataa acggattaat agacatactg aaagcatgcg
420

aaaaggcaaa aacagttaga aaattggttt tcacatcatc ggctggaact gtggacgtta
480

ctgaacatcc aaagtctatt attgatgaaa catgctggag tgacgttgac ttttgccgta
540

gagtcaaaat gaccggttgg atgtatttt
569

<210> 172
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<220>
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<223> Any nucleotide

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<222> (102)..(102)

<223> Any nucleotide

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<222> (123)..(123)

<223> Any nucleotide

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<221> misc_feature

<222> (154)..(154)

<223> Any nucleotide

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<222> (161)..(161)

<223> Any nucleotide

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<222> (322)..(322)

<223> Any nucleotide

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<223> Any nucleotide

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<223> Any nucleotide

<220>

<221> misc_feature

<222> (493)..(493)

<223> Any nucleotide

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60

gaagtgaana catacatggg ttccgaatca gaaatagttt gngttaccgg agcttcatgt
120

ttnatcggat cgtggcttgt tatgagactt atanagcgtg nctacacggc tcgagccacc
180

gttcgcgacc cagataacat gaagaagggtg aagcatttgg tggaactgcc gggtgcaaaa
240

agcaaatgtt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt
300

aaaggggtgca caggagtttt tnatgttgct acaccaatgg attttgaatc caaggaccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcnaa
420

aaggcaaaaa cagttaaaaa attggttttc acatcatcgg ctgnaactgt ggacgttact
480

gaacatccaa agn
493

<210> 173

<211> 580

<212> DNA

<213> *Trifolium repens*

<220>

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<222> (2)..(2)

<223> Any nucleotide

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<222> (13)..(13)

<223> Any nucleotide

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<223> Any nucleotide

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<222> (539)..(539)
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<222> (546)..(546)
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<220>
<221> misc_feature
<222> (576)..(576)
<223> Any nucleotide

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60

gaagtgaaaa catacatggg ttccgaatca gaaatagttt gtgttaccgg agcttcatgt
120

ttcatcggat cgtggcttgt tatgagactt atagagcgtg gctacacggg tcgagccacc
180

gttcgcgacc cagataacat gaagaagggtg aagcatttgg tggaactgcc gggtgcaaaa
240

agcaaattgt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt
300

aaaggggtgca caggagtttt tcatgttgct acaccaatgg attttgaatc caaggaccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcgaa
420

aaggcaaaaa cagttaaaaa attggttttc acatcatcgg ctggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtana
540

gtcaanatga cgggctggat gtattttgtt tcaaanaccc

580

<210> 174
<211> 581
<212> DNA
<213> Trifolium repens

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<222> (13)..(13)
<223> Any nucleotide

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<222> (22)..(22)
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<222> (36)..(36)
<223> Any nucleotide

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<222> (50)..(52)
<223> Any nucleotides

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<400> 174
gngtcttccg ttnaatttaa gnctatatattg aaaagnaaaa aaagagtagh nnanngaagt
60

gaagtgaataa catacatggg ttccgaatca gaaatagttt gtgttaccgg agcttcaggt
120

ttcatcggat cgtggcttgt tatgagactt atagagcgtg gctacacggg tcgagccacc
180

gttcgagacc cagataacat gaagaagggtg aagcatttgg tgggaactgcc ggggtgcaaaa
240

agcaaatgtt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt
300

aaaggggtgca caggagtttt tcatgttgct acaccaatgg attttgaatc caaggaccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgagaa
420

aaggcaaaaa cagttagaaa attggttttc acatcatcgg ctggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtaga
540

gtcaagatga ccggttggat gtattttgtt tcaaagaccc t
581

<210> 175
<211> 592
<212> DNA
<213> *Trifolium repens*

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<222> (2)..(2)
<223> Any nucleotide

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<222> (13)..(13)
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<222> (22)..(22)
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<222> (36)..(36)
<223> Any nucleotide

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<222> (50)..(52)
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60

gaagtgaaaa catacatggg ttccgaatca gaaatagttt gtgttaccgg agcttcaggt
120

ttcatcggat cgtggcttgt tatgagactt atagagcgtg gctacacggt tcgagccacc
180

gttcgcgacc cagataacat gaagaagggtg aagcatttgg tggaaactgcc ggggtgcaaaa
240

agcaaattgt ctcttttgga ggctgatctt gataaagagg ggagttttga tgaagcaatt
300

aaaggggtgca caggagtttt tcatgttgct acaccaatgg attttgaatc caaggaccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcgaa
420

aaggcaaaaa cagttagaaa attggttttc acatcatcgg ctggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtaga
540

gtcaagatga ccggttggat gtattttgtt tcaaagaccc tagcagagca ag
592

<210> 176

<211> 598

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (2)..(2)

<223> Any nucleotide

<220>

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<222> (13)..(13)

<223> Any nucleotide

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<221> misc_feature

<222> (19)..(19)

<223> Any nucleotide

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<221> misc_feature

<222> (22)..(22)

<223> Any nucleotide

<400> 176

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gaagtgaaaa catacatggg ttctgaatca gaaatagttt gtgttaccgg agcatcaggt
120

ttcatcggat cgtggcttgt tatgagactt atagagcgtg gctacacggt tcgagccact
180

gttcgcgacc cagataacat gaagaagggtg aagcatttgg tggaaactgcc ggggtgcaaaa
240

agcaaattgt ctcttttgga ggctgatctt gataaagagg ggagttttga tgaagcaatt

300

aaagggtgca caggagtttt tcatgttgct acaccaatgg attttgaatc caaggaccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcgaa
420

aaggcaaaaa cagttaaaaa attggttttc acatcatcgg ctggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtaga
540

gtcaagatga ccggttggat gtattttggt tcaaagaccc tagcagagca agaagctt
598

<210> 177

<211> 576

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (9)..(9)

<223> Any nucleotide

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<222> (12)..(12)

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<223> Any nucleotide

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<221> misc_feature

<222> (21)..(21)

<223> Any nucleotide

<400> 177

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60

aagtgaaaat atacatgggt tccgaatcgg aaatagtttg tgttaccgga gcttcagggt
120

tcatcgggtc gtggcttggt atgagactta tggagcgcgg ctacacggtt cgagccactg
180

ttcgcgaccc agataacatg aagaaggatga agcatttgat ggaactgccg ggtgcaaaaa
240

gcaaattgtc tctttggaag gctgatcttg ataaagaggg gagttttgat gaagcaatta
300

aagggtgcac aggagttttt catgttgcta caccaatgga ttttgaatcc aaggaccctg
360

196/390

agaacgaagt gataaagcct acaataaatg gactaataga cataactgaga gcatgtgaaa
420

aggcaaaaac aattagaaga ttgggttttca catcatcagc tggaactgtg gacgtaactg
480

aacactcaaa atcaattggt gatgaaacat gttggagtga cgttgacttt tgccgtagag
540

tcaaaatgac cggttggatg tattttgttt caaaga
576

<210> 178
<211> 587
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (12)..(12)
<223> Any nucleotide

<220>
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<222> (21)..(21)
<223> Any nucleotide

<400> 178
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60

aagtgaaaac atacatgggt tctgaatcag aaatagtttg tgttaccgga gcatcagggt
120

tcatcggtac gtggcttggt atgagactta tagagcgtgg ctacacgggt cgagccactg
180

ttcgcgaccc agataacatg aagaagggtga agcatttggt ggaactgccg ggtgcaaaaa
240

gcaaattgtc tctttggaag gctgatcttg ataaagaggg gagttttgat gaagcaatta
300

aagggtgcac aggagttttt catgttgcta caccaatgga ttttgaatcc aaggaccctg
360

agaatgaagt gataaagcct acaataaatg gattaataga cataactgaaa gcatgcgaaa
420

aggcaaaaac agttaaaaaa ttgggttttca catcatcggc tggaactgtg gacgttactg
480

aacatccaaa gtctattatt gatgaaacat gctggagtga cgttgacttt tgccgtagag
540

tcaagatgac cggttggatg tattttgttt caaagaccct agcagag
587

<210> 179
<211> 630
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (12)..(13)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (21)..(21)
<223> Any nucleotide

<400> 179
gggtcttccgt tnnattttaag nctatatattga aaaagaaaaa aagagtagag aagtgaagtg
60
aagtgaaaac atacatgggt tctgaatcag aaatagtttg tgttaccgga gcatcaggtt
120
tcatcggatc gtggcttggt atgagactta tagagcgtgg ctacacgggt cgagccactg
180
ttcgcgaccc agataacatg aagaagggtga agcatttggt ggaactgccg ggtgcaaaaa
240
gcaaattgtc tcttttgaag gctgatcttg ataaagaggg gagttttgat gaagcaatta
300
aaggggtgcac aggagttttt catgttgcta caccaatgga ttttgaatcc aaggaccctg
360
agaatgaagt gataaagcct acaataaatg gattaataga catactgaaa gcatgcaaaa
420
aggcaaaaac agttaaaaaa ttggttttca catcatcggc tggaactgtg gacgttactg
480
aacatccaaa gtctattatt gatgaaacat gctggagtga cgttgacttt tgccgtagag
540
tcaagatgac cggttggatg tattttgttt caaagaccct agcagagcaa gaagcttggg
600
agtattctaa agagcacacaac atagattttg
630

<210> 180
<211> 579
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (7)..(8)
<223> Any nucleotides

<220>
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<222> (11)..(11)
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<221> misc_feature
<222> (17)..(17)
<223> Any nucleotide

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<222> (20)..(20)
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60

agtgaaaata tacatggggtt ccgaatcgga aatagtttgt gttaccggag cttcaggttt
120

catcgggtcg tggcttggtta tgagacttat ggagcgcggc tacacgggttc gagccactgt
180

tcgcgaccca gataacatga agaaggtgaa gcatttgatg gaactgccgg gtgcaaaaag
240

caaattgtct ctttgggaagg ctgatcttga taaagagggg agttttgatg aagcaattaa
300

agggtgcaca ggagtttttc atgttgctac accaatggat tttgaatcca aggaccctga
360

gaacgaagtg ataaagccta caataaatgg actaatagac atactgagag catgtgaaaa
420

ggcaaaaaca attagaagat tggttttcac atcatcagct ggaactgtgg acgtaactga
480

acactcaaaa tcaattgttg atgaaacatg ttggagtgac gttgactttt gccgtagagt
540

caaaatgacc ggttggatgt attttgtttc aaagaccct
579

<210> 181
<211> 604
<212> DNA
<213> *Trifolium repens*

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<222> (12)..(12)
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<221> misc_feature
<222> (17)..(17)
<223> Any nucleotide

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<223> Any nucleotide

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<222> (52)..(53)
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<222> (55)..(57)
<223> Any nucleotides

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agtgaataca tacatgggtt ccgaatcaga aatagtttgt gttaccggag cttcaggttt
120

catcggtatg tggcttggtt tgagacttat agagcgtggc tacacggttc gagccaccgt
180

tcgcgaccca gataacatga agaaggtgaa gcatttggtg gaactgccgg gtgcaaaaag
240

caaattgtct ctttggaagg ctgatcttga taaagagggg agttttgatg aagcaattaa
300

agggtgcaca ggagtttttc atgttgctac accaatggat tttgaatcca aggaccctga
360

gaatgaagtg ataaagccta caataaatgg attaatagac atactgaaag catgcgaaaa
420

ggcaaaaaca gttagaaaat tggttttcac atcatcgggt ggaactgtgg acgttactga
480

acatccaaag tctattattg atgaaacatg ctggagtgac gttgactttt gccgtagagt
540

caagatgacc gggtggatgt attttgtttc aaagacccta gcagagcaag aagcttggaa
600

gtat
604

<210> 182
<211> 586
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (10)..(10)
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<400> 182
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gaaaatatac atgggttctg aatcggaaat agtttgtgtt accggagctt caggtttcat
120

cggttcgtgg cttgttatga gacttatgga gcgtggctac actgttcgag ccaccgttcg
180

tgaccagat aacatgaaga aggtgaagca ttgctggaa ctgccgggtg caaaaagcaa
240

attgtctctt tggaaggctg atcttgataa agaggggagt ttgatgaag caattaaagg
300

gtgcacagga gtttttcatg ttgctacacc aatggatttt gaatccaagg accctgagaa
360

tgaagtgata aagcctacaa taaacggatt aatagacata ctgaaagcat gcgaaaaggc
420

aaaaacagtt agaaaattgg ttttcacatc atcggctgga actgtggacg ttactgaaca
480

tccaaagtct attattgatg aaacatgctg gagtgacgtt gacttttgcc gtagagtcaa
540

aatgaccggt tggatgtatt ttgtttcaaa gaccctagca gagcag
586

<210> 183

<211> 586

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (2)..(2)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (11)..(11)

<223> Any nucleotide

<400> 183

gnagagaagt nacctggagt gaaaatatac atgggttctg aatcggaaat agtttgtgtt
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accggagctt caggtttcat cggttcgtgg cttgttatga gacttatgga gcgtggctac
120

actgttcgag ccaccgttcg tgaccagat aacatgaaga aggtgaagca ttgctggaa
180

ctgccgggtg caaaaagcaa attgtctctt tggaaggctg atcttgataa agaggggagt
240

ttgatgaag caattaaagg gtgcacagga gtttttcatg ttgctacacc aatggatttt
300

gagtccaagg accctgagaa tgaagtgata aagcctacaa taaacggatt aatagacata
360

201/390

ctgaaagcat gcgaaaaggc aaaaacagtt agaaaattgg ttttcacatc atcggctgga
420

actgtggacg ttactgaaca tccaaagtct attattgatg aaacatgctg gagtgacgtt
480

gacttttggc gtagagtcaa aatgaccggt tggatgtatt ttgtttcaaa gaccctagca
540

gagcaagaag cttggaagta ttcgaaagag cacaacatag actttg
586

<210> 184
<211> 570
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (10)..(11)
<223> Any nucleotides

<220>
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<222> (23)..(23)
<223> Any nucleotide

<400> 184
tactgaaagn ntgcgaaaag gcnaaaacag ttagaaaatt ggttttcaca tcatcggctg
60

gaactgtgga cgttactgaa catccaaagt ctattattga tgaaacatgc tggagtgcg
120

ttgacttttg ccgtagagtc aaaatgaccg gttggatgta ttttgtttca aagaccctag
180

cagagcaaga agcttgggaag tattcgaaaag agcacaacat agactttgtc tccatcattc
240

cacctcttgt tgttggcccc tttcttatgg cctcaatgcc acctagtcta atcactgctc
300

tttctcttat cacaggaaat gagggccatt actcaatcat aaagcaaggg caatacgtcc
360

atttagatga cctttgtctt gctcatatat ttctgtatga gaatccaaaa gctcaaggga
420

gatacatttg ctgttcacat gaagcaacca ttcatcaagt tgcaaaactt attaaagaaa
480

aatacccaga gttcaatgtc ccaacaaaaat tcaatgatat ccagatgaa ttggaaatta
540

ttaaattttc taaaaagaag atcacagact
570

<210> 185
<211> 833
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (3)..(3)
<223> Any nucleotide

<220>
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<222> (34)..(34)
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<400> 185
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60

acatcatggc tagtatcaaa caaattggaa acaagaaagc atgtgtgatt ggtggcactg
120

gttttggtgc atctatgttg atcaaacagt tacttgaaaa gggttatgct gttaatacta
180

ctgttagaga cccagatagt cctaagaaaa tatctcacct agtggcactg caaagtttgg
240

gggaactgaa tctatttaga gcagacttaa cagttgaaga agattttgat gctcctatag
300

caggatgtga gcttggtttt caacttgcta cacctgtgaa ctttgcttct caagatcctg
360

agaatgacat gataaagcca gcaatcaaag gtgtgttgaa tgtgttgaaa gcaagtgcaa
420

gagcaaaaaga agtcaaaaaga gttatcttaa catcttcggc agccgcggtg actataaatg
480

aactcaaagg gacaggtcat gttatggatg aaaccaactg gtcagatggt gaatttctga
540

acactgcaaa gccaccact tgggggttatc ctgcttcaaa aatgctagct gaaaaggctg
600

catggaaaatt tgctgaagaa aatgacattg atctaatac tgtgatacct agtttaacaa
660

ctggtccttc tctcacacca gatatcccat ctagtggttg cttggcaatg tctctaataa
720

caggcaatga tttcctcata aatgctctga aaggaatgca atttctgtcg ggttcgttat
780

ccatcactca tggtgaggat atttgocgag ctcatatatt tctggcagag aag
833

<210> 186
<211> 256
<212> PRT
<213> Trifolium repens

<400> 186

Met Ala Ser Ile Lys Gln Ile Gly Asn Lys Lys Ala Cys Val Ile Gly
1 5 10 15

Gly Thr Gly Phe Val Ala Ser Met Leu Ile Lys Gln Leu Leu Glu Lys
 20 25 30

Gly Tyr Ala Val Asn Thr Thr Val Arg Asp Pro Asp Ser Pro Lys Lys
 35 40 45

Ile Ser His Leu Val Ala Leu Gln Ser Leu Gly Glu Leu Asn Leu Phe
 50 55 60

Arg Ala Asp Leu Thr Val Glu Glu Asp Phe Asp Ala Pro Ile Ala Gly
 65 70 75 80

Cys Glu Leu Val Phe Gln Leu Ala Thr Pro Val Asn Phe Ala Ser Gln
 85 90 95

Asp Pro Glu Asn Asp Met Ile Lys Pro Ala Ile Lys Gly Val Leu Asn
 100 105 110

Val Leu Lys Ala Ser Ala Arg Ala Lys Glu Val Lys Arg Val Ile Leu
 115 120 125

Thr Ser Ser Ala Ala Ala Val Thr Ile Asn Glu Leu Lys Gly Thr Gly
 130 135 140

His Val Met Asp Glu Thr Asn Trp Ser Asp Val Glu Phe Leu Asn Thr
 145 150 155 160

Ala Lys Pro Pro Thr Trp Gly Tyr Pro Ala Ser Lys Met Leu Ala Glu
 165 170 175

Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Asp Ile Asp Leu Ile Thr
 180 185 190

Val Ile Pro Ser Leu Thr Thr Gly Pro Ser Leu Thr Pro Asp Ile Pro
 195 200 205

Ser Ser Val Gly Leu Ala Met Ser Leu Ile Thr Gly Asn Asp Phe Leu
 210 215 220

Ile Asn Ala Leu Lys Gly Met Gln Phe Leu Ser Gly Ser Leu Ser Ile
 225 230 235 240

Thr His Val Glu Asp Ile Cys Arg Ala His Ile Phe Leu Ala Glu Lys
 245 250 255

<210> 187
 <211> 576
 <212> DNA
 <213> Trifolium repens

<220>
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<223> Any nucleotide

<220>
<221> misc_feature
<222> (34)..(34)
<223> Any nucleotide

<400> 187
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acatcatggc tagtatcaaa caaattggaa acaagaaagc atgtgtgatt ggtggcactg
120
gttttgttgc atctatgttg atcaaacagt tacttgaaaa gggttatgct gttaatacta
180
ctgttagaga cccagatagt cctaagaaaa tatctcacct agtggcactg caagtttgg
240
gggaactgaa tctattttaga gcagacttaa cagttgaaga agattttgat gtcctatag
300
caggatgtga gcttggtttt caacttgcta cacctgtgaa ctttgcttct caagatcctg
360
agaatgacat gataaagcca gcaatcaaag gtgtgttgaa tgtgttgaaa gcaagtgcaa
420
gagcaaaaaga agtcaaaaaga gttatcttaa catcttcggc agccgcgggtg actataaatg
480
aactcaaagg gacaggtcat gttatggatg aaaccaactg gtcagatggt gaatttctga
540
acactgcaaa gccacccact tgggggttatc ctgctt
576

<210> 188
<211> 580
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (3)..(3)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (5)..(5)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (34)..(35)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (580)..(580)
<223> Any nucleotide

<400> 188
ggncntaaaa actgcactag tgtgtataag tttnttagtg aaaaaagagt gtgtaaatta
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acatcatggc tagtatcaaa caaattggaa acaagaaagc atgtgtgatt ggtggcactg
120
gttttggtgc atctatgttg atcaaacagt tacttgaaaa gggttatgct gttaatacta
180
ctgttagaga cccagatagt cctaagaaaa tatctcacct agtggcactg caaagtttgg
240
gggaactgaa tctatttaga gcagacttaa cagttgaaga agattttgat gtcctatag
300
caggatgtga gcttggtttt caacttgcta cacctgtgaa ctttgcttct caagatcctg
360
agaatgacat gataaagcca gcaatcaaag gtgtgttgaa tgtgttgaaa gcaagtgcaa
420
gagcaaaaaga agtcaaaaaga gttatcttaa catcttcggc agccgcggtg actataaatg
480
aactcaaagg gacaggtcat gttatggatg aaaccaactg gtcagatggt gaatttctga
540
acactgcaaa gccaccact tggggttatc ctgcttcaan
580

<210> 189
<211> 578
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (14)..(14)
<223> Any nucleotide

<220>
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<222> (29)..(30)
<223> Any nucleotides

<400> 189
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atggctagta tcaaacaaat tggaaacaag aaagcatgtg tgattgggtg cactgggttt
120
gttgcactta tgttgatcaa acagttactt gaaaagggtt atgctgttaa tactactgtt
180

agagacccag atagtcctaa gaaaatatct cacctagtgg cactgcaaag tttgggggaa
240

ctgaatctat ttagagcaga cttaacagtt gaagaagatt ttgatgctcc tatagcagga
300

tgtgagcttg tttttcaact tgctacacct gtgaactttg cttctcaaga tcctgagaat
360

gacatgataa agccagcaat caaaggtgtg ttgaatgtgt tgaaagcaag tgcaagagca
420

aaagaagtca aaagagttat cttaacatct tcggcagccg cggtgactat aaatgaactc
480

aaagggacag gtcatgttat ggatgaaacc aactggctcag atgttgaatt tctgaacact
540

gcaaagccac ccacttgggg ttatcctgct tcaaaaat
578

<210> 190

<211> 619

<212> DNA

<213> *Trifolium repens*

<400> 190

taaaaactgc actagtgtgt ataagtttct tggtgaaaaa agagtttgta aattaacatc
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atggctagta tcaaacaaat tggaaacaag aaagcatgtg tgattggtgg cactgggtttt
120

gttgcatcta tgttgatcaa gcagttactt gaaaagggtt atgctgttaa tactaccgtt
180

agagacccag atagccctaa gaaaatatct cacctagtgg cactgcaaag tttgggggaa
240

ctgaatctat ttagagcaga cttaacagtt gaagaagatt ttgatgctcc tatagcagga
300

tgtgaacttg tttttcaact tgctacacct gtgaactttg cttctcaaga tcctgagaat
360

gacatgataa agccagcaat caaaggtgtg ttgaatgtgt tgaaagcaat tgcaagagca
420

aaagaagtta aaagagttat cttaacatct tcggcagccg cggtgactat aaatgaactc
480

aaagggacag gtcatgttat ggatgaaacc aactggctctg atgttgaatt tctcaacact
540

gcaaaaccac ccacttgggg ttatcctgcc tcaaaaatgc tagctgaaaa ggctgcatgg
600

aaatttgctg aagaaaatg
619

<210> 191

<211> 619

<212> DNA

<213> Trifolium repens

<220>

<221> misc_feature

<222> (12)..(12)

<223> Any nucleotide

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<222> (14)..(14)

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<222> (45)..(45)

<223> Any nucleotide

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<221> misc_feature

<222> (53)..(53)

<223> Any nucleotide

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<222> (59)..(59)

<223> Any nucleotide

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<221> misc_feature

<222> (614)..(614)

<223> Any nucleotide

<400> 191

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60

tatcaaaciaa attggaaaca agaaagcatg tgtgattggt ggcactgggt ttgttgcac
120

tatgttgatc aagcagttac ttgaaaaggg ttatgctgtt aatactaccg ttagagaccc
180

agatagccct aagaaaatat ctcacctagt ggcactgcaa agtttggggg aactgaatct
240

atttagagca gacttaacag ttgaagaaga ttttgatgct cctatagcag gatgtgaact
300

tgtttttcaa cttgctacac ctgtgaactt tgcttctcaa gatcctgaga atgacatgat
360

aaagccagca atcaaagggtg tgttgaatgt gttgaaagca attgcaagag caaaagaagt
420

taaaagagtt atcttaacat cttcggcagc cgcggtgact ataaatgaac tcaaagggac
480

aggatcatgtt atggatgaaa ccaactggtc tgatgttgaa tttctcaaca ctgcaaaacc
540

accacttgg ggttatcctg cctcaaaaat gctagctgaa aaggctgcat ggaaatttgc
600

tgaagaaaat gacnttgat
619

<210> 192
<211> 586
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (2)..(2)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (4)..(4)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (23)..(23)
<223> Any nucleotide

<400> 192
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60

gcaggatgtg agcttggttt tcaacttgct acacctgtga cctttgcttc tcaagatcct
120

gagaatgaca tgataaagcc agcaatcaaa ggtgtgttga atgtgttgaa agcaagtgca
180

agagcaaaag aagtcaaaag agttatctta acatcttcgg cagccgcggt gactataaat
240

gaactcaaag ggacaggtca tggtatggat gaaaccaact ggtcagggtg tgaatttctg
300

aacactgcaa agccaccac ttgggggttat cctgcttcaa aaatgctagc tgaaaaggct
360

gcatggaaat ttgctgaaga aaatgacatt gatctaataca ctgtgatacc tagtttaaca
420

actggtcctt ctctcacacc agatatccca tctagtgttg gcttggcaat gtctctaata
480

acaggcaatg atttcctcat aaatgctctg aaaggaatgc aatttctgtc gggttcggtta
540

tccatcactc atggttgagga tatttgccga gctcatatat ttctgg
586

<210> 193
<211> 567
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (55)..(55)
<223> Any nucleotide

<400> 193
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60

gctacacctg tgacctttgc ttctcaagat cctgagaatg acatgataaa gccagcaatc
120

aaagggtgtg tgaatgtgtt gaaagcaagt gcaagagcaa aagaagtcaa aagagttatc
180

ttaacatctt cggcagccgc ggtgactata aatgaactca aagggacagg tcatgttatg
240

gatgaaacca actggtcaga tgttgaattt ctgaacactg caaagccacc cacttggggg
300

tattcctgctt caaaaatgct agctgaaaag gctgcatgga aatttgctga agaaaatgac
360

attgatctaa tcaactgtgat acctagttaa acaactgggc cttctctcac accagatatc
420

ccatctagtg ttggcttggc aatgtctcta ataacaggca atgatttcct cataaatgct
480

ctgaaaggaa tgcaatttct gtcggggttcg ttatccatca ctcatgttga ggatatttgc
540

cgagctcata tatttctggc agagaag
567

<210> 194
<211> 597
<212> DNA
<213> *Trifolium repens*

<400> 194
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60

aaagagatgg atgtcttggg tccacgtttt gatagcatat ttgaaaaaat gattggtgaa
120

cgtaagaaga aggaagtgga ggggaaagaa aatgaaagta aggattttct gcagtttttg
180

ttgaatttga aggatgaggg tgattctaag actccattca caattaccca tgttaaggct
240

ctactcatgg acatggttgt ggggtggatca gacacatcct ccaacacaat tgagtttgca
300

ttggcagaaa tgatgaacaa cccagaagta atgaggaagg ttcaagagga attagaagat
360

gtagttggga aagataactt agtagaagag tctcacattc ataagctacc ctacttgcat
420

210/390

gcagtgatga aagaaacact tcgtttacac ccagcacttc cacttttagt ccctcactgt
480

ccaagtga aa ccaccaatgt tggaggctac acaattccaa agggatctcg tgtgtttgtg
540

aacgtttggg ctattcatag agacccttcc atttgggaga aaccactaga atttgat
597

<210> 195

<211> 199

<212> PRT

<213> *Trifolium repens*

<400> 195

Gly Thr Asn Leu Ser Asp Phe Phe Pro Gly Leu Ala Arg Phe Asp Leu
1 5 10 15

Gln Gly Val Val Lys Glu Met Asp Val Leu Val Pro Arg Phe Asp Ser
20 25 30

Ile Phe Glu Lys Met Ile Gly Glu Arg Lys Lys Lys Glu Val Glu Gly
35 40 45

Lys Glu Asn Glu Ser Lys Asp Phe Leu Gln Phe Leu Leu Asn Leu Lys
50 55 60

Asp Glu Gly Asp Ser Lys Thr Pro Phe Thr Ile Thr His Val Lys Ala
65 70 75 80

Leu Leu Met Asp Met Val Val Gly Gly Ser Asp Thr Ser Ser Asn Thr
85 90 95

Ile Glu Phe Ala Leu Ala Glu Met Met Asn Asn Pro Glu Val Met Arg
100 105 110

Lys Val Gln Glu Glu Leu Glu Asp Val Val Gly Lys Asp Asn Leu Val
115 120 125

Glu Glu Ser His Ile His Lys Leu Pro Tyr Leu His Ala Val Met Lys
130 135 140

Glu Thr Leu Arg Leu His Pro Ala Leu Pro Leu Leu Val Pro His Cys
145 150 155 160

Pro Ser Glu Thr Thr Asn Val Gly Gly Tyr Thr Ile Pro Lys Gly Ser
165 170 175

Arg Val Phe Val Asn Val Trp Ala Ile His Arg Asp Pro Ser Ile Trp
180 185 190

Glu Lys Pro Leu Glu Phe Asp

195

<210> 196
<211> 700
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (2)..(2)
<223> Any nucleotide

<220>
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<222> (10)..(10)
<223> Any nucleotide

<220>
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<222> (22)..(22)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (698)..(698)
<223> Any nucleotide

<400> 196
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60

atcactcaat accaaacctt cctttacaaa gaactttcta tatccttttt cattttcttg
120

ataacccatt tcatcataag ttttctcttc aaaaaaaatc tcaaaaaact tccaccaggc
180

ccaaaaaggtt ttccagttgt tgggtgcactc ccactaatgg gatccatgcc tcatgttacc
240

ctattcaaaa tgtcacaaaa atatggtccc ataatgtacc taaaaatggg atcaaataac
300

atggtttag catcaactcc ttcttcagcc aaagcatttc tcaaaacact tgacctaaat
360

ttctccaata gaccgccgaa cgctggcgca actcacctag cttatgattc acaagacttg
420

gttttcgccg actatggatc taggtggaat ttacttagga aactaagtaa cttgcacatg
480

ctcggcgga aagccctcga aaattggtcg aaagtctgt agattgaaat gggtcacatg
540

attcgtacaa tgtacgattg tagcaagaaa gacgaatccg ttgttggtggc cgaaatgttg
600

acatatgcta tggccaatat gataggtcaa gttatattga gtctgcgcgt gttcgagaca
660

aaaggtagtg actcaaatga atttaaggat atgggttgntg
700

<210> 197
<211> 216
<212> PRT
<213> Trifolium repens

<220>
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<222> (216)..(216)
<223> Any amino acid

<400> 197

Met Val Met Ile Thr Gln Tyr Gln Thr Phe Leu Tyr Lys Glu Leu Ser
1 5 10 15

Ile Ser Phe Phe Ile Phe Leu Ile Thr His Phe Ile Ile Ser Phe Leu
20 25 30

Phe Lys Lys Asn Leu Lys Lys Leu Pro Pro Gly Pro Lys Gly Phe Pro
35 40 45

Val Val Gly Ala Leu Pro Leu Met Gly Ser Met Pro His Val Thr Leu
50 55 60

Phe Lys Met Ser Gln Lys Tyr Gly Pro Ile Met Tyr Leu Lys Met Gly
65 70 75 80

Ser Asn Asn Met Val Val Ala Ser Thr Pro Ser Ser Ala Lys Ala Phe
85 90 95

Leu Lys Thr Leu Asp Leu Asn Phe Ser Asn Arg Pro Pro Asn Ala Gly
100 105 110

Ala Thr His Leu Ala Tyr Asp Ser Gln Asp Leu Val Phe Ala Asp Tyr
115 120 125

Gly Ser Arg Trp Lys Leu Leu Arg Lys Leu Ser Asn Leu His Met Leu
130 135 140

Gly Gly Lys Ala Leu Glu Asn Trp Ser Lys Val Arg Glu Ile Glu Met
145 150 155 160

Gly His Met Ile Arg Thr Met Tyr Asp Cys Ser Lys Lys Asp Glu Ser
165 170 175

Val Val Val Ala Glu Met Leu Thr Tyr Ala Met Ala Asn Met Ile Gly
180 185 190

Gln Val Ile Leu Ser Arg Arg Val Phe Glu Thr Lys Gly Ser Asp Ser

195

200

205

Asn Glu Phe Lys Asp Met Val Xaa
210 215

<210> 198
<211> 584
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (2)..(2)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (10)..(10)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (27)..(27)
<223> Any nucleotide

<400> 198
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60
atcactcaat accaaacctt ccttttcaaa gaactttcta tctccttttt cattttcttg
120
ataacccggt tcatacataag ttttctcttc aaaaaaaatc tcaaaaaact tccaccaggc
180
ccaaagggtt ttccagttgt tgggtgcactc ccactaatgg gatccatgcc tcatgttacc
240
ctattcaaaa tgtcacaaaa atatgggtccc ataatgtacc taaaaatggg atcaaatagc
300
atggtttag catcaactcc ttcttcagcc aaagcatttc tcaaaacact tgacctaaat
360
ttctccaata gaccgccgaa cgctggcgcg actcacctag cttatgattc acaagacttg
420
gttttcgccg actatggatc taggtggaaa ttacttagga aactaagtaa cttgcacatg
480
ctcggcgga aagccctcga agattgggtcg aaagttcgtg agattgaaat gggtcacatg
540
attcgtacaa tgtatgattg tagcaagaaa gacgaatccg ttgt
584

<210> 199
<211> 694
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (2)..(2)
<223> Any nucleotide

<220>
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<222> (16)..(16)
<223> Any nucleotide

<220>
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<222> (20)..(21)
<223> Any nucleotides

<220>
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<222> (692)..(692)
<223> Any nucleotide

<400> 199
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60

caacaccaaaa ccttccttta caaagaactt tctatatacct ttttcatttt cttgataacc
120

catttcatca ttagttttct cttcaaaaaa aatctcaaaa aacttccacc aggcccaaaa
180

ggttttccag ttgttggtgc actccacta atgggatcca tgcctcatgt taccctattc
240

aaaatgtcac aaaaatatgg tcctataatg tacctaaaaa tgggatcaaa taacatggtt
300

gtagcatcaa ctctttcttc agccaaagca tttctcaaaa cacttgacct aaatttctcc
360

aataggccgg cgaacgctgg cgcaactcac ctagcttatg atccacaaga cttgggttttc
420

gccgactatg gatctagggtg gaaattactt aggaaactaa gtaacttgca catgctcggc
480

ggaaaagccc ttgaaaattg gtcgaaagtt cgtgagattg aaatgggtca catgattcgt
540

acaatgtacg attgtagcaa gaaagacgaa tccgttggtg tggccgaaat gttgacatat
600

gctatggcca atatgatagg tcaagttata ttgagtcgtc gcgtgttcga gacaaaagggt
660

agtgactcaa atgaatttaa ggatatgggtt gntg
694

<210> 200
<211> 580
<212> DNA

<213> Trifolium repens

<220>

<221> misc_feature

<222> (2)..(2)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (14)..(14)

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<222> (44)..(44)

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<221> misc_feature

<222> (55)..(56)

<223> Any nucleotides

<400> 200

cnaatctctt gaantnatac catttcttta caagaactta accntgggtga tgatnnctca
60

ataccaaacc ttccttttca aagaactttc tatctccttt ttcattttct tgataaccgg
120

tttcatcata agtcttctct tcaaaaaaaaa tctcaaaaaa cttccaccag gcccaaaggg
180

ttttccagtt gttgggtgcac tcccactaat gggatccatg cctcatgtta cctattcaa
240

aatgtcacia aaatatgggc ccataatgta cctaaaaatg ggatcaaata acatggttgt
300

agcatcaact ccttcttcag ccaaagcatt tctcaaaaaca cttgacctaa atttctccaa
360

tagaccgccg aacgotggcg cgactcacct agcttatgat tcacaagact tggttttcgc
420

cgactatgga tctaggtgga aattgcttag gaaactaagt aacttgcaca tgctcggcgg
480

aaaagccctc gaagattggc cgaaagtgcg cgagattgag atgggtcaca tgattcgtac
540

aatgtacgat tgtagcaaga aagacgaata tgttgttgtg
580

<210> 201

<211> 574

<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (8)..(8)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (12)..(12)
<223> Any nucleotide

<220>
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<222> (40)..(40)
<223> Any nucleotide

<220>
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<222> (51)..(52)
<223> Any nucleotides

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<222> (56)..(56)
<223> Any nucleotide

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<222> (569)..(569)
<223> Any nucleotide

<220>
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<222> (572)..(572)
<223> Any nucleotide

<400> 201
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60

caaaccttcc tttaaaaga actttctata tcctttttca ttttcttgat aaccatttc
120

atcattagtt ttctcttcaa aaaaaatctc aaaaaacttc caccaggccc aaaaggtttt
180

ccagttgttg gtgcactccc actaatggga tccatgcctc atgttacctt attcaaaatg
240

tcacaaaaat atggtcctat aatgtaccta aaaatgggat caaataacat ggttgtagca
300

tcaactcctt cttcagccaa agcattttctc aaaacacttg acctaaattt ctccaatagg
360

ccggcggaacg ctggcgcaac tcacctagct tatgattcac aagacttggt tttcgccgac
420

tatggatcta ggtggaaatt acttaggaaa ctaagtaact tgcacatgct cggcggaaaa
480

gcccttgaaa attggtcgaa agttcgtgag attgaaatgg gtcacatgat tcgtacaatg
540

tacgattgta gcaagaaaga cgaatccgnt gntg
574

<210> 202
<211> 1261
<212> DNA
<213> *Trifolium repens*

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120

agttatctct cacaacaaaa cactcttgag tcaagtttcg ttagggaaga agatgagcgt
180

ccaaaagttg cctacaataa cttcagcaac gagattccaa tcatttctct tgctggaatt
240

gatgagggtg atggtcgtag aacagagata tgtaacaaga ttgttgaagc ttgtgagaat

300

tggggtatatt ttcagggttgt tgatcatggg gttgatacaa aacttgtttc tgagatgacc
360

cgttttgcta gagagttttt tgctttgcc cgggaagaga agctccgggt tgacatgtcc
420

ggtggtaaaa aggggtgggtt cattgtctct agtcatctcc aaggagaagc agtgaaggat
480

tggagagagc tagtgacata tttttcatac ccaattaaac aaagagatta ttcaagggtg
540

ccagacaagc cagaaggatg gaaagaggta acagaaaaat acagtgaaaa cctaataaat
600

ttagcttgca aactattgga agttttatca gaagcaatgg gtttagaaaa agaagctcta
660

acaaaagcat gtgttgatat ggatcaaaaa gttgttataa attattaccc aaaatgcctt
720

gaacctgacc tcacacttgg ccttaaactg cacactgacc ctggcacaat tactcttttg
780

cttcaagatc aagttgggtg ccttcaagct accaaagata atggtaagac gtggattaca
840

gttcaaccag ttgaagggtg ttttggtgtt aatcttggag accatgggtca ctatctaagt
900

aatggacggg tcaaaaatgc tgaccaccaa gcagtgggtg attcgaacta cagccgntta
960

tcaatagcaa cattttcaaaa tccagctccc gatgcaactg tatacccttt gaagattaga
1020

gagggtgaaa aatctgtgtt ggaagaacca atcacttttg ctgaaatgta tagaaggaag
1080

atgaccaaag accttgaaat tgctaggatg aagaagttgg ctaaggaaca acaacttagg
1140

gacttggagg agaacaagac taaatatgag gccaaacctt tgaatgagat ctttgcttaa
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 35 40 45
 Glu Val Asp Gly Arg Arg Thr Glu Ile Cys Asn Lys Ile Val Glu Ala
 50 55 60
 Cys Glu Asn Trp Gly Ile Phe Gln Val Val Asp His Gly Val Asp Thr
 65 70 75 80
 Lys Leu Val Ser Glu Met Thr Arg Phe Ala Arg Glu Phe Phe Ala Leu
 85 90 95
 Pro Pro Glu Glu Lys Leu Arg Phe Asp Met Ser Gly Gly Lys Lys Gly
 100 105 110
 Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Ala Val Lys Asp Trp
 115 120 125
 Arg Glu Leu Val Thr Tyr Phe Ser Tyr Pro Ile Lys Gln Arg Asp Tyr
 130 135 140
 Ser Arg Trp Pro Asp Lys Pro Glu Gly Trp Lys Glu Val Thr Glu Lys
 145 150 155 160
 Tyr Ser Glu Asn Leu Met Asn Leu Ala Cys Lys Leu Leu Glu Val Leu
 165 170 175
 Ser Glu Ala Met Gly Leu Glu Lys Glu Ala Leu Thr Lys Ala Cys Val
 180 185 190
 Asp Met Asp Gln Lys Val Val Ile Asn Tyr Tyr Pro Lys Cys Pro Glu
 195 200 205
 Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp Pro Gly Thr Ile
 210 215 220
 Thr Leu Leu Leu Gln Asp Gln Val Gly Gly Leu Gln Ala Thr Lys Asp
 225 230 235 240
 Asn Gly Lys Thr Trp Ile Thr Val Gln Pro Val Glu Gly Ala Phe Val
 245 250 255
 Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn Gly Arg Phe Lys

220/390

260 265 270

Asn Ala Asp His Gln Ala Val Val Asn Ser Asn Tyr Ser Xaa Leu Ser
275 280 285

Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Thr Val Tyr Pro Leu
290 295 300

Lys Ile Arg Glu Gly Glu Lys Ser Val Leu Glu Glu Pro Ile Thr Phe
305 310 315 320

Ala Glu Met Tyr Arg Arg Lys Met Thr Lys Asp Leu Glu Ile Ala Arg
325 330 335

Met Lys Lys Leu Ala Lys Glu Gln Gln Leu Arg Asp Leu Glu Glu Asn
340 345 350

Lys Thr Lys Tyr Glu Ala Lys Pro Leu Asn Glu Ile Phe Ala
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180
ttgcctacaa taacttcagc aacgagattc caatcatttc tcttgctgga attgatgagg
240
ttgatggtcg tagaacagag atatgtaaca agattgttga agcttgtag aattggggta
300
tttttcaggt tgttgatcat ggtgttgata caaaacttgt ttctgagatg acccgttttg
360
ctagagagtt ttttgctttg ccaccggaag agaagctccg gtttgacatg tccggtggta
420
aaaagggtgg tttcattgtc tctagtcatc ttcaaggaga agcagtgaag gattggagag
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120

acaaaagact cttgagtcaa gtttcggttag ggaagaagat gagcgtccaa aagttgccta
180

caataacttc agcaacgaga ttccaatcat ttctcttgct ggaattgatg aggttgatgg
240

tcgcagaaca gagatatgta acaagattgt tgaagcttgt gagaattggg gtatTTTTTca
300

ggttggtgat catggtggtg atacaaagct tgtttctgag atgactcggt ttgctagaga
360

gttttttgcT ttgccgccgg aagagaagct ccggtttgac atgtccggtg gtaaaaaggg
420

tggtttcatt gtctctagtc atctccaagg agaagcagtg aaagattgga gagagctagt
480

gacatatttt tcatacccaa ttaaacaag agattattca aggtggccag acaagccaga
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180

caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt gctggaattg
240

atgaggttga tggtcgtaga acagagatat gtaacaagat tggtgaagct tgtgagaatt
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gggggtatatt tcaggttggt gatcatgggtg ttgatacaaa acttggttct gagatgacct
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gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt gacatgtccc
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gtggtaaaaa ggggtggtttc attgtctcta gtcattctca aggagaagca gtgaaggatt
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ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaagggtggc

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ttatctctca caacaaaaca ctctcgagtc aagtttcgtt aggaagaag atgagcgtcc
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aaaagttgcc tacaataact tcagcaacga gattccaatc atttctcttg ctggaattga
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tgaggttgat ggtcgtagaa cagagatatg taacaagatt gttgaagctt gtgagaattg
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ttttgctaga gagttttttg ctttgccacc ggaagagaag ctccggtttg acatgtccgg
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aggggaagaag atgagcgtcc aaaagttgcc tacaataact tcagcaacga gattccaatc
180

atttctcttg ctggaattga tgaggttgat ggtcgtagaa cagagatatg taacaagatt
240

gttgaagctt gtgagaattg gggatatttt caggttgttg atcatggtgt tgatacaaaa
300

cttgtttctg agatgaccgg ttttgctaga gagttttttg ctttgccacc ggaagagaag
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ctccggtttg acatgtccgg tggtaaaaag ggtggtttca ttgtctctag tcatctccaa
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ggagaagcag tgaaggattg gagagagcta gtgacatatt tttcataccc aattaaacaa
480

agagattatt caaggtggcc agacaagcca gaaggatgga aagaggtaac agaaaaatac
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agtgaaaacc taatgaattt agcttgcaaa ctattggaag ttttatcaga agcaatgggt
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aagatgagcg tccaaaagtt gcctacaata acttcagcaa cgagattcca atcatttctc
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ttgctggaat tgatgagggt gatggtcgta gaacagagat atgtaacaag attggtgaag
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cttgtgagaa ttgggggtatt tttcagggtg ttgatcatgg tgttgatata aaacttgttt
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ctgagatgac ccgttttgct agagagtttt ttgctttgcc accggaagag aagctccggt
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ttgacatgtc cggtggtaaa aagggtgggt tcattgtctc tagtcatctc caaggagaag
420
cagtgaagga ttggagagag ctagtgacat atttttcata cccaattaaa caaagagatt
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120
agaagatgag cgtccaaaag ttgcctacaa taacttcagc aacgagatcc caatcatttc
180
tcttgctgga attgatgagg ttgatggctg tagaacagag atatgtaaca agattggtga
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ttctgagatg acccgttttg ctagagagtt ttttgctttg ccaccggaag agaagctccg
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gtttgacatg tccggtggta aaaaggggtg tttcattgtc tctagtcac tcgaaggaga
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ttattcaagg tggccagaca agccagaagg atggaaagag gtaacagaaa aatacagtga
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aaacctaattg aatttagctt gcaaactatt ggaagnttta tcagaagcaa tgggtttaga
600
aaaagaagct ctaacaaang catgtgttga tatggatcaa aaagttgtta taaattatta
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240

gcttgatgaga attgggggtat ttttcagggt gttgatcatg gtgttgatac aaaacttggt
300

tctgagatga cccgttttgc tagagagttt tttgctttgc caccggaaga gaagctccgg
360

tttgacatgt ccggtggtaa aaaggggtgt ttcattgtct ctagtcatct ccaaggagaa
420

gcagtgaagg attggagaga gctagtgaca tattttttcat acccaattaa acaaagagat
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tattcaaggt ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtgaa
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aacctaataa atttagcttg caaactattg gaagttttat cagaagcaat gggtttagaa
600

aaagaagctc taacaaaagc atgtgttgat atggatcaaa aagttgttat aaattattac
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120

agatgaccgt ccaaaagttg cctacaatac cttcagcacc gagattccaa tcntttctct
180

tgctggaatt gatgaggttg atggccgaaa aacanaaatn ttaccaaga ttggnggggc
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ttgtnaaaat tggggtnntt ttcaggttgg tgatcatggg gtnnaacaaa acttgtttcc
300

canaaanccc nttttgntaa anagtttttt gcttttcccc cggaanaaaa cctccggttt
360

nacttnnccg ggggnaaaaa aggggggggt ttnattngnc nttaagnccc ncccaaggg
420

anaancccan nnaaggnttt ggaananncn nnn
453

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120
agaagatgag cgtccaaaag ttgcctacaa taacttcagc aacgagattc caatcatttc
180
tcttgctgga attgatgagg ttgatggncn cacancacac atctgnncca nattgctgga
240
acctngcgan agncgcoctn cctcncn
267

<210> 214
<211> 580
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120

gagcgtccaa aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct
180

ggaattgatg aggttgatgg tcgtagaaca gagatatgta acaagattgt tgaagcttgt
240

gagaattggg gtatTTTTtca gggtgttgat catgggtgtg atacaaaact tgtttctgag
300

atgacccgtt ttgctagaga gttttttgct ttgccaccgg aagagaagct ccggtttgac
360

atgtccggtg gtaaaaaggg tggtttcatt gtctctagtc atcttcaagg agaagcagtg
420

aaggattgga gagagctagt gacatatTTT tcatacccaa ttaaacaag agattattca
480

aggTggccag acaagccaga aggatggaaa gaggtaacag aaaaatacag tgaaaaccta
540

atgaatttag cttgcaagct attggaagtt ttatcagaag
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120

aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct ggaattgatg
180

aggttgatgg tcgcagaaca gagatatgta acaagattgt tgaagcttgt gagaattggg
240

gtatTTTTtca gggtgttgat catgggtgtg atacaaagct tgtttctgag atgactcgtt
300

ttgctagaga gttttttgct ttgccgccgg aagagaagct ccggtttgac atgtccggtg

360

gtaaaaaggg tggtttcatt gtctctagtc atctccaagg agaagcagtg aaagattgga
420

gggagctagt gacatatattt tcatacccaa ttaaacaag agattattca aggtggccag
480

acaagccaga aggatggaaa gaagtaacag aaaaatacag tgaaaaccta atgaatttag
540

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120

gcgtccaaaa gttgcctaca ataacttcag caacgagatt ccaatcattt ctcttgctgg
180

aattgatgag gttgatgggc gtagaacaga gatatgtaac aagattggtg aagcttgtga
240

gaattggggg atttttcagg ttgttgatca tgggtgtgat acaaaaacttg tttctgagat
300

gacccgtttt gctagagagt tttttgcttt gccaccggaa gagaagctcc ggtttgacat
360

gtncggtggg aaaaagggtg gtttcattgn ctctagtcac ctncaggan aagcannгаа
420

ngattggaga gagctngnga catatTTTTn
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<210> 217
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<222> (644)..(644)

<223> Any nucleotide

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120

gatgagcgtc caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt
180

gctggaattg atgaggttga tggtcgtaga acagagatat gtaacaagat tgttgaagct
240

tgtgagaatt ggggtatfff tcagggttgt gatcatggtg ttgatacaaa acttgtttct
300

gagatgaccc gttttgctag agagttffff gctttgccac cggaagagaa gctccggttt
360

gacatgtccg gtggtaaaaa ggggtggtttc attgtctcta gtcattctca aggagaagca
420

gtgaaggatt ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat
480

tcaagggtggc cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaaaac
540

ctaataaatt tagcttgcaa actattggaa gttttatcag aagcaatggg tttagaaaaa
600

gaagctctaa caaaagcatg tgttgatatg gatcaaaaag ttgntataaa ttattaccca
660

aaatgccctg aacctgacct c
681

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120
aagatgagcg tccaaaagtt gcctacaata acttcagcaa cgagattcca atcatttctc
180
ttgctggaat tgatgagggt gatggtcgaa gaacagagat atgtaacaag attggtgaag
240
cttgtgagaa ttgggggtatt tttcagggtg ttgatcatgg tgttgatata aaacttgttt
300
ctgagatgac ccgttttgct agagagtttt ttgctttgcc accggaagag aagctccggt
360
ttgacatgtc cggtggtaaa aagggtgggt tcattgtctc tagtcatctc caaggagaag
420
cagtgaagga ttggagagag ctagtgacat atttttcata cccaattaaa caaagagatt
480
attcaagggtg gccagacaag ccagaaggat ggaaagaggt aacagaaaaa tacagtgaag

540

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582

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120

tgagcgtcca aaagttgcct acaataactt cagcaacgag attccaatca tttctcttgc
180

tggaattgat gaggttgatg gtcgtagaac agagatatgt aacaagattg ttgaagcttg
240

tgagaattgg ggtatTTTTT aggttggtga tcatgggtgt gatacaaaac ttgtttctga
300

gatgaccggt tttgctagag agttttttgc ttgcccaccg gaagagaagc tccggtttga
360

catgtccggt ggtaaaaagg gtggtttcat tgtctctagt catctccaag gagaagcagt
420

gaaggattgg agagagctag tgacatattt ttcataccca attaaacaaa gagattattc
480

aagggtggcca gacaagccag aaggatggaa agaggtaaca gaaaaataca gtgaaaacct
540

aatgaattta gcttgcaagc tattggaagt tttatcagaa gcaatgggtt tagaaaaaga
600

agctctaaca
610

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120

gatgagcgtc caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt
180

gctggaattg atgaggttga tggtcgtaga acagagatat gtaacaagat tgttgaagct
240

tgtgagaatt ggggtatttt tcagggtgtt gatcatggtg ttgatacaaa acttgtttct
300

gagatgaccc gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt
360

gacatgtccg gtggtaaaaa ggggtggttc attgtctcta gtcattcttca aggagaagca
420

gtgaaggatt ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat
480

tcaaggtggc cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaaaac
540

ctaatagaatt tagcttgcaa gctattggaa gttttatcag aagcaatggg ttn
593

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<213> Trifolium repens

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aaactctaag ttatctctca caacaaaaca ctctcgagtc aagtttcggt agggaagaag
120

atgagcgctcc aaaagttgcc tacaataact tcagcaacga gattccaatc atttctcttg
180

ctggaattga tgaggttgat ggnnnnnggna ccngggnatg tggnnagagg acgnnn
236

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120

ccaaaagttg cctacaataa cttcagcaac nagattccaa tcattttctct tgctggaatt
180

gatgaggttg atggtcgnag aacanagata tgtaacaaga ttgttgaagc ttgtgagaat
240

tgggggtattt ttcangttgt tgatcatggn gtn
273

<210> 223
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120

gagcgtccaa aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct
180

ggaattgatg aggttgatgg tcgcagaaca gagatatgta acaagattgt tgaagcttgt
240

gagaattggg gtatTTTTca ggTTgTTgat catggTgTTg atacaaagct tgtttctgag
300

atgactcgTT ttgctagaga gttttttgct ttgccgccgg aagagaagct ccggTTtgac
360

atgtccggtg gtaaaaaggg tggTTTcatt gtctctagtc atctccaagg agaagcagtg
420

aaagattgga gagagctagt gacatTTTT tcataccCAA ttaaacaag agattattca
480

aggTggccag acaagccaga aggatggaaa gaagtaacag aaaaatacag tgaaaacct
540

atgaatttag cttgcaagct attggaagtt tt
572

<210> 224

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120

gagcgtccaa aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct
180

ggaattgatg aggttgatgg tcgtagaaca gagatatgta acaagattgt tgaagcttgt
240

gagaattggg gtatTTTTca ggTTgttgat catggTgttg atacaaaact tgTTTTctgag
300

atgacccggtt ttgctagaga gTTTTttgct ttgccaccgg aagagaagct ccggtttgac
360

atgtccggtg gtaaaaaggg tggTTtcatt gtctctagtc atctccaagg agaagcagtg

420

aaggattgga gagagctagt gacatatattt tcatacccaa ttaaacaag agattattca
480

agggtggccag acaagccaga aggatggaaa gaggtaacag aaaaatacag tgaaaaccta
540

atgaatttag cttgcaaact attggaagtt ttatc
575

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120

gtccaaaagt tgctacaat aacttcagca acgagattcc aatcatttct cttgctggaa
180

ttgatgaggt tgatggtcgt agaacagaga tatgtaacaa gattgttgaa gcttgatgaga
240

attggggtat ttttcagggt gttgatcatg gtgttgatac aaaacttggt tctgagatga
300

cccgttttgc tagagagttt tttgctttgc caccggaaga gaagctccgg tttgacatgt
360

ccggtggtaa aaagggtggt ttcattgtct ctagtcatct ccaaggagaa gcagtgaagg
420

attggagaga gctagtgaca tatttttcat acccaattaa acaaagagat tattcaaggt
480

ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtga aacctaatga
540

atttagcttg caaactattg gaagttttat cagaagcaat gggtttagaa aaagag
596

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120

caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt gctggaattg
180

atgagggtga tggtcgtaga acagagatat gtaacaagat tgttgaagct tgtgagaatt
240

gggggtatatt tcagggtggt gatcatgggt ttgatacaaa acttgtttct gagatgaccc
300

gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt gacatgtccg
360

gtggtaaaaa ggggtggttc attgtctcta gtcattctca aggagaagca gtgaaggatt
420

ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaagggtggc
480

cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaaaac ctaatgaatt
540

tagcttgcaa actattggaa gttttatcag aagcaatggg tttagaaaaa gaagctctaa
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caaaagcatg tg
612

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120
aaagttgcct acaataactt cagcaacgag attccaatca tttctcttgc tgggaattgat
180
gaggttgatg gtcgtagaac agagatatgt aacaagattg ttgaagcttg tgagaattgg
240
ggtatttttc aggttggtga tcatgggtgtt gatacaaaac ttgtttctga gatgaccogt
300
tttgctagag agttttttgc tttgccaccg gaagagaagc tccggtttga catgtccggt
360
ggtaaaaagg gtggtttcat tgtctctagt catctccaag gagaagcagt gaaggattgg
420
agagagctag tgacatattt ttcataccca attaaacaaa gagattattc aaggtggcca
480
gacaagccag aaggatggaa agaggtaaca gaaaaatata gtgaaaacct aatgc
535

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<222> (33)..(33)
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<222> (559)..(559)
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<400> 228
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251/390

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120
aaaagttgcc tacaataact tcagcaacga gattccaatc atttctcttg ctggaattga
180
tgaggttgat ggtcgtagaa cagagatatg taacaagatt gttgaagctt gtgagaattg
240
gggtatTTTT caggttgttg atcatggtgt tgatacaaaa cttgtttctg agatgacccg
300
ttttgctaga gagttttttg ctttgccacc ggaagagaag ctccggtttg acatgtccgg
360
tggtaaaaag ggtggtttca ttgtctctag tcatctccaa ggagaagcag tgaaggattg
420
gagagagcta gtgacatatt tttcatacc aattaaaca agagattatt caaggtggcc
480
agacaagcca gaaggatgga aagaggtaac agaaaaatac agtgaaaacc taatgaattt
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559

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120
caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt gctggaattg
180
atgaggttga tggtcgcaga acagagatat gtaacaagat tgttgaagct tgtgagaatt
240
ggggatTTTT tcaggttgtt gatcatggtg ttgatacaaa gcttgtttct gagatgactc
300
gttttgctag agagtttttt gctttgccgc cggaagagaa gctccggttt gacatgtccg
360
gtggtaaaaa ggggtggttc attgtctcta gtcattctca aggagaagca gtgaaagatt
420
ggagagagct agtgacatat tttcatacc caattaaaca aagagattat tcaaggtggc
480
cagacaagcc agaaggatgg aaagaagtaa cagaaaaata cagtgaaaac ctaatgaatt
540

tagcttgcaa gctattggaa gtttt
565

<210> 230
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120

gtccaaaagt tgccataaat aacttcagca acgagattcc aatcatttct cttgctggaa

180

ttgatgaggt tgatggtcga agaacagaga tatgtaacaa gattgttgaa gcttgtgaga
240

attgggggtat ttttcagggtt gttgatcatg gtgttgatac aaaacttggt tctgagatga
300

cccgttttgc tagagagttt tttgctttgc caccggaaga gaagctccgg tttgacatgt
360

ccgggtggtaa aaaggggtggt ttcattgtct ctagtcatct ccaaggagaa gcagtgaagg
420

attggagaga gctagtgaca tatttttcat acccaattaa acaaagagat tattcaaggt
480

ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtga aacctaatga
540

atntagcttg caaactattg gaagttttat cagaagcaat gggtttagaa n
591

<210> 231
<211> 609
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<400> 231

254/390

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gtacancaaa caccanaaac gagnccgttt cctnntcnaa catggcacca agccaaactc
120

tacaaaaagt tgcctacaat aacttcagca acgagattcc aatcatttct cttgctggaa
180

ttgatgaggt tgatggtcgt agaacagaga tatgtaacaa gattgttgaa gcttgtgaga
240

attgggggtat ttttcaggtt gttgatcatg gtgttgatac aaaacttggt tctgagatga
300

cccgttttgc tagagagttt tttgctttgc caccggaaga gaagctccgg tttgacatgt
360

ccggtggtaa aaaggggtgtt ttcattgtct ctagtcatct tcaaggagaa gcagtgaagg
420

attggagaga gctagtgaca tattttttcat acccaattaa acaaagagat tattcaaggt
480

ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtga aacctaataga
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atntagcttg caagctattg gaagttttat cagaagcaat gggtttagaa aaagaagctc
600

taacaaaag
609

<210> 232
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<223> Any nucleotide

<400> 232

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tccaacaaaa cactctcgag tcaagtttcg ttagggaaga agatgagcgt ccaaaagttg
120

cctacaataa cttcagcaac gagattccaa tcattttctct tgctggaatt gatgaggttg
180

atggtcgtag aacagagata tgtaacaaga ttggtgaagc ttgtgagaat tggggatattt
240

ttcaggttgt tgatcatggt gttgatacaa aacttgtttc tgagatgacc cgttttgcta
300

gagagttttt tgctttgcc aagggaagaga agctccgggt tgacatgtcc ggtggtaaaa
360

aggggtgggtt cattgtctct agtcatctcc aaggagaagc agtgaaggat tggagagagc
420

tagtgacata tttttcatat ccaattaaac aaagagatta ttcaagggtg ccagacaagc
480

cagaaggatg gaaagaggta acagaaaaat acagtgaaaa cctaataaat ttagcttgca
540

agctattgga agttttatca gaagcaatgg gtttagaaaa agaagctcta acaaaaag
597

<210> 233

<211> 418

<212> DNA

<213> *Trifolium repens*

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tctctcacia caaaacactc ttgagtcaag tttcgttagg gaagaagatg agcgtccaaa
120

agttgcctac aataacttca gcaacgagat tccaatcatt tctcttgctg gaattgatga
180

ggttgatggt cgtagaacag agatatgtaa caagattggt gaagcttgctg agaattgggg
240

tatttttcag gttgttgatc atggtgttga tacaaaactt gtttctgaga tgaccogttt

300

tgctagagag ttttttgctt tgccaccgga agagaagctc cggtttgaca tgtncggtgg
360

naaaaaggnt ggctccantg cctgtancca tctccaagga gaaccacccn angantgn
418

<210> 234

<211> 570

<212> DNA

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<222> (31)..(32)

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<400> 234

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60

gttatctctc acaacaaaac actcttgagt caagtttcgt tagggaagaa gatgagcgtc
120

caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt gctggaattg
180

atgaggttga tggctcgtaga acagagatat gtaacaagat tggtgaagct tgtgagaatt
240

gggggtatatt tcagggtgtt gatcatgggtg ttgatacaaa acttgtttct gagatgaccc
300

gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt gacatgtccg
360

gtggtaaaaa ggggtggtttc attgtctcta gtcattctcca aggagaagca gtgaaggatt
420

ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaagggtggc
480

cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaaaac ctaatgaatt
540

tagcttgcaa actattggaa gttttatcag
570

<210> 235

<211> 608

<212> DNA
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120
aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct ggaattgatg
180
aggttgatgg tcgtagaaca gagatatgta acaagattgt tgaagcttgt gagaattggg
240
gtatTTTTca ggTtgTtgat catggTgTtg atacaaaact tgtttctgag atgaccgTt
300
ttgctagaga gttttttgct ttgccaccgg aagagaagct ccggtttgac atgtccggtg
360
gtaaaaaggg tggtttcatt gtctctagtc atctccaagg agaagcagtg aaggattgga
420
gagagctagt gacatatTTT tcataccCAA ttaaataaag agattattca aggtggccag
480
acaagccaga aggatggaaa gaggtaacag aaaaatacag tgaaaaccta atgaatttag
540
cttgcaaact attggaagtt ttatcagaag caatgggTtt agaaaaagaa gctctaacaa
600
aagcatgt
608

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<211> 602
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<400> 236
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ctcacacaaa aaaaccgtcg agtcaagttt cgttagggaa gaagatgagc gtccaaaagt
120
tgccatacaat aacttcagca acgagattcc aatcatttct cttgctggaa ttgatgaggt
180
tgatgggtcgc agaacagaga tatgtaacaa gattgttgaa gcttgtgaga attgggggtat
240
ttttcagggtt gttgatcatg gtgttgatac aaagcttggt tctgagatga ctcgttttgc
300
tagagagttt tttgctttgc cgccggaaga gaagctccgg tttgacatgt ccggtggtaa
360
aaagggtggt ttcattgtct ctagtcgtct ccaaggagaa gcagtgaaag attggagaga
420
gctagtgaca tattttttcat acccaattaa acaaagagat tattcaaggt ggccagacaa
480
gccagaagga tggaaagaag taacanaaaa atacagtga aacctaata atttancttg
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600

nt

602

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120
ctacaataac ttcagcaacg agattccaat cattnctctt gctggaattg atgaggttga
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tggtcgcaga acagagatat gtaacaagat tgttgaagct tgtgagaatt ggggtatctt
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tcaggttggt gatcatgggtg ttgatacaaa ncttgtttct gagatgaccc gttttgctag
300
agagtttttt gctntgccac cggaagagaa gtcctgggtt gacatgtccg gtggtaaaaa
360
gggtgggttc attgtctcta gtcactnca agganaagca ntgaaggatt ggagagagct
420
agtgacatat ttttcatacc caattaaaca aagagattat tcaagggtggc cagacaagcc
480
agaaggatgg aaagaggtna cagaaaaata cagcgaaaac ctaatgaatt tanctn
536

<210> 238
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<212> DNA
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ctctcacacac aaaagactct tgagtcnagt ttcggttaggg aagaagatga gcgtccacaaa
120

gttgcttaca ataacttcag caacgagatt ccaatcattt ctcttgctgg aattgatgag
180

gttgatgggtc gcagaacaga gatatgtaac aagattggtg aagcttgtga gaattgggggt
240

atttttcagg ttgttgatca tgggtgttgat acaaagcttg tttctgagat gactcgtttt
300

gctagagagt tttttgcttt gccgccggaa gagaagctcc ggtttgacat gtccgggtggt
360

aaaaaggggtg gtttcattgt ctctagtcac ctccaaggag aagcagtga agattggagg
420

gagctagtga catatttttc ataccacatt aaacaaagag attattcaag gtggccagac
480

aagccagaag gatggaaaga agtaacagaa aaatacagtg aaaacctaata gaatttagct
540

tgcaagctat tggaagtttt atcagaagca at
572

<210> 239

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tctcncaaca aaacactctc gagtcaagtt tcggttaggga agaagatgag cgtccaaaag
120

ttgcctacaa taacttcagc aacgagattc caatcatttc tcttgctgga attgatgagg
180

ttgatgggtcg aagaacagag atatgtaaca agattgttga agcttgtgag aattggggta
240

tttttcaggt tggtgatcat ggtgttgata caaaacttgt ttctgagatg acccgttttg

300

ctagagagtt ttttgctttg ccaccggaag agaagctccg gtttgacatg tccgggtgta
360

aaaaggggtgg tttcattgtc tctagtcac tc caaggaga agcagtgaag gattggagag
420

agctagtgaac atatTTTTTca tacccaatta aacaaagaga ttattcaagg tggccagaca
480

agccagaagg atggaaagag gtaacagaaa aatacagtga aaacctaatg aatttagctt
540

gcaaactatt ggaagtttta tcagaagcaa tgg
573

<210> 240
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<212> DNA
<213> *Trifolium repens*

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ctcacaacaa aagactcttg agtcaagttt cgttagggaa gaagatgagc gtccaaaagt
120

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tgccataaat aacttcagca acgagattcc aatcatttct cttgctggaa ttgatgaggt
180

tgatgggtcgc agaacagaga tatgtaacaa gattgttgaa gcttgtgaga attgggggtat
240

ttttcaggtt gttgatcatg gtgttgatac aaagcttggt tctgagatga ctcgttttgc
300

tagagagttt tttgctttgc cgccggaaga gaagctccgg tttgacatgt ccggtggtaa
360

aaagggtggt ttcattgtct ctagtcatct ccaaggagaa gcagtgaaag attggagggga
420

gctagtgaca tattttttcat acccaattaa acaaagagat tattcaaggt ggccagacaa
480

gccagaagga tggaaagaag taacagaaaa atacagtga aacctaata atttagcttg
540

caagctattg gaagttttat cagaagcaat ggg
573

<210> 241
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120
tgcctacaat aacttcagca acgagattcc aatcatttct cttgctggaa ttgatgaggt
180
tgatggtcgc agaacagaga tatgtaacaa gattgttgaa gcttgtgaga attggggtat
240
ttttcaggtt gttgatcatg gtgttgatac aaagcttggt tctgagatga ctcgttttgc
300
tagagagttt tttgctttgc cgccggaaga gaagctccgg tttgacatgt ccggtggtaa
360
aaagggtggt ttcattgtct ctagtcatct ccaaggagaa gcagtgaaag attggagaga
420
gctagtgaca tattttttcat acccaattaa acaaagagat tattcaaggt ggccagacaa
480
gccagaagga tggaaagaag taacagaaaa atacagtga aacctaata atttagcttg
540
caagctattg gaagttttat cagaagcaat gggattagaa aaag
584

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tccaaaagtt gcctacaata acttcagcaa cgagattcca atnatttctc ttgctggaat
120

tgatgagggt gatggtcgca gaacagagat atgtaacaag attggtgaag cttgtgagaa
180

ttgggggtatt tttcagggtg ctgatcatgg tggtgatata aagcttggtt ctgagatgac
240

tcgtttttgc agagagtttt ttgctttgcc gccggaagag aagctccggt ttgacatgtc
300

cggtggtaaa aagggtggtt tcattgtctc tnntcatctc caaggagaag cagngaaaga
360

ttggaganag ctagtgacat attntcata cccaattaaa caagagatt atncaagggt
420

gtcanacnag ccagaaggat ggaaagaagt aacagaaaaa tacagtgaac acctaatgaa

480

tttacctngc aagctattgg aagttttata ataancnatg gnattaaga
529

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120

ggaagagaag ctccggtttg acatgtccgg tggtaaaaag ggtggtttca ttgtctctag
180

tcattctcaa ggagaagcag tgaaggattg gagagagcta gtgacatatt tttcataccc
240

aattaaacaa agagattatt caaggtggcc agacaagcca gaaggatgga aagaggtaac
300

agaaaaatac agtgaaaacc taatgaattt agcttgcaaa ctattggaag ttttatcaga
360

agcaatgggt ttagaaaaag aagctctaac aaaagcatgt gttgatatgg atcaaaaagt
420

tgttataaat tattacccaa aatgccctga acctgacctc acacttggcc ttaaacgtca
480

270/390

cactgaccct ggcacaatta ctcttttgct tcaagatcaa gttggtgggc ttcaagctac
540

caaagataat ggtaagacgt ggattacagt tcaaccagtt gaaggtgctt ttgttggttaa
600

tcttgagac catggtcact atctaagtaa tggacgggtc aaaaatgctg accatcaagc
660

agtggatgaat tcgaactaca gccgnttatc aatagcaa
698

<210> 244
<211> 579
<212> DNA
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<400> 244
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ttaaagccca cactgaccct ggnacaatta ctcttttgct tcaagatcaa gttggtggcc
120

ttcaagctac caaagataat ggtaagacgt ggattacagt tcaaccagtt gaaggtgctt
180

ttgttggttaa tcttgagac catggtcatt atctaagtaa tggacgggtc aaaaatgctg
240

accaccaagc agtggatgaat tcgaactaca gccgtttatc aatagcaaca tttcaaaatc
300

cagctcccgat tgcaactgta taccctttga agattagaga gggtgaaaaa tctgtgttgg
360

aagaaccaat cacttttgct gaaatgtata gaaggaagat gaccaaagac cttgaaattg
420

ctaggatgaa gaagttggct aaggaacaac aacttaggga ctggaggag aacaagacta
480

aatatgaggc caaacctttg aatgagatct ttgcttaatt aattagtctt aatttaaata
540

attaataaat tttagactta atttacatat aataatttt
579

<210> 245
<211> 601
<212> DNA
<213> *Trifolium repens*

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<222> (22)..(22)
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<222> (30)..(30)
<223> Any nucleotide

<400> 245
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60

aagtaaaata ccataacaca ataatatgaa taccataatc ttgaatcata caaacaacct
120

tggatcaaac aaaacaacaa ccatgggtga tctagaaaca gaaccaagtt caccatttat
180

tcaatcccca gaacacagac caaaatcctc aataatcatt gctgaaggta tccctcta
240

tgatctcact cctataaact acaaagatga aatcatcacc aaccacttt ccattgaaga
300

cttagtcaaa gaaataggca aagcatgtaa agaatggggt ttctttcaag tgattaatca
360

caaagttcct ttggataaac gtgaaaggat tgaagaatct tcaaagaagt tttttgaact
420

tagtttggag gaaaaactta aggtgagaag agatgaagtt aatttgcttg gttatattga
480

agctgagcat acaaaaaatg ttagggactg gaaggaaatt tatgatttta atgtgcaaca
540

accaactttt ataccacctt cggatgacca aagttttcag tttcaatggg aaaatcga
600

g
601

<210> 246
 <211> 172
 <212> PRT
 <213> Trifolium repens

<400> 246

Met Asn Thr Ile Ile Leu Asn His Thr Asn Asn Leu Gly Ser Asn Lys
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Thr Thr Thr Met Val Asp Leu Glu Thr Glu Pro Ser Ser Pro Phe Ile
 20 25 30

Gln Ser Pro Glu His Arg Pro Lys Ser Ser Ile Ile Ile Ala Glu Gly
 35 40 45

Ile Pro Leu Ile Asp Leu Thr Pro Ile Asn Tyr Lys Asp Glu Ile Ile
 50 55 60

Thr Asn Pro Leu Ser Ile Glu Asp Leu Val Lys Glu Ile Gly Lys Ala
 65 70 75 80

Cys Lys Glu Trp Gly Phe Phe Gln Val Ile Asn His Lys Val Pro Leu
 85 90 95

Asp Lys Arg Glu Arg Ile Glu Glu Ser Ser Lys Lys Phe Phe Glu Leu
 100 105 110

Ser Leu Glu Glu Lys Leu Lys Val Arg Arg Asp Glu Val Asn Leu Leu
 115 120 125

Gly Tyr Phe Glu Ala Glu His Thr Lys Asn Val Arg Asp Trp Lys Glu
 130 135 140

Ile Tyr Asp Phe Asn Val Gln Gln Pro Thr Phe Ile Pro Pro Ser Asp
 145 150 155 160

Asp Gln Ser Phe Gln Phe Gln Trp Glu Asn Arg Trp
 165 170

<210> 247
 <211> 585
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 <213> Trifolium repens

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cagctttctt caaatccaga aaataggcca aaactttcca taatccaagc tgaaggaatt
120

cctgtaatca atctctcccc attaatccac cacacagttc aagactcctc tgccattgaa
180

agcttagtca aagaaatagg aaatgcttgc aaggaatggg gtttcttcca agtaacaaac
240

catgggtgtcc ctctaaatct aaggctcaga ctcgaggaag ctaccaaagt tttctttgca
300

cagagtttgg aggagaagag gaagcttacc gtagatgata acagtttgcc tggttatcat
360

gatacagagc acaccaagaa tgtcagagac tggaaagaag tgtttgattt tttatccaaa
420

gaccccaactt tgattcctct gaattctgat gaacatgatg atcgagtcac tcaatggact
480

aatccatccc ctcaatatcc tccaaacttc aaagttattt tggaagagta tattaaagag
540

atggaaaagc taggctttaa gttgctagag cttatagctt tgagc
585

<210> 248

<211> 187

<212> PRT

<213> Trifolium repens

<400> 248

Met Leu Val Tyr Gln Glu Arg Trp Glu Arg Trp Ile Gln Leu Ser Ser
1 5 10 15

Asn Pro Glu Asn Arg Pro Lys Leu Ser Ile Ile Gln Ala Glu Gly Ile
20 25 30

Pro Val Ile Asn Leu Ser Pro Leu Ile His His Thr Val Gln Asp Ser
35 40 45

Ser Ala Ile Glu Ser Leu Val Lys Glu Ile Gly Asn Ala Cys Lys Glu
50 55 60

Trp Gly Phe Phe Gln Val Thr Asn His Gly Val Pro Leu Asn Leu Arg
65 70 75 80

Leu Arg Leu Glu Glu Ala Thr Lys Val Phe Phe Ala Gln Ser Leu Glu
85 90 95

Glu Lys Arg Lys Leu Thr Val Asp Asp Asn Ser Leu Pro Gly Tyr His
100 105 110

Asp Thr Glu His Thr Lys Asn Val Arg Asp Trp Lys Glu Val Phe Asp
115 120 125

Phe Leu Ser Lys Asp Pro Thr Leu Ile Pro Leu Asn Ser Asp Glu His
 130 135 140

Asp Asp Arg Val Thr Gln Trp Thr Asn Pro Ser Pro Gln Tyr Pro Pro
 145 150 155 160

Asn Phe Lys Val Ile Leu Glu Glu Tyr Ile Lys Glu Met Glu Lys Leu
 165 170 175

Gly Phe Lys Leu Leu Glu Leu Ile Ala Leu Ser
 180 185

<210> 249
 <211> 604
 <212> DNA
 <213> Trifolium repens

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 60
 atggcgtttag ctggagtttt caatattggt gattttgttc ctgctttgga atgggttagat
 120
 attcaagggtg tacaaggaaa aatgaagaaa ttacataaaa gatttgatgc atttttaact
 180
 agcattattg aagatcacat gatttccaag agtgagaagc ataatgactt attgagtacg
 240
 ttgttatcac taaaagaaaa agttgatgag gatggtgaca aacttaatga tactgagatc
 300
 aaagcattac tcttgaacat gttcacagct ggaacagaca catcatcaag cacaacagag
 360
 tgggctattg ctgaactaat aaaaaatcca aaactaatga ttogtggttca aaatgagttg
 420
 gacactgttg tgggcogaga caagcttgta actgaacaag acttggccca tcttccttac
 480
 ttagaggctg taataaagga gacatttcgt ctccatccat caaccctctt ttctctccca
 540
 cgtgttgcaa caaatagttg tgaaatcctc gactatcaca ttcccaaagg tgcaactctc
 600
 ttgg
 604

<210> 250
 <211> 201
 <212> PRT
 <213> Trifolium repens

<400> 250

Gly Asn Gly Gly Gly Glu Cys Asp Pro Arg Ala Asp Glu Leu Val Met
 1 5 10 15

Val Val Glu Leu Met Ala Leu Ala Gly Val Phe Asn Ile Gly Asp Phe
20 25 30

Val Pro Ala Leu Glu Trp Leu Asp Ile Gln Gly Val Gln Gly Lys Met
35 40 45

Lys Lys Leu His Lys Arg Phe Asp Ala Phe Leu Thr Ser Ile Ile Glu
50 55 60

Asp His Met Ile Ser Lys Ser Glu Lys His Asn Asp Leu Leu Ser Thr
65 70 75 80

Leu Leu Ser Leu Lys Glu Lys Val Asp Glu Asp Gly Asp Lys Leu Asn
85 90 95

Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Met Phe Thr Ala Gly Thr
100 105 110

Asp Thr Ser Ser Ser Thr Thr Glu Trp Ala Ile Ala Glu Leu Ile Lys
115 120 125

Asn Pro Lys Leu Met Ile Arg Val Gln Asn Glu Leu Asp Thr Val Val
130 135 140

Gly Arg Asp Lys Leu Val Thr Glu Gln Asp Leu Ala His Leu Pro Tyr
145 150 155 160

Leu Glu Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro
165 170 175

Leu Ser Leu Pro Arg Val Ala Thr Asn Ser Cys Glu Ile Leu Asp Tyr
180 185 190

His Ile Pro Lys Gly Ala Thr Leu Leu
195 200

<210> 251

<211> 581

<212> DNA

<213> Trifolium repens

<400> 251

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ttatggcggt agctggagtt ttcaatattg gtgattttgt tcctgctttg gaatgggttag
120

atattcaagg tgtacaagga aaaatgaaga aattacataa aagatttgat gcatttttaa
180

ctagcattat tgaagatcac atgatttcca agagtgagaa gcataatgac ttattgagta

240

cgttggttatc actaaaagaa aaagttgatg aggatgggtga caaacttaat gatactgaga
300

tcaaagcatt actccttgaac atgttcacag ctggaacaga cacatcatca agcacaacag
360

agtgggctat tgctgaacta ataaaaaatc caaaactaat gattcgtggt caaaatgagt
420

tggacactgt tgtgggccga gacaagcttg taactgaaca agacttggcc catcttccct
480

acttagaggc tgtaataaag gagacatttc gtctccatcc atcaaccctt cttctctctc
540

cacgtgttgc aacaaatagt tgtgaaatcc tcgactatca c
581

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<211> 603

<212> DNA

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120

ttcaagggtgt acaaggaaaa atgaagaaat tacataaaaag atttgatgca tttttaacta
180

gcattattga agatcacatg atttccaaga gtgagaagca taatgactta ttgagtacgt
240

tgttatcact aaaagaaaaa gttgatgagg atggtgacaa acttaatgat actgagatca
300

aagcattact cttgaacatg ttcacagctg gaacagacac atcatcaagc acaacagagt
360

gggctattgc tgaactaata aaaaatccaa aactaatgat tcgtgttcaa aatgagttgg
420

acactgttgt gggccgagac aagcttgtaa ctgaacaaga cttggcccat cttccttact
480

tagaggctgt aataaaggag acatttcgtc tccatccatc aaccctctt tctctccac
540

gtgttgcaac aaatagttgt gaaatcctcg actatcacat tcccaaaggt gcaactctct
600

tgg

603

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 <222> (598)..(598)
 <223> Any nucleotide

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ctccctaaaa attctatagc taccacatca ncacaacata acannaatta agaaatattn
 120

tatntactat tttaagatat ggaagtagta gcagcagcaa tcacaaaaaa caatggcaag
 180

attgattcat tttgcttgaa tcatgctaata gctaataaca tgaaagtga tggtgctgat
 240

cctttgaatt ggggtgtggc tgctgaggca atgaaggga gtcacttga tgaggtgaag
 300

cgatgggtgg aggaataccg gaaaccggtt gtccgtcttg gtggcgagac actgacgatt
 360

tctcaggtgg ctgccattgc tgcacacgat ggtgcaacgg tggagctatc ggaatctgct
 420

agagccggcg ttaaggcgag cagtgactgg gttatggaga gtatgaacaa aggtacagac
 480

agttatggtg tcactacagg gttcggcgct acctcgacc gccgaaccaa acaaggtggt
 540

gctttgcaga aagagctcat aaggtnnttt gaatgcagga atatttgga atggaacntg
 600

agacaaagcc acacactacc c
 621

<210> 254
 <211> 159
 <212> PRT
 <213> Trifolium repens

<400> 254

Met Glu Val Val Ala Ala Ala Ile Thr Lys Asn Asn Gly Lys Ile Asp
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Ser Phe Cys Leu Asn His Ala Asn Ala Asn Asn Met Lys Val Asn Gly
 20 25 30

Ala Asp Pro Leu Asn Trp Gly Val Ala Ala Glu Ala Met Lys Gly Ser
 35 40 45

His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg Lys Pro Val
50 55 60

Val Arg Leu Gly Gly Glu Thr Leu Thr Ile Ser Gln Val Ala Ala Ile
65 70 75 80

Ala Ala His Asp Gly Ala Thr Val Glu Leu Ser Glu Ser Ala Arg Ala
85 90 95

Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met Asn Lys Gly
100 105 110

Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr Ser His Arg
115 120 125

Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu Ile Arg Phe Glu
130 135 140

Cys Arg Asn Ile Trp Lys Trp Asn Arg Gln Ser His Thr Leu Pro
145 150 155

<210> 255
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ctccctaaaa attctatagc taccacatca ncacaacata acannaatta agaaatattn
120

tatntactat ttttaagatat ggaagtagta gcancagcaa tcacaaaaaa caatggcaag
180

attgattcat tttgcttgaa tcatgctaatt gctaataaca tgaaagttaa tgggtgctgat
240

cctttgaatt ggggtgtggc tgctgaggca atgaaggga gtcacttgga tgaggtgaag
300

cgtatggtgg aggaataaccg gaaaccgggtt gtccgtcttg gtggcgagac gctgacgatt
360

tctcaggtgg ctgccattgc tgcacacgat ggtgcaacgg tgganctatc ggaatctgct
420

agagccggcg ttaaggcgag cagtgactgg gttatggaga gcatgaacaa aggtacagac
480

agttatggtg tcactacggg gttcggcgct acctcncacc gccgaaccaa acaaggtggt
540

gctttgcana aagagctcat aagctaattt gcttgtgtca at
582

<210> 256
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60

ctccctaaaa attctatagc taccacatca ncacaacata acannaatta agaaatattn
120

tatntactat nttaagatat ggaagtagta gcagcagcaa tcacaaaaaa caatggcaag
180

attgattcat tttgcttgaa tcatgctaatt gctaataaca tgaaagtga tggtgctgat
240

cctttgaatt ggggtgtggc tgctgaggca atgaaggga gtcacttgga tgaggtgaag
300

cgtatgggtgg aggaataccg gaaaccggtt gtccgtcttg gtggcgagac actaaccatt
360

tctcaggtgg ctgccattgc tgcacacgat ggtgcaacgg tggagctatc ggaatctgct
420

agagccggcg ttaaggcaag cagtgactgg gttatggaga gtatgaacaa aggtaccgac
480

agctacggtg tcccaacagg gttcggcgct acctcgacc gccgaaccaa acaaggtggt

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120tttaagnnat ggaagtagta gcagcagcaa tcacaaaaaa caacggaaag attgattcat
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360ctgccattgc tgcacacgat ggtgcgacgg tggagctatc ggaatctgct agagccggcg
420ttaaggcgag cagtgactgg gttatggaaa gtatgaacaa aggtactgac agttatgggtg
480tcactacagg gttcggcgct acctcgcacc gccgaaccaa acaaggtggt gctttgcaga
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120

ctttctacac accccctct caactattat taactaacat aatggaggga attaccaatg
180

gccatgctga agcaactttt tgcgtgacca aaagtgttg tgatccactc aactggggtg
240

cagccgcgga gtcgttgatg gggagtcat tggatgaggt gaagcgtatg gtggaggaat
300

accgtaatcc attggttaaa attggcggcg agacgcttac cattgctcag gtggctggaa
360

ttgcttctca tgatagtggg gtgagggtgg agctgtctga gtccgccagg gccggcgta
420

aggcgagtag tgattgggtg atggacagca tgaacaatgg gactgatagt tatggtgta
480

ccaccggttt cggcgccacc tctcaccgga gaaccaagca gggtggtgcc ttgcagaagg
540

agctaattag gtttttgaat gctggaatat ttggcaatgg tacagaatct aactgtacac
600

taccacacac agcaaccaga gctgcaatgc ttgtgagaat caacactctt cttcaagagg
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693

<210> 259

<211> 177

<212> PRT

<213> Trifolium repens

<400> 259

286/390

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Lys Ser Val Gly Asp Pro Leu Asn Trp Gly Ala Ala Ala Glu Ser Leu
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Met Gly Ser His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg
35 40 45

Asn Pro Leu Val Lys Ile Gly Gly Glu Thr Leu Thr Ile Ala Gln Val
50 55 60

Ala Gly Ile Ala Ser His Asp Ser Gly Val Arg Val Glu Leu Ser Glu
65 70 75 80

Ser Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val Met Asp Ser
85 90 95

Met Asn Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala
100 105 110

Thr Ser His Arg Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu
115 120 125

Ile Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Ser Asn
130 135 140

Cys Thr Leu Pro His Thr Ala Thr Arg Ala Ala Met Leu Val Arg Ile
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Leu

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120
ttaactangc ataatggagg gaattaccaa tggccagctg ctttcaaaaa aaaaccaatg
180
gccatgctga aacaactttt tgcgtgacca aaagtgttgg tgatccactc aactgggggtg
240
cagccgcgga gtcgttgacg ggtagtcatt tggatgaggt gaagcgtatg gtggaggagt
300
accgtaatcc gttgggttaa attggcggcg agacgcttac cattgctcag gtggctggaa
360
ttgcttctca tgatagtggg gtgagggtgg agctgtccga gtccgcaagg gccggcggtta
420
aggcgagtag tgattgggtg atggatagca tgaacaatgg gactgatagt tacggtgtta
480
ccaccggttt tgggtgccacc tctcaccgga gaaccaagca ggggtggtgcc ttgcagaagg
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taatggaggg aattaccaat ggccatgctg aagcaacttt ttgcgtgacc aaaagtgtg
180

gtgatccact caactggggg gcagccgcgg agtcgttgat ggggagtcac ttggatgagg
240

tgaagcgtat ggtggaggaa taccgtaatc cattgggttaa aattggcggc gagacgctta
300

ccattgctca ggtggctgga attgcttctc atgatagtgg tgtgaggggtg gagctgtctg
360

agtcgcgcgag ggccggcggt aaggcgagta gtgattgggt gatggacagc atgaacaatg
420

ggactgatag ttatggtggt accaccggtt tcgggtgccac ctctcaccgg agaaccaagc
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aaggtggtgc cttgcagaag gagctaatta ggtttttgaa tgctggaata tttggcaatg
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tcaacactct tcttcaag
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120

taatggaggg aattactaat ggccatgctg aagcaacttt ttgcgtnacc aaaagtgttg
180

gtgatccact caactggggg gcagccgcgg agtcgntgat ggggagtnat ttggatgagg
240

tgaancgtat ggtggaggaa taccgtaatc cattgggttaa aattggcggc gagacgctta
300

ccattgctca ggtggctgga attgcttctc atgatagnngn tgtgaggggtg gagctgtctg
360

agtnccgag ggccggcggt aangcgagta gtgattgngt gatggacagn atgaacaatg
420

ggactgatag ttatggngtn accaccggtt tcggcgccac ctctcaccgg agaaccaagc
480

aggggtggtgc cttgcaaaag gagctaatta tgtttttgaa tgctggaata tttggcaatg
540

gtacagaatc taactgtaca cttcnacaca cagcaaccan agntgcattg ctttggtgca
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120

atggagggaa ttactaatgg ccatgctgaa gcaacttttt gcgtgaccaa aagtgttggt
180

gatccactca actgggggtgc agccgcggag tcgttgatgg ggagtcattt ggatgagggtg
240

aagcgtatgg tggaggaata ccgtaatcca ttgggttaaaa ttggcggcga gacgcttacc
300

attgctcagg tggctggaat tgcttctcat gatagtgggtg tgagggtgga gctgtctgag
360

tccgccaggg cgggcgttaa ggcgagtagt gattgggtga tggacagcat gaacaatggg
420

actgatagtt atggtgttac caccggtttc ggcgccacct ctcaccggag aaccaagcag
480

ggtggtgcct tgcagaagga gctaattagg tttttgaatg ctggaatatt tggcaatggt
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120

atggagggaa ttaccaatgg ccatgctgaa gcaacttttt gcgtgaccaa aagtgttggt
180

gatccactca actgggggtgc agccgcggag tcgttgatgg ggagtcattt ggatgaggtg
240

aagcgtatgg tggaggaata ccgtaatcca ttggttaaaa ttggcggcga gacgcttacc
300

attgctcagg tggctggaat tgcttctcat gatagtgggtg tgaggggtgga gctgtctgag
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tccgccaggg ccggcggttaa ggcgagtagt gggtgggtga tggacagcat gaacaatggg
420

actgatagtt atggtgttac cactgggtttc ggcgccacct ctcaccggag aaccaagcag
480

ggtggtgcct tgcagaagga gctaattagg tttttgaatg ccggaatatt tggcaatggt
540

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120

tggaggggaat taccaatggc catgctgaaa caactttttg cgtgaccaa agtggtggtg
180

atccactcaa ctgggggtgca gccgcggagt cgttgacggg gagtcatttg gatgaggtga
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agcgtatggt ggaggagtac cgtaatccgt tggctaaaat tggcggcgag acgcttacca
300

ttgctcaggt ggctggaatt gcttctcatg atagtgggtg gaggggtggag ctgnncgagt
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420

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tggagggaat taccaatggc catgctgaag caactttttg cgtgaccaa agtggttggtg
180

atccactcaa ctgggggtgca gccgcggagt cgttgatggg gagtcatttg gatgaggtga
240

agcgtatggt ggaggaatac cgtaatccat tgggttaaaat tggcggcgag acgcttacca
300

ttgctcaggt ggctggaatt gcttctcatg atagtgggtg gaggggtggag ctgtctgagt
360

ccgccagggc cggcggttaag gcgagtagtg gttgggtgat ggacagcatg aacaatggga
420

ctgatagtta tgggtgttacc actggtttcg gcgccacctc tcaccggaga accaagcagg
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gtggtgcctt gcagaaggag ctaattaggt ttttgaatgc cggaatatat ggcaatggta
540

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120

tttgcgtagac caaaagtgtt ggtgatccac tcaactgggg tgcagccgcg gagtcgtcga
180

cggggagtca tttggatgag gtgaagcgta tggaggagga gtaccgtaat ccgttggtta
240

aaattggcgg cgagacgctt accattgctc aggtggctgg aattgcttct catgatagtg
300

gtgtgagggg ggagctgtcc gagtccgcaa gggccggcgt taaggcgagt agtgattggg
360

tgatggatag catgaacaat gggactgata gttacggtgt taccaccggt tttggtgcca
420

cctctcaccg gagaaccaag caggggtgtg ccttgagaa ggagctaatt aggtttttga
480

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120

cgatgtttca aggaacaagg ccattcatgg tggttaacttt caaggaacac ctattggagt
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ttcaatggat aacacacggt tagctcttgc ttcaattggg aaactcatgt ttgctcaatt
240

ctctgaactt gttaatgatt tttacaacaa cgggttgctt tcgaatctta ctgctagtag
300

gaacccgagc ttggactatg gtttcaaggg atcggaaatt gccatggctt cgtattgttc
360

cgagttacaa tatcttgcta atcctgtcac caccatgtc caaagtgccg agcaacacaa
420

ccaagatggt aactccttgg gtttgatttc atctagaaaa acaaatgaag ctattgagat

300/390

480

tctcaagctc atgtcttcca ctttcttgat tgcattatgt caagcaatcg acttaaggca
540

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579

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Ile Glu Val Ile Arg Phe Ser Thr Lys Ser Ile Glu Arg Glu Ile Asn
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Ser Val Asn Asp Asn Pro Leu Ile Asp Val Ser Arg Asn Lys Ala Ile
35 40 45

His Gly Gly Asn Phe Gln Gly Thr Pro Ile Gly Val Ser Met Asp Asn
50 55 60

Thr Arg Leu Ala Leu Ala Ser Ile Gly Lys Leu Met Phe Ala Gln Phe
65 70 75 80

Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn Gly Leu Pro Ser Asn Leu
85 90 95

Thr Ala Ser Arg Asn Pro Ser Leu Asp Tyr Gly Phe Lys Gly Ser Glu
100 105 110

Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu Gln Tyr Leu Ala Asn Pro
115 120 125

Val Thr Thr His Val Gln Ser Ala Glu Gln His Asn Gln Asp Val Asn
130 135 140

Ser Leu Gly Leu Ile Ser Ser Arg Lys Thr Asn Glu Ala Ile Glu Ile
145 150 155 160

Leu Lys Leu Met Ser Ser Thr Phe Leu Ile Ala Leu Cys Gln Ala Ile
165 170 175

Asp Leu Arg His Leu Glu Glu Asn Leu Arg Asn Thr Val Lys Asn Thr
180 185 190

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120
caattggctg gaatcaatac cgagttcttt gaattacaac caaaagaagg tcttgcaactt
180
gttaatggaa ctgctgttgg ttctgggtta gcttctattg ttctttttga ggctaacata
240
ttggcgggtg tgtctgaagt tctatcggca attttcgctg aagttatgca agggaagccc
300
gaatttactg atcatttgac acataagttg aagcaccacc ctggtcaaat tgaggctgct
360
gctattatgg aacacatttt ggatgggagt gcttatgtta aagacgcgaa gaagttgcat
420
gagatggacc ctttacagaa gccaaagcaa gatagatatg cacttagaac ttcaccacaa
480
tggcttggtc ctttgattga agtgattaga ttttcaacca agtcaattga gagagagatc
540
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591

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Leu Leu Thr Gly Arg Xaa Asn Ser Lys Ala His Gly Pro Thr Gly Glu
 20 25 30

Val Leu Asn Ala Lys Glu Ala Phe Gln Leu Ala Gly Ile Asn Thr Glu
 35 40 45

Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly Thr
 50 55 60

Ala Val Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu Ala Asn Ile
 65 70 75 80

Leu Ala Val Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val Met
 85 90 95

Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys His
 100 105 110

His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile Leu Asp
 115 120 125

Gly Ser Ala Tyr Val Lys Asp Ala Lys Lys Leu His Glu Met Asp Pro
 130 135 140

Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro Gln
 145 150 155 160

Trp Leu Gly Pro Leu Ile Glu Val Ile Arg Phe Ser Thr Lys Ser Ile
 165 170 175

Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val Ser
180 185 190

Arg Asn Lys Ala Leu
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120

ctattaagat atggaagtag tagcagcagc aatcacaaaa aacaacggca agattgattc
180

attttgcttg aatcatgcta atgctaataa catgaaagtg aatgatgctg atcctttgaa
240

ttgggggtgtg gctgctgagg caatgaaggg aagtcacttg gatgaggtga aacgtatggt
300

ggaggagtac cggaagccga ttgtccgtct tgggtggcgag acgctgacga tttctcaggt
360

ggctgccatt gctgcacacg atggtgcat ggttgagctg tcggaatctg ctagagccgg
420

cgtaaaggca agcagtgatt gggttatgga gagtatgaac aaagggtactg acagttatgg
480

tgtcaccaca gggttcggcg ctacctnca ccgccgaacc aaacaagggtg gtgctttaca
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Ser Phe Cys Leu Asn His Ala Asn Ala Asn Asn Met Lys Val Asn Asp
20 25 30

Ala Asp Pro Leu Asn Trp Gly Val Ala Ala Glu Ala Met Lys Gly Ser
35 40 45

His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg Lys Pro Ile
50 55 60

Val Arg Leu Gly Gly Glu Thr Leu Thr Ile Ser Gln Val Ala Ala Ile
65 70 75 80

Ala Ala His Asp Gly Ala Met Val Glu Leu Ser Glu Ser Ala Arg Ala
85 90 95

Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met Asn Lys Gly
100 105 110

Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr Xaa His Arg
115 120 125

Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Gly Leu Ile Arg Phe Leu
130 135 140

Asn Ala Gly Ile Phe Xaa Asn Xaa Thr Xaa
145 150

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120

accaatggcc atgctgaaac aacttttagc gtgacaaaa gtgnngnga tccactcaac
180

tggcgngcag ccgcgagtc gtcgacggg agtcatttg atgaggtgaa gcgtatggng
240

gaggagtacc gtaatccgnt ggtaaaatt ggcgcgaga cgcttaccat tgctnnggta
300

nctggaattg cttctcatga tagtggagtg aggggtggagc tgtccgagtt cgcaagggcc
360

ggcgtaagg cgagtagtga ttgngtgatg gatagcatga acaatgggac tgataggttac
420

ggtgttacca ccgcntttgg tgccacctgt caccggagaa ccaagccang gtggtgcctt
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gcagaaggag ctaaattnng gtgttttgaa ngctggnaat antttggcnn tggttcagaa
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atctnaactt gtncacttac cacacc
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Lys Ser Xaa Xaa Asp Pro Leu Asn Trp Xaa Ala Ala Ala Glu Ser Ser
 20 25 30

Thr Gly Ser His Leu Asp Glu Val Lys Arg Met Xaa Glu Glu Tyr Arg
 35 40 45

Asn Pro Xaa Val Lys Ile Gly Gly Glu Thr Leu Thr Ile Ala Xaa Val
 50 55 60

Xaa Gly Ile Ala Ser His Asp Ser Gly Val Arg Val Glu Leu Ser Glu
 65 70 75 80

Phe Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Xaa Val Met Asp Ser
 85 90 95

Met Asn Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Xaa Phe Gly Ala
 100 105 110

Thr Cys His Arg Arg Thr Lys Pro Xaa Trp Cys Leu Ala Glu Gly Ala
 115 120 125

Lys Xaa Xaa Cys Phe Glu Xaa Trp Xaa Xaa Phe Gly Xaa Gly Ser Glu
130 135 140

Ile Xaa Thr Cys Xaa Leu Thr Thr
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120

accaatggcc atgctgaaac aacttttttgc gtgacaaaaa gtgtnggnga tnnantgnnc
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tgtcgngn

188

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120

ttatcgtgac caaaagtgnt ggtgatccac tcaactgggg tgcagccgcg gagtcgtcga
180

cggggagtc tttggatgag gtgaagcgta tggnggagga gtaccgtaat ccgntgggta
240

aaattggcgg cgagacgctt accattgctn nggtanctgg aattgcttct catgatagtg
300

gagtgagggt ggagctgtcc gagttcgcaa gggccggcgt taaggcgagt agtgattgng
360

tgatggatag catgaacaat gggactgata gttacggtgt taccaccgcn tttggtgcca
420

cctgtcaccg gagaaccaag ccanggtggt gccttgacaga aggagctaaa tttnnggtgtt
480

ttgaangctg gnaatanttt ggcnnrtggtt cagaaatctn aacttgtntca cttaccacac
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120

atcaagagtc ttcttgaaaa tggatactct gttaatacca ctattagagc tgatccagaa
180

cgtaagaggg atgtaagctt cctaacaaat ctacccggcg catccgaaag gctacatttc
240

ttcaacgccg atctagacga cccagagagt ttcaacgaag caattgaagg ttgtgtcggg
300

atattccaca ccgcttcacc aatcgatttc gccgtgagtg agccagaaga aatagtgaca
360

aaaagaacag tggatggagc attaggaatt ttaaaagcat gtgtgaattc aaagacagtg
420

aagagattta ttacacttc aagnggttct gctgtttcat tcaatggaaa aaacaaagat
480

gnntnggatg agagtgattg gagtgatggt gatttgctta gaagtgttaa accatttggt
540

tggagttatg gngtgttcaa gactttggct gagaaagcag tgcttgaatt tgggtcnacaa
600

aatgggattg atgttggttac tttgattcctt cctttttattg ttggagggtt tgtttggtccc
660

aagcttcctg attctgttga gaaagctcctt gttttggtac taggcaaaaa ggaacaaatt
720

gggtattataa gtttccacat ggtacatgta gatgatgtgg ctagagcaca tatctatcta
780

cttgagaatc ctgttccagg aggtagatat aattgttcac cattctttgt atctattgaa
840

gaaatgtcac agcttctctc agccaaatat ccagaatatc aaatactatc agtagatgag
900

ttgaaggaaa ttaaaggggc aagattgcc a gatttgaact cgaagaagct cgtggacgct
960

ggttttgagt ttaagtatag tgtcgatgat atgttcgatg atgcgattca atgctgcaag
1020

gaaaaaggct atctctaagc atgtatttga aaattccatg aagttgagaa aacaataatg
1080

tgccataaaat caatgatggc taatgagatg tacaagttta tgcattaagt tattttgtgat
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caatcaaata atgaaataat ctgttcattt ttccgaaaaa aaaaa
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316/390

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Asn Thr Thr Ile Arg Ala Asp Pro Glu Arg Lys Arg Asp Val Ser Phe
 35 40 45

Leu Thr Asn Leu Pro Gly Ala Ser Glu Arg Leu His Phe Phe Asn Ala
 50 55 60

Asp Leu Asp Asp Pro Glu Ser Phe Asn Glu Ala Ile Glu Gly Cys Val
 65 70 75 80

Gly Ile Phe His Thr Ala Ser Pro Ile Asp Phe Ala Val Ser Glu Pro
 85 90 95

Glu Glu Ile Val Thr Lys Arg Thr Val Asp Gly Ala Leu Gly Ile Leu
 100 105 110

Lys Ala Cys Val Asn Ser Lys Thr Val Lys Arg Phe Ile Tyr Thr Ser
 115 120 125

Xaa Gly Ser Ala Val Ser Phe Asn Gly Lys Asn Lys Asp Xaa Xaa Asp
 130 135 140

Glu Ser Asp Trp Ser Asp Val Asp Leu Leu Arg Ser Val Lys Pro Phe
 145 150 155 160

Gly Trp Ser Tyr Xaa Val Phe Lys Thr Leu Ala Glu Lys Ala Val Leu
 165 170 175

Glu Phe Gly Xaa Gln Asn Gly Ile Asp Val Val Thr Leu Ile Leu Pro
 180 185 190

Phe Ile Val Gly Gly Phe Val Cys Pro Lys Leu Pro Asp Ser Val Glu
 195 200 205

Lys Ala Leu Val Leu Val Leu Gly Lys Lys Glu Gln Ile Gly Ile Ile
 210 215 220

Ser Phe His Met Val His Val Asp Asp Val Ala Arg Ala His Ile Tyr
 225 230 235 240

Leu Leu Glu Asn Pro Val Pro Gly Gly Arg Tyr Asn Cys Ser Pro Phe
 245 250 255

Phe Val Ser Ile Glu Glu Met Ser Gln Leu Leu Ser Ala Lys Tyr Pro
 260 265 270

Glu Tyr Gln Ile Leu Ser Val Asp Glu Leu Lys Glu Ile Lys Gly Ala
 275 280 285

Arg Leu Pro Asp Leu Asn Ser Lys Lys Leu Val Asp Ala Gly Phe Glu
290 295 300

Phe Lys Tyr Ser Val Asp Asp Met Phe Asp Asp Ala Ile Gln Cys Cys
305 310 315 320

Lys Glu Lys Gly Tyr Leu
325

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gctgaaggaa aaggaagggt ttgtgttact ggaggaacag gttttcttgg ttcattggatc
120
atcaagagtc ttcttgaaaa tggatactct gttaatacca ctattagagc tgatccagaa
180
cgtaagaggg atgtaagctt cctaacaaat ctacccggcg catccgaaag gctacatttc
240
ttcaacgccg atctagacga cccagagagt ttcaacgaag caattgaagg ttgtgtcggg
300
atattccaca cgcgttcacc aatcgatttc gccgtgagtg agccagaaga aatagtgaca
360
aaaagaacag tggatggagc attaggaatt ttaaaagcat gtgtgaattc aaagacagt
420
aagagattta ttacacttc aagnggttct gctgtttcat tcaatgnaaa aancaaagat
480
gnntnnnatg ana
493

<210> 281
<211> 601
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<222> (50)..(51)
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<220>

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<222> (552)..(552)
<223> Any nucleotide

<400> 281
agagttgaga aaaaanncca ataaagtaaa cnctatntag aaagagagtn naaaatggct
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gaaggaaaag gaagggtttg tggtactgga ggaacagggt ttcttggttc atggatcatc
120
aagagtcttc ttgaaaatgg atactctgtt aataccacta ttagagctga tccagaacgt
180
aagaggggatg taagcttcct aacaaatcta cccggcgcat ccgaaaggct acatttcttc
240
aacgccgata tagacgaccc agagagtttc aacgaagcaa ttgaagggtg tgcggggata
300
ttccacaccg cttcaccaat cgatttcgcc gtgagtgagc cagaagaaat agtgacaaaa
360
agaacagtgg atggagcatt aggaatttta aaagcatgtg tgaattcaaa gacagtgaag
420
agatttattt acacttcaag tggttctgct gtttcattca atggaaaaaa caaagatgtt
480
ttggatgaga gtgattggag tgatgttgat ttgcttagaa gtgttaaacc atttggttgg
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agttatggtg tnttcaagac tttggctgag aaagcagtgc ttgaatttgg tcaacaaaat
600
g
601

<210> 282
<211> 613
<212> DNA
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<220>
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<222> (2)..(2)
<223> Any nucleotide

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<222> (45)..(46)
<223> Any nucleotides

<400> 282
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atgttggttac tttgattctt ccttttattg ttggagggtt tgtttgctct aagcttcctg
120
attctgttga gaaagctctt gttttggtac taggcaaaaa ggaacaaatt ggtattataa
180

gtttccacat ggtacatgtg gatgatgtgg ctagagcaca tatctatcta cttgagaatc
240

ctgttccagg aggtagatat aattgttcac cattctttgt atctattgaa gaaatgtcac
300

agcttctttc agccaaatat ccagaatatc aaatactatc tgtagatgag ttgaaggaaa
360

ttaaaggggc aagggtgcc a gatttgaact cgaagaagct cgtggacgct ggttttgagt
420

ttaagtatag tgtcgatgat atgttcgatg atgcgattca atgctgcaag gaaaaaggct
480

atctctaagc atgtgtttga aaattccatg aagttgagaa aacaatactg tgcctaaaat
540

caatgatggc taatgagatg tacaagttta tgcattaagt tattttgtgat caatcaaata
600

atgaaataat ctg
613

<210> 283
<211> 602
<212> DNA
<213> *Trifolium repens*

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<222> (8)..(8)
<223> Any nucleotide

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<223> Any nucleotide

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<222> (37)..(37)
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<400> 283
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ctttgattct tccttttatt gttggagggt ttgtttgtcc taagcttctt gattctgttg
120

agaaagctct tgttttggt a ctaggcaaaa aggaacaaat tgggtattata agtttccaca
180

tggtagatgt ggatgatgtg gctagagcac atatctatct acttgagaat cctgttccag
240

gaggtagata taattgttca ccattctttg tatctattga agaaatgtca cagcttcttt
300

cagccaaata tccagaatat caaatactat ctgtagatga gttgaaggaa attaaagggg

360

caaggttgcc agatttgaac tcgaagaagc tcgtggacgc tggttttgag ttttaagtata
420

gtgtcgatga tatgttcgat gatgcgattc aatgctgcaa ggaaaaaggc tatctctaag
480

catgtgtttg aaaattccat gaagttgaga aaacaatact gtgcctaaaa tcaatgatgg
540

ctaattgagat gtacaagttt atgcattaag ttatttgtga tcaatcaaataa
600

tc
602

<210> 284
<211> 575
<212> DNA
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<220>
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<222> (1)..(2)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (13)..(13)
<223> Any nucleotide

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<223> Any nucleotide

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<222> (56)..(56)
<223> Any nucleotide

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<222> (575)..(575)
<223> Any nucleotide

<400> 284
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120

aggcaaaaag gaacaaattg gtattataag tttccacatg gtacatgtag atgatgtggc
180

tagagcacat atctatctac ttgagaatcc tgttocagga ggtagatata attgttcacc
240

attcttttgta tctattgaag aaatgtcaca gcttctctca gccaaatattc cagaatatca
300

aatactatca gtagatgagt tgaaggaaat taaagggtgca agattgccag atttgaactc
360

gaagaagctc gtggacgctg gttttgagtt taagtatagt gtcgatgata tgtttgatga
420

tgcgattcaa tgctgcaagg aaaaaggcta tctctaagca tgtatttgaa aattccatga
480

agttgagaaa acaataatgt gcctaaaatc aatgatggct aatgagatgt acaagtttat
540

gcattaagtt atttgtgatc aatcaaataa tgaan
575

<210> 285
<211> 604
<212> DNA
<213> *Trifolium repens*

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<222> (1)..(2)
<223> Any nucleotides

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<222> (14)..(15)
<223> Any nucleotides

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<222> (56)..(56)
<223> Any nucleotide

<400> 285
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120

aggcaaaaag gaacaaattg gtattataag tttccacatg gtacatgtag atgatgtggc
180

tagagcacat atctatctac ttgagaatcc tgttccagga ggtagatata attgttcacc
240

attcttttgta tctattgaag aaatgtcaca gcttctctca gccaaatattc cagaatatca
300

aatactatca gtagatgagt tgaaggaaat taaagggtgca agattgccag atttgaactc
360

gaagaagctc gtggacgctg gttttgagtt taagtatagt gtcgatgata tgtttgatga
420

tgcgattcaa tgctgcaagg aaaaaggcta tctctaagca tgtatttgaa aattccatga
480

agttgagaaa acaataatgt gctaaaaatc aatgatggct aatgagatgt acaagtttat
540

gcattaagtt atttgtgatc aatcaaataa tgaaataatc tgttcatttt tccgaaaaaa
600

aaaa
604

<210> 286
<211> 695
<212> DNA
<213> *Lolium perenne*

<400> 286
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ctttgttgct tcttggttg tcaaaagact actcgagtcc gggtataatg ttctaggac
120

agtcagagac ccaggcaatc agaagaagggt agcacacctc tggaacttag caggggccaa
180

ggaaagggtg gagcttgtca aagctgacct cttggaagaa gggagcttcg atgatgctgt
240

gatggcctgt gaggggtgtct tccacactgc atcacctatc atcaccaa atcgataccaa
300

ggaagaaatg cttgattctg caattaacgg cactctaaac gtgctgagat cgtgcaagaa
360

gaatcctttt ctcaaaaggg ttgttctcac gtcacatcgc tcaaccgtga ggctgaggga
420

tgaagctgaa ttcccaccca acgtgttgct ggatgaaaca tcatggagct ccgtggagtt
480

ctgtgaaagt atccaggtat ggtatggtgt cgcgaagatc cttgctgaga aatcagcttg
540

ggagttcgcc aaggagaaca acatcgacct agtggctgtt cttccaacgt tcgtgattgg
600

acctaattctc tcgtctgaat taggaccac tgttttagat gtccttggct tatttaaagg
660

agagacagag aagttcacca tgtttkggaa ggatg
695

<210> 287
<211> 231
<212> PRT
<213> *Lolium perenne*

<400> 287

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Gly Ala Ser Gly Phe Val Ala Ser Trp Leu Val Lys Arg Leu Leu Glu

20					25					30					
Ser	Gly	Tyr	Asn	Val	Leu	Gly	Thr	Val	Arg	Asp	Pro	Gly	Asn	Gln	Lys
	35					40						45			
Lys	Val	Ala	His	Leu	Trp	Asn	Leu	Ala	Gly	Ala	Lys	Glu	Arg	Leu	Glu
	50					55					60				
Leu	Val	Lys	Ala	Asp	Leu	Leu	Glu	Glu	Gly	Ser	Phe	Asp	Asp	Ala	Val
65						70					75				80
Met	Ala	Cys	Glu	Gly	Val	Phe	His	Thr	Ala	Ser	Pro	Ile	Ile	Thr	Lys
				85					90					95	
Ser	Asp	Thr	Lys	Glu	Glu	Met	Leu	Asp	Ser	Ala	Ile	Asn	Gly	Thr	Leu
			100					105					110		
Asn	Val	Leu	Arg	Ser	Cys	Lys	Lys	Asn	Pro	Phe	Leu	Lys	Arg	Val	Val
		115					120					125			
Leu	Thr	Ser	Ser	Ser	Ser	Thr	Val	Arg	Leu	Arg	Asp	Glu	Ala	Glu	Phe
	130					135					140				
Pro	Pro	Asn	Val	Leu	Leu	Asp	Glu	Thr	Ser	Trp	Ser	Ser	Val	Glu	Phe
145						150					155				160
Cys	Glu	Ser	Ile	Gln	Val	Trp	Tyr	Gly	Val	Ala	Lys	Ile	Leu	Ala	Glu
				165					170					175	
Lys	Ser	Ala	Trp	Glu	Phe	Ala	Lys	Glu	Asn	Asn	Ile	Asp	Leu	Val	Ala
			180					185					190		
Val	Leu	Pro	Thr	Phe	Val	Ile	Gly	Pro	Asn	Leu	Ser	Ser	Glu	Leu	Gly
		195					200					205			
Pro	Thr	Val	Leu	Asp	Val	Leu	Gly	Leu	Phe	Lys	Gly	Glu	Thr	Glu	Lys
	210					215					220				
Phe	Thr	Met	Phe	Gly	Lys	Asp									
225						230									

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 <212> DNA
 <213> Lolium perenne

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 <223> Any nucleotide

<400> 288
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120
caggcaatca gaagaaggta gcacacctct ggaacttagc aggggccaag gaaaggttgg
180
agcttgctcaa agctgacctc ttggaagaag ggagcttcga tgatgctgtg atggcctgtg
240
agggtgtctt ccacactgca tcacctatca tcaccaaate tgataccaag gaagaaatgc
300
ttgattctgc aattaacggc actctaaacg tgctgagatc gtgcaagaag aatccttttc
360
tcaaaagggg tgttctcacg tcatcatcgt caaccgtgag gctgagggat gaagctgaat
420
tcccacccaa cgtgttgctg gatgaaacat catggagctc cgtggagttc tgtgaaagta
480
tccaggtatg gtatggtgtc gcgaagatcc ttgctgagaa atcagcttgg gagttcgcca
540
aggagaacaa catcgacctc gtggctgttc ttccaacggt cgtgattgga cctaattctc
600
cgtctgaatt aggaccact gtttttagatg tccttggcctt atttaaagga gagacagaga
660
agttcac
667

<210> 289
<211> 688
<212> DNA
<213> *Lolium perenne*

<220>
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<222> (23)..(23)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (651)..(651)
<223> Any nucleotide

<400> 289
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gcttcttggc ttgtcaaaag actactcgag tccggttata atgttctagg gacagtcaga
120
gaccaggca atcagaagaa ggtagcacac ctctggaact tagcaggggc caaggaaagg
180
ttggagcttg tcaaagctga cctcttgga gaaggagct tcgatgatgc tgtgatggcc

240

tgtgaggggtg tcttccacac tgcacacact atcatcacca aatctgatac caaggaagaa
300

atgcttgatt ctgcaattaa cggcactcta aacgtgctga gatcgtgcaa gaagaatcct
360

tttctcaaaa gggttgttct cactcatca tcgtcaaccg tgaggctgag ggatgaagct
420

gaattccac ccaacgtgtt gctggatgaa acatcatgga gctccgtgga gttctgtgaa
480

agtatccagg tatggtatgg tgcgcgaag atccttgctg agaaatcagc ttgggagttc
540

gccaaaggaga acaacatcga cctagtggct gttcttccaa cgctcgtgat tggacctaat
600

ctctcgtctg aattaggacc cactgtttta gatgtccttg gcttatttaa nggagagaca
660

gagaagttca ccatgttttg gaaggatg
688

<210> 290
<211> 425
<212> DNA
<213> Lolium perenne

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<222> (3)..(3)
<223> Any nucleotide

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<223> Any nucleotide

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<223> Any nucleotide

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<223> Any nucleotide

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<222> (363)..(363)
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<222> (387)..(387)
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<222> (390)..(390)
<223> Any nucleotide

<220>
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<222> (396)..(396)
<223> Any nucleotide

<220>
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<222> (404)..(404)
<223> Any nucleotide

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<222> (409)..(409)
<223> Any nucleotide

<220>
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<222> (423)..(423)
<223> Any nucleotide

<220>
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<222> (425)..(425)
<223> Any nucleotide

<400> 290
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tnaaagacta ctogagtccg gttataatgt tctagggaca gtcagagacc caggcaatca
120
gaagaaggta gcacacctct ggaacttagc aggggcccaag gaaagggttg agcttggtcaa
180

agctgacctc ttggaagaag ggagcttcga tgatgctgtg atggcctgtg aggggtgtctt
240

ccacactgca tcacctatca tcaccaaatac tgataccaag gaagaaatgc ttgattctgc
300

aattaacggc actctaaacg ngctgagatc gngcaagaag aatncttttc tnaaaagggn
360

tgntctcacg tcatcatcgc caccocngan gctganggat gaantgant tcccacccaa
420

cgngn
425

<210> 291
<211> 691
<212> DNA
<213> *Lolium perenne*

<220>
<221> misc_feature
<222> (691)..(691)
<223> Any nucleotide

<400> 291
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tgttgcttcc tggcttgtca aaagacttct cgagtccggt tataatgttc tagggacagt
120

cagagaccca ggcaatcaga agaaggtagc acacctctgg agcttagcag gggccaagga
180

aaggctggag cttgtcagag ctgacctctt ggaagaaggg agcttcgatg atgccgtgat
240

ggcctgtgag ggtgtcttcc aactgcatc acctatcatc accaaatctg ataccaagga
300

agaaatgctt gattctgcaa taaacggcac tctaaacgtg ctgagatcgt gcaagaagaa
360

tccttttctc aaaagggttg ttctcacgtc atcatcgtca accgtgaggc tgagggatga
420

agctgaattc ccacccaacg tgttgctgga tgaacatca tggagctccg tggagtctctg
480

tgaagtatc caggtatggt acggtgtcgc aaagatcctt gccgagaaat cagcctggga
540

gtttgccaag gagaacaaca tcgacctagt ggctgttctt ccaacattcg tgattggacc
600

taatctctcg tctgaattag gaccactgt ttagatgtc cttggcttat ttaaaggaga
660

gacagagaag ttcaccatgt ttgggaagga n
691

<210> 292

<211> 365
<212> DNA
<213> Lolium perenne

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<222> (29)..(29)
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<222> (356)..(356)
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<400> 292
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120
gtcagagacc caggcaatca gaagaaggta gcacacctct ggagcttagc aggggccaag
180
gaaaggctgg agcttgtcag agctgacctc ttggaagaag ggagcttcga tgatgccgtg
240
atggcctgtg aggggtgtctt ccacactgca tcacctatca tcaccaaata tgataccaag
300
gaagaaatgc ttgattctgc aataaacggc nctctaaacg tgctgnnatc cgggtnaaaa
360

aaaan
365

<210> 293
<211> 524
<212> DNA
<213> Lolium perenne

<220>
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<400> 293
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caccgcgcgc acttcctaaa gcttctcaag gacctcttcc cgcagtactc cttcaccgcc
120
aagtgcgaag acgacggcaa gcccatggcg aagccgtaca agttctccna ccagaggctc
180
agggacctgg gattaaaatt cactccgctg gcggaaagtt tgtacgagac cgtgacgtgc
240
ctgcaaaaaa atggccacct gcctctgccc gctcccatgg cgccaaagcg tgcataccta
300
taatactaca aagacacggc cgggatcgac aagccaagaa acagaggatt ctcccgaggt
360
tcaccatgga attgtgtatt tcacaaagtt tgaattctta ttttttttat tatgaagaaa
420
tacggaaaac caatactgta taccagaggc aagtgtaca atgtaaatag tcgtgtaa
480
cttgttcaag aatgaatgat aaagtatttt ttgcaaaaaa aaaa
524

<210> 294
<211> 100
<212> PRT
<213> Lolium perenne

<220>
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<222> (57)..(57)
<223> Any amino acid

<400> 294
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Gly Ala Val Leu His Arg Ala His Phe Leu Lys Leu Leu Lys Asp Leu
20 25 30
Phe Pro Gln Tyr Ser Phe Thr Ala Lys Cys Glu Asp Asp Gly Lys Pro
35 40 45
Met Ala Lys Pro Tyr Lys Phe Ser Xaa Gln Arg Leu Arg Asp Leu Gly
50 55 60
Leu Lys Phe Thr Pro Leu Ala Glu Ser Leu Tyr Glu Thr Val Thr Cys
65 70 75 80
Leu Gln Lys Asn Gly His Leu Pro Leu Pro Ala Pro Met Ala Pro Lys
85 90 95

Arg Ala Tyr Leu
100

<210> 295
<211> 524
<212> DNA
<213> Lolium perenne

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<222> (482)..(482)
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<222> (519)..(519)
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<400> 295
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caccgcgcgc acttcctaaa gcttctcaag gacctcttcc cgcagtactc cttcaccgcc
120

aagtgcgaag acgacggcaa gcccatggcg aagccgtaca agttctccaa ccagaggctc
180

agggacctgg gattaaaatt cactccgctg gcggaaagtt tgtacgagac cgtgacgtgc
240

ctgcaaaaaa atggccacct gcctctgccc gctcccgtgg cgccaaagcg tgcataccta
300

taatantacc aagacacggc cgggatcgac aagccaagaa acagaggatt ctcccgaggt
360

tcaccatgga attgtgtatt tcagaaagtt tgaattctta ttttttttat tatgaaggaa
420

tacggataac caatactgta taccagaggc aagtgtaca atgtaaatag tcgtgtaaat
480

cntgttcaag attgaatgat aaagtatttt ttgcaaaaana aaaa
524

<210> 296
<211> 374
<212> DNA
<213> Lolium perenne

<220>
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<222> (19)..(19)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (25)..(26)

<223> Any nucleotides

<400> 296

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120

gctcccatgg cgccaaagcg tgcataccta taatactaca aagacacggc cgggatcgac
180

aagccaagaa acagaggatt ctcccagagt tcacatgga attgtgtatt tcacaaagtt
240

tgaattctta ttttttttat tatgaagaaa tacggaaaac caatactgta taccagagggc
300

aagtgtaca atgtaaatag tcgtgtaaat cttgttcaag aatgaatgat aaagtatttt
360

ttgcaaaaaa aaaa
374

<210> 297

<211> 363

<212> DNA

<213> Lolium perenne

<220>

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<222> (7)..(8)

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<222> (363)..(363)

<223> Any nucleotide

<400> 297

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120

gccaaagcgt gcatacctat aatactacaa agacacggcc gggatcgaca agccaagaaa
180

cagaggattc tcccagaggtt caccatggaa ttgtgtattt cacaaagttt gaattcttat
240

tttttttatt atgaagaaat acggaaaacc aatactgtat accagaggca agtgtacaa
300

tgtaaatagt cgtgtaaatc ttgttcaaga atgaatgata aagtattttt tgcaaaaaaa

360

aan

363

<210> 298
<211> 1381
<212> DNA
<213> Lolium perenne

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<222> (1338)..(1338)
<223> Any nucleotide

<400> 298
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tcagctaacc attcctcaac tagaataagc atggctccgg cgatgtccaa ccctctcctc
120

agtgatcggg tggcacgctc caagaaagtc ccatctagcc acgttagagc ggtgggagac
180

cgcccagacc tcgccaatgt cgaccacgag tccggcgcg gcatccgct catcgacctg
240

aagcagctcg aaggtccagg gcgccgcagg gtcgtcgagg ccatcggtc cgcgtgcgag
300

aacgatgggt ttttcatggt gacgaatcat ggcattcccag aggcggctcgt ggaggggatg
360

ctgagcgtgg cgagggagtt cttccacctg ccggagtcgg agcgggtcaa gtgctactcc
420

gacgacccca agaaggcggt ccggctgtcg acgagcttca acgtgcgcac ggagaagggtg
480

agcaactggc gcgacttcct ccggctgcat tgctaccctc ttgagagctt cgtcgaccag
540

tggccgtcga acccgcccg cttcaggcaa gtcgtcggca cctactcgac ggaagcgaga
600

gcgctggcgc tgaggctcct ggaggcgata tcggagagcc tagggctgga gagaggccac
660

atgggtgaagg ccatggggcg gcacgcgcag cacatggcgg tgaactacta cccgccgtgc
720

ccgcagccgg agctcaccta cggctctgcca gggcacacgg accccaacgc cctcaccatc
780

ctcctcatgg atccccacgt ctccggcctc caggctctca gggacggcgc caagtggatc
840

gccgtccacc cacgccccaa cgccctgggtc atcaacctag ggcaccagct acaggcgctg
900

agcaacggcg cgtacaagag cgtgtggcac cgggcagtgg tgaacgcgga gcaggagcgt
960

ctgtcggtag catctttcct gtgcccgtgc aacagcgcgg ttatctgccc cgcgccgagg
1020

ctcgtcggcg acgggggagga ccccgctctac cggagctaca cctacgacga gtactacaag
1080

aggttttggg gcaggaacct ggatcaggag cactgcctcg agctcttcag gagtcagcac
1140

tgatgcttga accttgagtt actagctagc tctccttaac agtgcaaadc catggcccaa
1200

gagggccccg attgcatggt tacttatggt gtttgaactg gtattgctta agtgcctaata
1260

aacattgcta cattctactn ctatcttctc cgttttaaata tataagatgg cctaaccttt
1320

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1380

a

1381

<210> 299

<211> 346

<212> PRT

<213> Lolium perenne

<400> 299

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Pro	Ser	Ser	His	Val	Arg	Ala	Val	Gly	Asp	Arg	Pro	Asp	Leu	Ala	Asn
			20					25					30		

Val	Asp	His	Glu	Ser	Gly	Ala	Gly	Ile	Pro	Leu	Ile	Asp	Leu	Lys	Gln
		35					40					45			

Leu	Glu	Gly	Pro	Gly	Arg	Arg	Arg	Val	Val	Glu	Ala	Ile	Gly	Ser	Ala
	50					55					60				

Cys	Glu	Asn	Asp	Gly	Phe	Phe	Met	Val	Thr	Asn	His	Gly	Ile	Pro	Glu
65					70					75					80

Ala	Val	Val	Glu	Gly	Met	Leu	Ser	Val	Ala	Arg	Glu	Phe	Phe	His	Leu
				85					90						95

Pro Glu Ser Glu Arg Leu Lys Cys Tyr Ser Asp Asp Pro Lys Lys Ala
 100 105 110

Val Arg Leu Ser Thr Ser Phe Asn Val Arg Thr Glu Lys Val Ser Asn
 115 120 125

Trp Arg Asp Phe Leu Arg Leu His Cys Tyr Pro Leu Glu Ser Phe Val
 130 135 140

Asp Gln Trp Pro Ser Asn Pro Pro Ala Phe Arg Gln Val Val Gly Thr
 145 150 155 160

Tyr Ser Thr Glu Ala Arg Ala Leu Ala Leu Arg Leu Leu Glu Ala Ile
 165 170 175

Ser Glu Ser Leu Gly Leu Glu Arg Gly His Met Val Lys Ala Met Gly
 180 185 190

Arg His Ala Gln His Met Ala Val Asn Tyr Tyr Pro Pro Cys Pro Gln
 195 200 205

Pro Glu Leu Thr Tyr Gly Leu Pro Gly His Thr Asp Pro Asn Ala Leu
 210 215 220

Thr Ile Leu Leu Met Asp Pro His Val Ser Gly Leu Gln Val Leu Arg
 225 230 235 240

Asp Gly Ala Lys Trp Ile Ala Val His Pro Arg Pro Asn Ala Leu Val
 245 250 255

Ile Asn Leu Gly Asp Gln Leu Gln Ala Leu Ser Asn Gly Ala Tyr Lys
 260 265 270

Ser Val Trp His Arg Ala Val Val Asn Ala Glu Gln Glu Arg Leu Ser
 275 280 285

Val Ala Ser Phe Leu Cys Pro Cys Asn Ser Ala Val Ile Cys Pro Ala
 290 295 300

Pro Arg Leu Val Gly Asp Gly Glu Asp Pro Val Tyr Arg Ser Tyr Thr
 305 310 315 320

Tyr Asp Glu Tyr Tyr Lys Arg Phe Trp Ser Arg Asn Leu Asp Gln Glu
 325 330 335

His Cys Leu Glu Leu Phe Arg Ser Gln His
 340 345

<210> 300
<211> 755
<212> DNA
<213> Lolium perenne

<220>
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<222> (5)..(5)
<223> Any nucleotide

<400> 300
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120
agtgatcggg tggcacgctc caagaaagtc ccatctagcc acgttagagc ggtgggagac
180
cgcccagacc tcgccaatgt cgaccacgag tccggcgcg gcatccgct catcgacctg
240
aagcagctcg aagggtccagg gcgccgcagg gtcgtcgagg ccatcggtc cgcggtcgag
300
aacgatgggt ttttcatggt gacgaatcat ggcattccag aggcggtcgt ggaggggatg
360
ctgagcgtgg cgagggagtt cttccacctg cgggagtcgg agcgggtcaa gtgctactcc
420
gacgacccca agaaggcggt ccggctgtcg acgagcttca acgtgcgcac ggagaagggtg
480
agcaactggc ggaacttcct ccggctgcat tgctaccctc ttgagagctt cgtcgaccag
540
tggccgtcga acccgcccg cttcaggcaa gtcgtcggca cctactcgac ggaagcgaga
600
gcgctggcgc tgaggctcct ggaggcgata tcggagagcc tagggctgga gagaggccac
660
atggtgaagg ccatggggcg gcacgcgcag cacatggcgg tgaactacta cccgccgtgc
720
ccgcagccgg agctcaccta cggctctgcc gggca
755

<210> 301
<211> 780
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (21)..(21)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (778)..(778)

<223> Any nucleotide

<400> 301

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120

tgatcgggtg gcacgctcca agaaagtccc atctagccac gttagagcgg tgggagaccg
180

cccagacctc gccaatgtcg accacgagtc cggcgcgggc attccgctca tcgacctgaa
240

gcagctcgaa ggtccagggc gccgcagggc cgtcgaggcc atcggctccg cgtgcgagaa
300

cgatggggtt ttcatgggtga cgaatcatgg catcccagag gcggtcgtgg aggggatgct
360

gagcgtggcg agggagttct tccacctgcc ggagtcggag cggctcaagt gctactccga
420

cgaccccaag aaggcgggtc ggctgtcgac gagcttcaac gtgcgcacgg agaaggtgag
480

caactggcgc gacttcctcc ggctgcattg ctacctctt gagagcttcg tcgaccagtg
540

gccgtcgaaac ccgccgcct tcaggcaagt cgtcggcacc tactcgacgg aagcgagagc
600

gctggcgctg aggctcctgg aggcgatatc ggagagccta gggctggaga gaggccacat
660

ggtgaaggcc atggggcggc acgcgcagca catggcgggtg aactactacc cgccgtgccc
720

gcagccggag ctcacctacg gtctgccagg gcacacggac cccaatgccc tcaccatnct
780

<210> 302

<211> 793

<212> DNA

<213> Lolium perenne

<220>

<221> misc_feature

<222> (64)..(64)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (692)..(692)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (750)..(750)

<223> Any nucleotide

<400> 302
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120
taccgcgggt gccccgagcc ggacctcacc tacggcctgc ccaagcacac ggaccccaac
180
gccctcacca tctctctcat ggatccccac gtctccggcc tccaggctct cagggacggc
240
gccaagtgga tcgccgtcca cccacgcccc aacgccctgg tcatcaacct aggcgaccag
300
ctacaggcgc tgagcaacgg cgcgtacaag agcgtgtggc accgggcagt ggtgaacgcg
360
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420
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480
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540
aggagtgcgc actgatgctt gaaccttgag ttactagcta gctctcctta acagtgcaaa
600
tccatggccc aagaggggccc cgattgcatg gttacttatg ttgtttgaac tggatttgct
660
taagtgccta ataacattgc tacattctac tnctatcttg tccgtttaaa attataagat
720
ggcctaacct ttttcttaat tgtatgcatt ctgaacatat ttaagtgtgt gtgttcagac
780
agtttagtct gca
793

<210> 303
<211> 1395
<212> DNA
<213> *Lolium perenne*

<400> 303
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taaccacggg agcgagtggc aagactagca gaaagtacgg acatcagcta accattcctc
120
aactagaata agcatggctc cggcgatgtc caaccctctc ctcagtgatc ggggtggcacg
180
ctccaagaaa gtcccatcta gccacgttag agcgggtggga gaccgcccag acctcgccaa
240
tgtcgaccac gagtccggcg cgggcattcc gctcatcgac ctgaagcagc tcgaaggctc
300

agggcgccgc aggggtcgctg aggccatcgg ctccgcgtgc gagaacgatg ggtttttcat
360
ggtgacgaat catggcatcc cagaggcggg cgtggagggg atgctgagcg tggcgagggg
420
gttcttccac ctgccggagt cggagcggct caagtgctac tccgacgacc ccaagaaggc
480
ggtccggctg tcgacgagct tcaacgtgcg cacggagaag gtgagcaact ggcgcgactt
540
cctccggctg cattgctacc ctcttgagag cttcgtcgac cagtggccgt cgaacccgcc
600
cgccttcagg caagtgcgct gcacctactc gacggaagcg agagcgctgg cgctgaggct
660
cctggaggcg atatcggaga gcctagggct ggagagaggc cacatgggtga aggccatggg
720
gcggcacgcg cagcacatgg cggatgaacta ctacccgccg tgcccgcagc cggagctcac
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840
ctccggcctg cagggtccagc gcgacggccg gtgggtggcc gtcaaccggg tgcccaacgc
900
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960
gaaccacaga gtgatcgta acagcgcgag cgagaggatt tcggtgccga cgttctactg
1020
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1080
ggcctaccag cccttcacgt accaggagta ctacgaggag ttctggaaga tgggccttca
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1260
tcctccctcc ggaaaagaaa aataaaacag agtggagacc actagaaccg tcagatagca
1320
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1380
atcactagtg aattc
1395

<210> 304
<211> 348
<212> PRT
<213> Lolium perenne

<400> 304

Met Ala Pro Ala Met Ser Asn Pro Leu Leu Ser Asp Arg Val Ala Arg

1	5	10	15
Ser Lys Lys Val Pro Ser Ser His Val Arg Ala Val Gly Asp Arg Pro	20	25	30
Asp Leu Ala Asn Val Asp His Glu Ser Gly Ala Gly Ile Pro Leu Ile	35	40	45
Asp Leu Lys Gln Leu Glu Gly Pro Gly Arg Arg Arg Val Val Glu Ala	50	55	60
Ile Gly Ser Ala Cys Glu Asn Asp Gly Phe Phe Met Val Thr Asn His	65	70	75
Gly Ile Pro Glu Ala Val Val Glu Gly Met Leu Ser Val Ala Arg Glu	85	90	95
Phe Phe His Leu Pro Glu Ser Glu Arg Leu Lys Cys Tyr Ser Asp Asp	100	105	110
Pro Lys Lys Ala Val Arg Leu Ser Thr Ser Phe Asn Val Arg Thr Glu	115	120	125
Lys Val Ser Asn Trp Arg Asp Phe Leu Arg Leu His Cys Tyr Pro Leu	130	135	140
Glu Ser Phe Val Asp Gln Trp Pro Ser Asn Pro Pro Ala Phe Arg Gln	145	150	155
Val Val Gly Thr Tyr Ser Thr Glu Ala Arg Ala Leu Ala Leu Arg Leu	165	170	175
Leu Glu Ala Ile Ser Glu Ser Leu Gly Leu Glu Arg Gly His Met Val	180	185	190
Lys Ala Met Gly Arg His Ala Gln His Met Ala Val Asn Tyr Tyr Pro	195	200	205
Pro Cys Pro Gln Pro Glu Leu Thr Tyr Gly Leu Pro Gly His Lys Asp	210	215	220
Pro Asn Ala Ile Thr Leu Leu Leu Gln Asp Gly Val Ser Gly Leu Gln	225	230	235
Val Gln Arg Asp Gly Arg Trp Val Ala Val Asn Pro Val Pro Asn Ala	245	250	255
Leu Val Ile Asn Ile Gly Asp Gln Leu Gln Ala Leu Ser Asn Asp Arg	260	265	270

341/390

Tyr Lys Ser Val Asn His Arg Val Ile Val Asn Ser Ala Ser Glu Arg
 275 280 285

Ile Ser Val Pro Thr Phe Tyr Cys Pro Ser Pro Asp Thr Val Val Ala
 290 295 300

Pro Ala Asp Ala Leu Val Asp Asp Ala His Pro Arg Ala Tyr Gln Pro
 305 310 315 320

Phe Thr Tyr Gln Glu Tyr Tyr Glu Glu Phe Trp Lys Met Gly Leu Gln
 325 330 335

Ser Ala Ser Cys Leu Asp Arg Phe Arg Arg Ile Glu
 340 345

<210> 305
 <211> 1309
 <212> DNA
 <213> Trifolium repens

<400> 305
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tataagttttc ttggtgaaaa aagagtttgt aaattaacat catggctagt atcaaacaaa
 120

ttggaacaaa gaaagcatgt gtgattgggtg gcactgggtt tgttgcattc atgttgatca
 180

agcagttact tgaaaagggt tatgctgtta atactaccgt tagagacca gatagcccta
 240

agaaaatatc tcacctagtg gcactgcaaa gtttggggga actgaatcta tttagagcag
 300

acttaacagt tgaagaagat tttgatgctc ctatagcagg atgtgaactt gtttttcaac
 360

ttgctacacc tgtgaacttt gcttctcaag atcctgagaa tgacatgata aagccagcaa
 420

tcaaagggtgt gttgaatgtg ttgaaagcaa ttgcaagagc aaaagaagtt aaaagagtta
 480

tcttaacatc ttcggcagcc gcggtgacta taaatgaact caaagggaca ggtcatgtta
 540

tgatgaaac caactgggtc gatgttgaat ttctcaacac tgcaaaacca ccacttggg
 600

gttatcctgc ctcaaaaatg ctagctgaaa aggctgcatg gaaatttgct gaagaaaatg
 660

acattgatct aatcactgtg atacctagtt taacaactgg tccttctctc acaccagata
 720

tcccatctag tgttggcttg gcaatgtctc taataacagg caatgatttt ctcataaatg
 780

ctttgaaagg aatgcagttt ctgtcgggtt cgttatccat cactcatgtt gaggatattt
840

gccgagctca tatatttctt gcagagaaag aatcagcttc tggtagatac atttgctgtg
900

ctcacaatac tagtgttccc gagcttgcaa agttttctcaa caaacgatat cctcagtata
960

aagttccaac tgaatttgat gattgcccc a gcaaggcaaa gttgataatc tcttctgaaa
1020

agcttatcaa agaagggttc agtttcaagc atggtattgc cgaaactttc gaccagactg
1080

tcgagtattt taagactaag ggggcactga agaattagat tttgatattt ctaattcaat
1140

agcaaaactct aagcttggtta tgtgtttgtg aagttcagag tgaaatatca aatgaataag
1200

tggagagagc acaataagag gagagcacia taattttgga aaaaaaaaaa aaaaaaaaaa
1260

aaaaaaaaagt actctgcgtt gttaccactg cttaatcact agtgaattc
1309

<210> 306

<211> 338

<212> PRT

<213> Trifolium repens

<400> 306

Met Ala Ser Ile Lys Gln Ile Gly Asn Lys Lys Ala Cys Val Ile Gly
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Gly Thr Gly Phe Val Ala Ser Met Leu Ile Lys Gln Leu Leu Glu Lys
20 25 30

Gly Tyr Ala Val Asn Thr Thr Val Arg Asp Pro Asp Ser Pro Lys Lys
35 40 45

Ile Ser His Leu Val Ala Leu Gln Ser Leu Gly Glu Leu Asn Leu Phe
50 55 60

Arg Ala Asp Leu Thr Val Glu Glu Asp Phe Asp Ala Pro Ile Ala Gly
65 70 75 80

Cys Glu Leu Val Phe Gln Leu Ala Thr Pro Val Asn Phe Ala Ser Gln
85 90 95

Asp Pro Glu Asn Asp Met Ile Lys Pro Ala Ile Lys Gly Val Leu Asn
100 105 110

Val Leu Lys Ala Ile Ala Arg Ala Lys Glu Val Lys Arg Val Ile Leu
115 120 125

Thr Ser Ser Ala Ala Ala Val Thr Ile Asn Glu Leu Lys Gly Thr Gly
 130 135 140
 His Val Met Asp Glu Thr Asn Trp Ser Asp Val Glu Phe Leu Asn Thr
 145 150 155 160
 Ala Lys Pro Pro Thr Trp Gly Tyr Pro Ala Ser Lys Met Leu Ala Glu
 165 170 175
 Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Asp Ile Asp Leu Ile Thr
 180 185 190
 Val Ile Pro Ser Leu Thr Thr Gly Pro Ser Leu Thr Pro Asp Ile Pro
 195 200 205
 Ser Ser Val Gly Leu Ala Met Ser Leu Ile Thr Gly Asn Asp Phe Leu
 210 215 220
 Ile Asn Ala Leu Lys Gly Met Gln Phe Leu Ser Gly Ser Leu Ser Ile
 225 230 235 240
 Thr His Val Glu Asp Ile Cys Arg Ala His Ile Phe Leu Ala Glu Lys
 245 250 255
 Glu Ser Ala Ser Gly Arg Tyr Ile Cys Cys Ala His Asn Thr Ser Val
 260 265 270
 Pro Glu Leu Ala Lys Phe Leu Asn Lys Arg Tyr Pro Gln Tyr Lys Val
 275 280 285
 Pro Thr Glu Phe Asp Asp Cys Pro Ser Lys Ala Lys Leu Ile Ile Ser
 290 295 300
 Ser Glu Lys Leu Ile Lys Glu Gly Phe Ser Phe Lys His Gly Ile Ala
 305 310 315 320
 Glu Thr Phe Asp Gln Thr Val Glu Tyr Phe Lys Thr Lys Gly Ala Leu
 325 330 335

Lys Asn

<210> 307

<211> 1005

<212> DNA

<213> Trifolium repens

<400> 307

gaattcgcatt aagcagtggt aacaacgcag agtacgcggg gacttaaaca ttgacacaag
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tcccaaataa aaaagatctg aaacaacata gtcaccccat tttttaacat taaactaaaa
 120
 atatgtcggc catcaccgca atccaagtcg agaaçcttga atttccggct gtgggttactt
 180
 ctccggccac cggtaaagtca tattttcttg gtgggtgcagg ggagagaggt ttgactattg
 240
 aaggaaaactt catcaagttc actgccatag gagtatatatt ggaagatgta gcagtggctt
 300
 cacttgccac taaatggaag ggtaaâtccct ctgaggagtt gcttgagact cttgacttct
 360
 atagagacat catttcagga ccctttgaaa agttgattcg aggatcgaag attaggggaat
 420
 tgagtgggtcc tgagtactca aggaaggtta atgaaaactg cgtggcacac ttaaaatctg
 480
 ttgggactta tggagatgct gaagctgaag ctatgcaaaa atttgttgaa gccttcaagc
 540
 ctattaatth tccacctggg gcctctgttt ttacaggca atcacctgat ggaatattag
 600
 ggcttagttt ctctcaagat gcaagtatac cagaaaagga ggctgcagta atagagaaca
 660
 aggcagcttc atcggcagtg ttagaaaacta tgattgggtga acatgctgtt tctcctgatt
 720
 taaagcgttg tttggctgca agattacctg ccttgttgaa cgagggtact ttcaagattg
 780
 aatgaaaact gattattatt atctccaaaa gcattgcagc acaagattga gtcatttatg
 840
 agcatggaca tttttatgtc cacacatgtt taacttttgt atctctcttt agattctcat
 900
 caatatcaat aataactaata tgaaacgaag tcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
 960
 aaaagtactc tgcgttggtta ccaactgctta atcactagtg aattc
 1005

<210> 308
 <211> 220
 <212> PRT
 <213> Trifolium repens

<400> 308

Met Ser Ala Ile Thr Ala Ile Gln Val Glu Asn Leu Glu Phe Pro Ala
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Val Val Thr Ser Pro Ala Thr Gly Lys Ser Tyr Phe Leu Gly Gly Ala
 20 25 30

Gly Glu Arg Gly Leu Thr Ile Glu Gly Asn Phe Ile Lys Phe Thr Ala
 35 40 45

Ile Gly Val Tyr Leu Glu Asp Val Ala Val Ala Ser Leu Ala Thr Lys
 50 55 60

Trp Lys Gly Lys Ser Ser Glu Glu Leu Leu Glu Thr Leu Asp Phe Tyr
 65 70 75 80

Arg Asp Ile Ile Ser Gly Pro Phe Glu Lys Leu Ile Arg Gly Ser Lys
 85 90 95

Ile Arg Glu Leu Ser Gly Pro Glu Tyr Ser Arg Lys Val Asn Glu Asn
 100 105 110

Cys Val Ala His Leu Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu Ala
 115 120 125

Glu Ala Met Gln Lys Phe Val Glu Ala Phe Lys Pro Ile Asn Phe Pro
 130 135 140

Pro Gly Ala Ser Val Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu Gly
 145 150 155 160

Leu Ser Phe Ser Gln Asp Ala Ser Ile Pro Glu Lys Glu Ala Ala Val
 165 170 175

Ile Glu Asn Lys Ala Ala Ser Ser Ala Val Leu Glu Thr Met Ile Gly
 180 185 190

Glu His Ala Val Ser Pro Asp Leu Lys Arg Cys Leu Ala Ala Arg Leu
 195 200 205

Pro Ala Leu Leu Asn Glu Gly Thr Phe Lys Ile Glu
 210 215 220

<210> 309
 <211> 1105
 <212> DNA
 <213> Trifolium repens

<400> 309
 gaattcacta gtgattaagc agtggttaaca acgcagagta cgcggggaca ttacaactca
 60

caacaccttc tccattacca tctatcttct actaagttca acgagatcaa tggcacttcc
 120

ttctgtcacc gctttgaata tcgagaacaa tctattccct cctaccgtca caccaccggg
 180

atccaccaac aattttcttcc tcggcggtgc aggagagcgg ggtcttcaaa ttcaagacaa
 240

atttgtcaaa ttcaccgcta ttggtgttta tctacaggac attgctgttc cttacctcgc
 300

cactaaatgg aagggttaaga ctgctcaaga gctaacggaa actgttcoctt tcttcagggg
360

catcggttaca ggtccatttg agaaatttat gcaggtgaca atgatcttgc cattgactgg
420

gcaacaatac tcagagaaaag tgtcagaaaa ttgtgtagct atttggaagt ctcttgggat
480

ttataccgac gaagaagcca aagcaattga gaagtttggt tctgtcttca aagatgaaac
540

attcccacca ggctcctcta tcctttttcac agtattaccc aaaggattag gatcactaac
600

gataagtttc tctaaagatg gatccattcc agagaccgag tctgcagtta tagagaataa
660

gtactctca caagctgtgc ttgagtcgat gataggggag cacgggtgtct cccctgcagc
720

aaaacagagt ttggccacca gggtatccga gttattcaac gaggttggtg atgctagcaa
780

ctgattatat caacaaaacg aaaatgaaag tcctttctgc aataaagacc aagcggaaat
840

tttatttttag gtgcactttg aaatgacctc tttggcgact ttttcttgta ctaataataa
900

agagtgtggt tgtatcatgt tgtaatttta ttttagaaaa agtgaggtaa gaaaggagtc
960

cttatgttta tttcaattat tgaaaaatta tttgcatgta taattgattt caactgatgt
1020

tatttaatca cgttttttct aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gtactctgcg
1080

ttgttaccac tgcttaatcg aattc
1105

<210> 310

<211> 224

<212> PRT

<213> Trifolium repens

<400> 310

Met	Ala	Leu	Pro	Ser	Val	Thr	Ala	Leu	Asn	Ile	Glu	Asn	Asn	Leu	Phe
1				5					10					15	

Pro	Pro	Thr	Val	Thr	Pro	Pro	Gly	Ser	Thr	Asn	Asn	Phe	Phe	Leu	Gly
			20					25					30		

Gly	Ala	Gly	Glu	Arg	Gly	Leu	Gln	Ile	Gln	Asp	Lys	Phe	Val	Lys	Phe
		35					40					45			

Thr	Ala	Ile	Gly	Val	Tyr	Leu	Gln	Asp	Ile	Ala	Val	Pro	Tyr	Leu	Ala
		50					55						60		

Thr Lys Trp Lys Gly Lys Thr Ala Gln Glu Leu Thr Glu Thr Val Pro
 65 70 75 80

Phe Phe Arg Asp Ile Val Thr Gly Pro Phe Glu Lys Phe Met Gln Val
 85 90 95

Thr Met Ile Leu Pro Leu Thr Gly Gln Gln Tyr Ser Glu Lys Val Ser
 100 105 110

Glu Asn Cys Val Ala Ile Trp Lys Ser Leu Gly Ile Tyr Thr Asp Glu
 115 120 125

Glu Ala Lys Ala Ile Glu Lys Phe Val Ser Val Phe Lys Asp Glu Thr
 130 135 140

Phe Pro Pro Gly Ser Ser Ile Leu Phe Thr Val Leu Pro Lys Gly Leu
 145 150 155 160

Gly Ser Leu Thr Ile Ser Phe Ser Lys Asp Gly Ser Ile Pro Glu Thr
 165 170 175

Glu Ser Ala Val Ile Glu Asn Lys Leu Leu Ser Gln Ala Val Leu Glu
 180 185 190

Ser Met Ile Gly Ala His Gly Val Ser Pro Ala Ala Lys Gln Ser Leu
 195 200 205

Ala Thr Arg Leu Ser Glu Leu Phe Asn Glu Val Gly Asp Ala Ser Asn
 210 215 220

<210> 311
 <211> 1272
 <212> DNA
 <213> Trifolium repens

<400> 311
 gaattcgatt aagcagtggg aacaacgcag agtacgcggg gattcaaaca tagctcaaag
 60

tgtgtaacaa atttcttaac ttaaaacatt ttcaacccaa caaaaaaaaa caaagacaaa
 120

aacatgggta gtgttgaaat tocaacaaag gttcttacta acagttctag tcaagtgaag
 180

atgcctgtgg ttggaatggg atcagcacct gatttcacat gtaagaaaga cacaaaagat
 240

gcaatcattg aagccatcaa acagggttat agacactttg atactgctgc tgcttatggc
 300

tcagaacaag ctcttggtga aggtttgaaa gaagcaattg aacttggtct tgtcactaga
 360

gaagaccttt ttgttacttc taaactttgg gtcactgaaa atcatcctca tcttgttggg

420

cctgctcttc aaaaatctct caagactctt caattggagt acttggactt gtatttgatc
480

cattggccac ttagttctca gcctggaaag ttttcatttc caattgatgt ggcagatctc
540

ttgccatttg atgtgaaggg tgtttgggaa tccatggaag aaggcttgaa acttggactc
600

actaaagcta ttggtgtag taacttctct gtcaagaaac ttcaaatct tgtctcagtt
660

gccactgttc ttctgtctgt caatcaagtg gagatgaacc ttgcatggca acaaaagaag
720

cttagagaat tttgcaatgc aaatggaata gtgttaactg cattttcacc attgagaaaa
780

ggtgcaagca ggggaccaa tgaagttatg gaaaatgata tgcttaaaga gattgcagat
840

gctcatggaa agtctgttgc acaaatttca ttgagatggg tatatgaaca aggagtcact
900

tttgttccca agagctatga taaggaaaga atgggtcaaa atttggctat ctttgattgg
960

acattggcaa aagaagatca tgagaaaatt gatcaaatta agcagaaccg tttgatccct
1020

ggaccaacca agccaggact cagtgcacta tgggatgatg aaatataaag tggaagatgt
1080

taaaagtccc ttaagctcac tcaatatcta tctatttgtt actttttgca tttgggggtt
1140

gaaattgagt cacccttggt tctgtatcga tttaaaattt aaataatcaa tttttcatta
1200

caaaaaaaaa aaaaaaaaaa aaaaaaaaaa agtactctgc gttgttacca ctgcttaac
1260

actagtgaat tc
1272

<210> 312

<211> 314

<212> PRT

<213> Trifolium repens

<400> 312

Met Gly Ser Val Glu Ile Pro Thr Lys Val Leu Thr Asn Ser Ser Ser
1 5 10 15

Gln Val Lys Met Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr
20 25 30

Cys Lys Lys Asp Thr Lys Asp Ala Ile Ile Glu Ala Ile Lys Gln Gly
35 40 45

Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Glu Gln Ala Leu
 50 55 60

Gly Glu Gly Leu Lys Glu Ala Ile Glu Leu Gly Leu Val Thr Arg Glu
 65 70 75 80

Asp Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His
 85 90 95

Leu Val Val Pro Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Glu
 100 105 110

Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Leu Ser Ser Gln Pro Gly
 115 120 125

Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu Pro Phe Asp Val
 130 135 140

Lys Gly Val Trp Glu Ser Met Glu Glu Gly Leu Lys Leu Gly Leu Thr
 145 150 155 160

Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Asn Leu
 165 170 175

Val Ser Val Ala Thr Val Leu Pro Ala Val Asn Gln Val Glu Met Asn
 180 185 190

Leu Ala Trp Gln Gln Lys Lys Leu Arg Glu Phe Cys Asn Ala Asn Gly
 195 200 205

Ile Val Leu Thr Ala Phe Ser Pro Leu Arg Lys Gly Ala Ser Arg Gly
 210 215 220

Pro Asn Glu Val Met Glu Asn Asp Met Leu Lys Glu Ile Ala Asp Ala
 225 230 235 240

His Gly Lys Ser Val Ala Gln Ile Ser Leu Arg Trp Leu Tyr Glu Gln
 245 250 255

Gly Val Thr Phe Val Pro Lys Ser Tyr Asp Lys Glu Arg Met Gly Gln
 260 265 270

Asn Leu Ala Ile Phe Asp Trp Thr Leu Ala Lys Glu Asp His Glu Lys
 275 280 285

Ile Asp Gln Ile Lys Gln Asn Arg Leu Ile Pro Gly Pro Thr Lys Pro
 290 295 300

Gly Leu Ser Asp Leu Trp Asp Asp Glu Ile

305

310

<210> 313
<211> 1548

<212> DNA

<213> *Trifolium repens*

<400> 313

gaattcgatt aagcagtggt atcaacgcag agtacgcggg gacaacaact ataacttcct
60

gttattaacc aattgagttc aaattacata catagcagga actatactaa agatatcaac
120

atgggttagtg tttctgaaat tcgcaaggct caaagggctg aaggccctgc aactattttg
180

gccattggta ctgcaaatcc agcaaactgt gttgaccaga gtacatatcc tgatttctac
240

ttcaaaatca ctaacagtga gcataagggt gagcttaaag agaaatttca gcgcatgtgt
300

gataaatcta tgatcaagag cagatacatg tatctaacag aagagatttt gaaagaaaat
360

cctagtcttt gtgaatacat ggcaccttca ttggatgcta ggcaagacat ggtggtggtt
420

gaggtaccta gacttgggaa ggaggctgca gtgaaagcta tcaaagaatg ggggtcaacca
480

aagtcaaaga ttactcactt aatcttttgc accacaagtg gtgttgacat gcctggtgcc
540

gattaccaac tcacaaaact cttaggtctt cgcccatatg tgaagaggta catgatgtac
600

caacaagggt gctttgcagg tgggacgggt cttcgtttgg ccaaggattt ggccgagaac
660

aacaaagggt ctcgtgtgtt ggttgtttgc tctgaagtaa ccgcagtcac attccgcggc
720

ccagtgaca ctcat ttgga cagtcttggt ggacaagcac tattcggaga tggagctgct
780

gcactcattg ttggctcaga ccagttacca gaaattgaga agccaatatt tgagatggtt
840

tggaccgcac agacaattgc tccagatagt gaagggtcca ttgatgggtca tcttcgtgaa
900

gctggactaa catttcatct tcttaaagat gttcctggga ttgtctcaaa gaacattgat
960

aaggcattgg ttgaggcatt ccaaccatta aacatctctg attacaattc aatcttttgg
1020

attgctcatc cagggtggtcc tgcaattcta gaccaagttg agataaagtt gggcttaaaa
1080

cctgaaaaaa tgaaggccac cagagatgta cttagtgaat atggtaacat gtcaagtgca
1140

tgtgtattgt tcattcttaga tgagatgaga aagaaatcgg ctgaaaatgg acttaaaacc
1200

acaggagaag gacttgactg ggggtgtgtg tttggatttg ggcccggact taccattgaa
1260

actgttggtc tacatagtgt ggctatatga gaatgagaga cttgatttgt ttttattgta
1320

ttgtattgta ttactttaaa tcttggttga acctccattt taagaataaa tatggagtgc
1380

aatatggacc atcctgttaa aataatatat cgtaaatagc tattatttta gtgtctgttt
1440

ctttttacta aactatttta ttttagtatt tgtttttgac caaaaaaaaa aaaaaaaaaa
1500

aaaaaaagta ctctgcgttg ttaccactgc ttaatcacta gtgaattc
1548

<210> 314

<211> 389

<212> PRT

<213> Trifolium repens

<400> 314

Met Val Ser Val Ser Glu Ile Arg Lys Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Ile Leu Ala Ile Gly Thr Ala Asn Pro Ala Asn Arg Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His
35 40 45

Lys Val Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr

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145 150 155 160
 Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
 165 170 175
 Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
 180 185 190
 Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
 195 200 205
 Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
 210 215 220
 Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
 225 230 235 240
 Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
 245 250 255
 His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
 260 265 270
 Gly Ile Val Ser Lys Asn Ile Asp Lys Ala Leu Val Glu Ala Phe Gln
 275 280 285
 Pro Leu Asn Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
 290 295 300
 Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Ile Lys Leu Gly Leu Lys
 305 310 315 320
 Pro Glu Lys Met Lys Ala Thr Arg Asp Val Leu Ser Glu Tyr Gly Asn
 325 330 335
 Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys
 340 345 350
 Ser Ala Glu Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly
 355 360 365
 Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu
 370 375 380
 His Ser Val Ala Ile
 385

<210> 315
 <211> 1447
 <212> DNA

<213> Trifolium repens

<400> 315

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acgcatatta tatatatata tatatagtct ataattgaaa gaaactgcta aagatattat
120

taagatatgg tgagtgtagc tgaaattcgc aaggctcaga gggctgaagg ccctgcaacc
180

attttgccca ttggcactgc aaatccacca aaccgtgttg agcagagcac atatcctgat
240

ttctacttca aaattacaaa cagtgagcac aagactgagc tcaaagagaa gttccaacgc
300

atgtgtgaca aatccatgat caagagcaga tacatgtatc taacagaaga gattttgaaa
360

gaaaatccta gtctttgtga atacatggca ccttcattgg atgctaggca agacatgggtg
420

gtggttgagg tacctagact tgggaaggag gctgcagtca aggccattaa agaatgggggt
480

caaccaaagt caaagattac tcaacttaatc ttttgacca caagtgggtg tgacatgcct
540

ggtgctgatt accaactcac aaaactctta ggtcttcgcc catatgtgaa aaggatatatg
600

atgtaccaac aaggttgttt tgcaggaggc acggtgcttc gtttggcaaa agatttggcc
660

gagaacaaca aagggtgctcg tgtgctagtt gtttgttctg aagtcaccgc agtcacattt
720

cgcggcccca gtgatactca cttggacagt cttggttgac aagcattgtt tggagatgga
780

gccgctgcac taattgttgg ttctgatcca gtgcctgaaa ttgagaaacc aatatttgag
840

atggtttgga ctgcacaaac aattgctcca gacagtgaag gtgccattga tggatcatctt
900

cgtgaagctg ggctaacatt tcatcttctt aaagatgttc ctgggattgt atcaaagaac
960

attaataaag cattggttga ggctttccaa ccattaggaa tttctgacta caactcaatc
1020

ttttggattg cacaccggg tggacctgca attcttgatc aagtagaaca aaagctagcc
1080

ttgaagcccg aaaagatgag ggccacgagg gaagttctaa gtgaatatgg aaacatgtca
1140

agcgcagtgt tattgttcat cttagatgag atgcggaaga aatcggctca aaatggactt
1200

aagacaactg gagaaggact tgattgggggt gtgttggttcg gcttcggacc aggacttacc
1260

attgaaaccg ttgttcttcg tagcgtggct atataagatg tgtgattggt tttatttttaa
1320

tgtattactt ttaatcttgc tgccttgaat ttcgatttaa gaataaataa atatatcttt
1380

tgataaaaaa aaaaaaaaaa aaaaaaaaaa aagtactctg cggtgttacc actgcttaat
1440

cgaattc
1447

<210> 316
<211> 389
<212> PRT
<213> Trifolium repens

<400> 316

Met Val Ser Val Ala Glu Ile Arg Lys Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Ile Leu Ala Ile Gly Thr Ala Asn Pro Pro Asn Arg Val Glu
20 25 30

Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr
145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
180 185 190

Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
 195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
 210 215 220

Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
 225 230 235 240

Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
 245 250 255

His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
 260 265 270

Gly Ile Val Ser Lys Asn Ile Asn Lys Ala Leu Val Glu Ala Phe Gln
 275 280 285

Pro Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
 290 295 300

Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Gln Lys Leu Ala Leu Lys
 305 310 315 320

Pro Glu Lys Met Arg Ala Thr Arg Glu Val Leu Ser Glu Tyr Gly Asn
 325 330 335

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys
 340 345 350

Ser Ala Gln Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly
 355 360 365

Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu
 370 375 380

Arg Ser Val Ala Ile
 385

<210> 317
 <211> 2394
 <212> DNA
 <213> Trifolium repens

<400> 317
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 60

aaattcactc attgcataga aaaccataca catttgatct tgcaaagaag aaatatggga
 120

gacgaaggta tagtgagagg tgtcacaaag cagacaaccc ctgggaaggc tactatatattg
180

gctcttggca aggcattccc tcaccaactt gtgatgcaag agtgtttagt tgatgggttat
240

tttagggaca ctaattgtga caatcctgaa cttaagcaga aacttgctag actttgtaag
300

acaaccacgg taaaaacaag gtatgttggt atgaatgagg agatactaaa gaaatatcca
360

gaacttgttg tcgaaggcgc ctcaactgta aaacaacgtt tagagatatg taatgaggca
420

gtaacacaaa tggcaattga agcttcccaa gtttgcctaa agaattgggg tagatcctta
480

tggacataa ctcatgtggt ttatgtttca tctagtgaag ctagattacc cgggtggtgac
540

ctatacttgt caaaaggact aggactaaac cctaaaattc aaagaaccat gctctatttc
600

tctggatgct cgggaggcgt agccggcctt cgcgttgca aagacgtagc tgagaacaac
660

cctggaagta gagttttgct tgctacttcg gaaactacaa ttattggatt caagccacca
720

agtggtgata gaccttatga tcttggttgg gtggcactct ttggagatgg tgctggtgca
780

atgataattg gctcagaccc ggtatttgaa actgagacac cattgtttga gctgcatact
840

tcagctcagg agtttatacc agacaccgag aagaaaattg atgggcggct gacggaggag
900

ggcataagtt tcacactagc aagggaactt ccgcagataa tcgaagacaa tgttgagggg
960

ttctgtaata aactaattga tgttggtggg ttggagaata aggagtacaa taagttgttt
1020

tgggctgtgc atccagggtg gcctgcgata ttgaatcgcg tggagaagcg gcttgagttg
1080

tcgccgcaga agctgaatgc tagtagaaaa gctctaattg attatggaaa tgctagcagc
1140

aatactattg tttatgtgct ggaatatatg ctagaagagg aaaagaagat taaaaaggcg
1200

ggtaggaggag attctgaatg gggattgata cttgcttttg gacctggaat tacttttgag
1260

gggattctag caaggaactt gtgtgcatga agtcttatac aattgtgatg catgacttat
1320

actcttattt ctactaatta ttatatataag caaattcaga acttttaagt aatgatttaa
1380

tgaagaatac ttatagtata ttgaacttat tcactttcaa agcaagttta tgatcctaag
1440

acatggtaga acttgagcat gtggaatagt tgtaacaaaa actctaagca aatagagact
 1500
 ttatgtagta taaagcattt ccagacatga taaataatgg tacctcagaa cataaaatat
 1560
 atttagctat ctttcatccc caactttaca catccaccaa ggtacagaat aagcatatgt
 1620
 caacacaaaa tgtactctaa gtctaacatg agtaaccaa catgatgcct gattaagtta
 1680
 aaagaaaaga aaatctgagg gcatagatct tcaatcacac cactccagag ggaaggcgta
 1740
 gaacaagctg tccgccgaaa aactgcaat tcaataaata tcattaggac aacagtgcag
 1800
 agtcatgcgg gaaatgtctt aagtcactgt actaaaaata taggattata ttatgaacta
 1860
 tactaacctt ttcacataat agtaacagaa atcagctaag atgaatgtct ggacaatttc
 1920
 tgagataaga accatgacgg ccataagcca taccccaagg caaccaataa atgtccacgg
 1980
 gtatctaaca cctggttgcaa gaaatagtaa gttattagga gatgtgcggt tacgaaattc
 2040
 aagctacaca acaaaaggag gccagaacaa cagcaatctt gtaaccagat gacaacaata
 2100
 aaatgtaaac ttaaagagac cgaacacaca aacattgcaa ctcagatgga attgctgcca
 2160
 tgtaactagt aggagatttg ggacgtcaaa tcagtatat attgcaaatac aaggatatgac
 2220
 cgccttgtct attgtagcat acaacaaacg tacagtgggt ttgtccctct caaaatggca
 2280
 ggatotttac agcacaatat ttggttttgt catacttata ccataaaaaa aaaaaaaaaa
 2340
 aaaaaaaaaa aaagtactct gcgttggtac cactgcttaa tcactagtga attc
 2394

<210> 318
 <211> 391
 <212> PRT
 <213> Trifolium repens

<400> 318

Met	Gly	Asp	Glu	Gly	Ile	Val	Arg	Gly	Val	Thr	Lys	Gln	Thr	Thr	Pro
1				5					10					15	

Gly	Lys	Ala	Thr	Ile	Leu	Ala	Leu	Gly	Lys	Ala	Phe	Pro	His	Gln	Leu
			20					25					30		

Val	Met	Gln	Glu	Cys	Leu	Val	Asp	Gly	Tyr	Phe	Arg	Asp	Thr	Asn	Cys
		35					40					45			

Asp Asn Pro Glu Leu Lys Gln Lys Leu Ala Arg Leu Cys Lys Thr Thr
 50 55 60

Thr Val Lys Thr Arg Tyr Val Val Met Asn Glu Glu Ile Leu Lys Lys
 65 70 75 80

Tyr Pro Glu Leu Val Val Glu Gly Ala Ser Thr Val Lys Gln Arg Leu
 85 90 95

Glu Ile Cys Asn Glu Ala Val Thr Gln Met Ala Ile Glu Ala Ser Gln
 100 105 110

Val Cys Leu Lys Asn Trp Gly Arg Ser Leu Ser Asp Ile Thr His Val
 115 120 125

Val Tyr Val Ser Ser Ser Glu Ala Arg Leu Pro Gly Gly Asp Leu Tyr
 130 135 140

Leu Ser Lys Gly Leu Gly Leu Asn Pro Lys Ile Gln Arg Thr Met Leu
 145 150 155 160

Tyr Phe Ser Gly Cys Ser Gly Gly Val Ala Gly Leu Arg Val Ala Lys
 165 170 175

Asp Val Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Leu Ala Thr Ser
 180 185 190

Glu Thr Thr Ile Ile Gly Phe Lys Pro Pro Ser Val Asp Arg Pro Tyr
 195 200 205

Asp Leu Val Gly Val Ala Leu Phe Gly Asp Gly Ala Gly Ala Met Ile
 210 215 220

Ile Gly Ser Asp Pro Val Phe Glu Thr Glu Thr Pro Leu Phe Glu Leu
 225 230 235 240

His Thr Ser Ala Gln Glu Phe Ile Pro Asp Thr Glu Lys Lys Ile Asp
 245 250 255

Gly Arg Leu Thr Glu Glu Gly Ile Ser Phe Thr Leu Ala Arg Glu Leu
 260 265 270

Pro Gln Ile Ile Glu Asp Asn Val Glu Gly Phe Cys Asn Lys Leu Ile
 275 280 285

Asp Val Val Gly Leu Glu Asn Lys Glu Tyr Asn Lys Leu Phe Trp Ala
 290 295 300

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Val His Pro Gly Gly Pro Ala Ile Leu Asn Arg Val Glu Lys Arg Leu
 305 310 315 320

Glu Leu Ser Pro Gln Lys Leu Asn Ala Ser Arg Lys Ala Leu Met Asp
 325 330 335

Tyr Gly Asn Ala Ser Ser Asn Thr Ile Val Tyr Val Leu Glu Tyr Met
 340 345 350

Leu Glu Glu Glu Lys Lys Ile Lys Lys Ala Gly Gly Gly Asp Ser Glu
 355 360 365

Trp Gly Leu Ile Leu Ala Phe Gly Pro Gly Ile Thr Phe Glu Gly Ile
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Leu Ala Arg Asn Leu Cys Ala
 385 390

<210> 319
 <211> 1663
 <212> DNA
 <213> Trifolium repens

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 120

tccaattcct taatataacc tatcagtact caccatcttt tcttctctcc tgctaacttt
 180

agactcagag aagatgggtga atgttaatga gatccgccag gcacagagag ctgaaggccc
 240

tgccaccgtg ttggcaatcg gactgcaac tctccaaac tgtgtcgatc agagtacata
 300

cccagactac tacttccgca tcacaaacag tgagcacaag acagagctca aagaaaaatt
 360

ccagcgcagtg tgtgacaaat ctatgattaa gaagagatac atgcatttga cagaagagat
 420

tttgaaggag aatccaagtt tatgtgagta catggcacct tcattggatg caagacaaga
 480

catgggtggtt gtggaagtac caaggctagg aaaagaggct gcaacaaagg ctatcaagga
 540

atgggggtcaa cctaagtcca agattactca cctcatcttt tgcaccacaa gtgggtgtgga
 600

catgcctggc gccgactatc agcttacaaa gcttttaggc cttcgtccgc atgtgaagcg
 660

ttatatgatg taccaacaag gttgtttcgc tgggtggtacg gtgcttcggt tgggctaaaga
 720

360/390

cttggtgaa aacaacaaag gtgcccgtgt gttggtggtt tgttcagaga tcaactgcggt
780

tactttccgt ggacccagtg acactcatct tgatagcctt gtggggcaag cattgtttgg
840

agatggtgca gcagctgtga ttgtaggttc agaccatta ccacaagttg agaagccctt
900

gtttgaattg gtatggactg ctcaaacaat ccttcagac agtgaaggag ccattgatgg
960

gcaccttcgt gaagtcgggc tgacattcca tctcctcaag gatgttcctg gactcatctc
1020

aaagaacatt gagaaagctc ttgttgaggc ctttcaacct ttaggtatct ctgattacaa
1080

ttctatatatt tggatcgac atcctggtgg acctgcaatt ctggaccaag tggaagccaa
1140

attaagctta aagccagaga aaatgcaagc caccggcat gtgcttagcg agtatggtaa
1200

catgtcaagt gcatgtgtgt tatttatctt ggatgagatg aggaggaagt caaagaaga
1260

tggacttgcc acaacaggcg aggggctgga atgggggtgta ctattcggtt ttggaccggg
1320

actcactggt gagactgtat tgctccatag tgttgccact taaattgcct agatatgcta
1380

taactatatg cttatttaat tctttgttcc tgggggattt tatcttcact tacttcactg
1440

agcatttgaa taaagtttgt tttaattatt cataatgtaa tatggtgttg cttaatgtac
1500

ccatccatat aatatttgta atacatatat taatcaactt gcaatttcac gaaaaaaaaa
1560

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaggaaaaaa aaaaaaaaaa aaaaaaaaaa
1620

aagtactctg cgttgttacc actgcttaat cactagttaa ttc
1663

<210> 320

<211> 389

<212> PRT

<213> Trifolium repens

<400> 320

Met Val Asn Val Asn Glu Ile Arg Gln Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Pro Asn Cys Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
 50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu Lys Glu Asn
 65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
 85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Thr Lys
 100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
 115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
 130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro His Val Lys Arg Tyr Met Met Tyr
 145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
 165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
 180 185 190

Ile Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
 195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Val Ile Val
 210 215 220

Gly Ser Asp Pro Leu Pro Gln Val Glu Lys Pro Leu Phe Glu Leu Val
 225 230 235 240

Trp Thr Ala Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala Ile Asp Gly
 245 250 255

His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
 260 265 270

Gly Leu Ile Ser Lys Asn Ile Glu Lys Ala Leu Val Glu Ala Phe Gln
 275 280 285

Pro Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
 290 295 300

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Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Ala Lys Leu Ser Leu Lys
 305 310 315 320

Pro Glu Lys Met Gln Ala Thr Arg His Val Leu Ser Glu Tyr Gly Asn
 325 330 335

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Arg Lys
 340 345 350

Ser Lys Glu Asp Gly Leu Ala Thr Thr Gly Glu Gly Leu Glu Trp Gly
 355 360 365

Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr Val Leu Leu
 370 375 380

His Ser Val Ala Thr
 385

<210> 321
 <211> 1653
 <212> DNA
 <213> Trifolium repens

<400> 321
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 120

gatttgaatg gaagttcctc ggtgaatgga gcacgtgcta gacgtgctcc tactcagggga
 180

aaggcaacga tacttgcat aggaaaggct ttccccgccc aggtcctccc tcaagagtgc
 240

ttggtggaag gattcattcg cgacactaag tgtgacgata cttatatataa ggagaaattg
 300

gagcgtcttt gcaaaaacac aactgtgaaa acaagatata cagtaatgtc aaaggagatc
 360

ttagacaact atccagagct agccatagat ggaacaccaa caataaggca aaagcttgaa
 420

atagcaaata cagcagtagt tgaaatggca acaagagcaa gcaaagattg catcaaagaa
 480

tggggaagggt cacctcaaga tatcacacac atagtctatg tttcctcgag cgaaattcgt
 540

ctaccgggtg gtgaccttta tcttgcaaata gaactcgggt taaacagcga tgttaatcgc
 600

gtaatgctct atttcctcgg ttgctacggc ggtgtcactg gcttacgtgt cgccaaagac
 660

atcgccgaaa ataaccctgg tagtaggggt ttactcacia catccgagac cactattctc
 720

363/390

ggtttttcgac caccgagtaa agctagacct tatgacctcg ttggcgctgc acttttcggt
780

gatggcgccg ctgctgcaat aattggaaca gacctatat tgaatcaaga atcacctttc
840

atggaattga accatgcagt ccaaaaattc ttgcctgata cacaaaatgt gattgatggt
900

agaatcactg aagagggtat taattttaag cttggaagag accttcctca aaaaattgaa
960

gacaatattg aagaattttg caagaaaatt atggctaaaa gtgatgttaa ggaatttaat
1020

gacttattttt gggctgttca tcctgggtggg ccagctatac tcaataagct agaaaatata
1080

ctcaaattga aaagtgataa attggattgt agtaggaagg cattaatgga ttatggaaat
1140

gttagtagca atactatatt ctatgtgatg gagtatatga gagattattt gaaggaagat
1200

ggaagtgaag aatggggatt aggattggct tttggaccag ggattacttt tgaaggggtt
1260

ctcctccgta gcctttaatc ttgaaataat aattcatatg aaattacttg tcttaagatt
1320

gtgataggaa gatgaatatg tattggatta atattgatat ggtgttattt taagttgatt
1380

ttaaaaaaag tttattaata aagtatgatg taacaattgt tgtttgaatg ttaaaaggga
1440

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1500

aattgttcta tgatatcttc attgttgata ctgtaataat ataatatcta atttggctgg
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1620

cgttgttacc actgcttaat cactagtgaa ttc
1653

<210> 322

<211> 389

<212> PRT

<213> Trifolium repens

<400> 322

Met Pro Gln Gly Asp Leu Asn Gly Ser Ser Ser Val Asn Gly Ala Arg
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Ala Arg Arg Ala Pro Thr Gln Gly Lys Ala Thr Ile Leu Ala Leu Gly
20 25 30

Lys Ala Phe Pro Ala Gln Val Leu Pro Gln Glu Cys Leu Val Glu Gly
35 40 45

Phe Ile Arg Asp Thr Lys Cys Asp Asp Thr Tyr Ile Lys Glu Lys Leu
 50 55 60

Glu Arg Leu Cys Lys Asn Thr Thr Val Lys Thr Arg Tyr Thr Val Met
 65 70 75 80

Ser Lys Glu Ile Leu Asp Asn Tyr Pro Glu Leu Ala Ile Asp Gly Thr
 85 90 95

Pro Thr Ile Arg Gln Lys Leu Glu Ile Ala Asn Pro Ala Val Val Glu
 100 105 110

Met Ala Thr Arg Ala Ser Lys Asp Cys Ile Lys Glu Trp Gly Arg Ser
 115 120 125

Pro Gln Asp Ile Thr His Ile Val Tyr Val Ser Ser Ser Glu Ile Arg
 130 135 140

Leu Pro Gly Gly Asp Leu Tyr Leu Ala Asn Glu Leu Gly Leu Asn Ser
 145 150 155 160

Asp Val Asn Arg Val Met Leu Tyr Phe Leu Gly Cys Tyr Gly Gly Val
 165 170 175

Thr Gly Leu Arg Val Ala Lys Asp Ile Ala Glu Asn Asn Pro Gly Ser
 180 185 190

Arg Val Leu Leu Thr Thr Ser Glu Thr Thr Ile Leu Gly Phe Arg Pro
 195 200 205

Pro Ser Lys Ala Arg Pro Tyr Asp Leu Val Gly Ala Ala Leu Phe Gly
 210 215 220

Asp Gly Ala Ala Ala Ala Ile Ile Gly Thr Asp Pro Ile Leu Asn Gln
 225 230 235 240

Glu Ser Pro Phe Met Glu Leu Asn His Ala Val Gln Lys Phe Leu Pro
 245 250 255

Asp Thr Gln Asn Val Ile Asp Gly Arg Ile Thr Glu Glu Gly Ile Asn
 260 265 270

Phe Lys Leu Gly Arg Asp Leu Pro Gln Lys Ile Glu Asp Asn Ile Glu
 275 280 285

Glu Phe Cys Lys Lys Ile Met Ala Lys Ser Asp Val Lys Glu Phe Asn
 290 295 300

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Asp Leu Phe Trp Ala Val His Pro Gly Gly Pro Ala Ile Leu Asn Lys
 305 310 315 320

Leu Glu Asn Ile Leu Lys Leu Lys Ser Asp Lys Leu Asp Cys Ser Arg
 325 330 335

Lys Ala Leu Met Asp Tyr Gly Asn Val Ser Ser Asn Thr Ile Phe Tyr
 340 345 350

Val Met Glu Tyr Met Arg Asp Tyr Leu Lys Glu Asp Gly Ser Glu Glu
 355 360 365

Trp Gly Leu Gly Leu Ala Phe Gly Pro Gly Ile Thr Phe Glu Gly Val
 370 375 380

Leu Leu Arg Ser Leu
 385

<210> 323
 <211> 1600
 <212> DNA
 <213> Trifolium repens

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 120

tatcttgggt acatcttttg ttacctccaa caaaaaaatg gtgaccgtag aagagattcg
 180

taacgccccaa cgttcaaagtg gccctgccac tatcttagct tttggcacag ccactccttc
 240

taactgtgtc actcaagctg attatcctga ttactacttt cgtatcacca acagcgaaca
 300

tatgactgat ctttaaggaaa aattcaagcg gatgtgtgat agatcaatga taaagaaacg
 360

ttacatgcac ctaacagaag actttctgaa ggagaatcca aatatgtgtg aatacatggc
 420

accatcacta gatgtaagac gagacatagt ggttggttgaa gtaccaaagc taggtaaaga
 480

agcagcaaaa aaagccatat gtgaatgggg acaacaaaaa tccaaaatca cacatcttgt
 540

tttctgcacc acttccggtg ttgacatgcc gggagccgat taccaactca ccaaactttt
 600

aggcttaaaa ccttctgtca agcgtctcat gatgtatcaa caaggttgtt tcgctggcgg
 660

cacagttctc cgcttagcaa aagaccttgt tgagaataac aaaaatgcaa gagttcttgt
 720

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tgtttgttct gaaattactg cggttacttt tcgtggacca tcggatactc atcttgattc
780

gctcgtggga caggcgcttt ttggtgatgg agccgcagca atgattattg gtgcggatcc
840

tgatttaacc gtggagcgtc cgattttcga gattgtttcg gctgctcaga ctattcttcc
900

tgattctgat ggcgcaattg atggacatct tcgtgaagtg gggctcactt ttcatttatt
960

gaaagatgtt cgggggatta tttcaaagaa cattgaaaaa agtttagttg aagcttttgc
1020

gcctattggg attaatgatt ggaactcaat attttgggtt gcacatccag gtggaccggc
1080

tatttttagac caggttgaag agaaactcca tcttaaagag gagaaactcc ggtccacccg
1140

gcatgtgctt agtgaatatg gaaatatgtc aagtgcattg gttttattta ttttggatga
1200

aatgagaaaag aggtctaaaag aggaagggat gattacaact ggtgaagggt tggaatgggg
1260

tgtgttgttt gggtttggac cgggtttaac tgttgaaacc gttgtgcttc atagtgttcc
1320

ggttcagggt tgaatttatt atacatagat tggaaaataa aatttgcctg ccgagagatg
1380

tgaactaact ttgtaggcaa gctcaaatta aagtttgaga taatattgtg ctttagttat
1440

tatggtatgt aatgtaatgt ttttactttt ttcgaaattc atgtaatttg atatgtaaag
1500

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1560

aaaaagtact ctgcgttggt accactgctt aatcgaattc
1600

<210> 324

<211> 391

<212> PRT

<213> Trifolium repens

<400> 324

Met Val Thr Val Glu Glu Ile Arg Asn Ala Gln Arg Ser Asn Gly Pro
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Ala Thr Ile Leu Ala Phe Gly Thr Ala Thr Pro Ser Asn Cys Val Thr
20 25 30

Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Met Thr Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp Arg Ser Met

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50						55										60
Ile	Lys	Lys	Arg	Tyr	Met	His	Leu	Thr	Glu	Asp	Phe	Leu	Lys	Glu	Asn	
65					70					75					80	
Pro	Asn	Met	Cys	Glu	Tyr	Met	Ala	Pro	Ser	Leu	Asp	Val	Arg	Arg	Asp	
				85					90					95		
Ile	Val	Val	Val	Glu	Val	Pro	Lys	Leu	Gly	Lys	Glu	Ala	Ala	Lys	Lys	
			100					105					110			
Ala	Ile	Cys	Glu	Trp	Gly	Gln	Pro	Lys	Ser	Lys	Ile	Thr	His	Leu	Val	
		115					120					125				
Phe	Cys	Thr	Thr	Ser	Gly	Val	Asp	Met	Pro	Gly	Ala	Asp	Tyr	Gln	Leu	
	130					135					140					
Thr	Lys	Leu	Leu	Gly	Leu	Lys	Pro	Ser	Val	Lys	Arg	Leu	Met	Met	Tyr	
145					150					155					160	
Gln	Gln	Gly	Cys	Phe	Ala	Gly	Gly	Thr	Val	Leu	Arg	Leu	Ala	Lys	Asp	
				165					170					175		
Leu	Val	Glu	Asn	Asn	Lys	Asn	Ala	Arg	Val	Leu	Val	Val	Cys	Ser	Glu	
			180					185					190			
Ile	Thr	Ala	Val	Thr	Phe	Arg	Gly	Pro	Ser	Asp	Thr	His	Leu	Asp	Ser	
		195					200					205				
Leu	Val	Gly	Gln	Ala	Leu	Phe	Gly	Asp	Gly	Ala	Ala	Ala	Met	Ile	Ile	
	210					215					220					
Gly	Ala	Asp	Pro	Asp	Leu	Thr	Val	Glu	Arg	Pro	Ile	Phe	Glu	Ile	Val	
225					230					235					240	
Ser	Ala	Ala	Gln	Thr	Ile	Leu	Pro	Asp	Ser	Asp	Gly	Ala	Ile	Asp	Gly	
				245					250					255		
His	Leu	Arg	Glu	Val	Gly	Leu	Thr	Phe	His	Leu	Leu	Lys	Asp	Val	Pro	
			260					265					270			
Gly	Ile	Ile	Ser	Lys	Asn	Ile	Glu	Lys	Ser	Leu	Val	Glu	Ala	Phe	Ala	
		275					280					285				
Pro	Ile	Gly	Ile	Asn	Asp	Trp	Asn	Ser	Ile	Phe	Trp	Val	Ala	His	Pro	
	290					295					300					
Gly	Gly	Pro	Ala	Ile	Leu	Asp	Gln	Val	Glu	Glu	Lys	Leu	His	Leu	Lys	
305					310					315					320	

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Arg
340 345 350

Ser Lys Glu Glu Gly Met Ile Thr Thr Gly Glu Gly Leu Glu Trp Gly
355 360 365

Val	Leu	Phe	Gly	Phe	Gly	Pro	Gly	Leu	Thr	Val	Glu	Thr	Val	Val	Leu
	370					375					380				

His Ser Val Pro Val Gln Gly
385 390

<210>	325
<211>	1333
<212>	DNA
<213>	Trifolium repens

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120

tttgcgtcac cggcggcagc ggatgcatcg gttcatggct agtccatctc cttctcctcc
180

gaggctacac tgtttacgcc accgtccaaa atctcaatga tgagaacgaa acgaagcatc
240

tagaagctct cgaaggagca caaactaatc tccgtctctt ccagatcgat ctcccttaact
300

acgacacaat cctcgctgct gtccgcgggt gcgtcggaat ttccacctc gcttcacctt
360

gcactgtaga caaagttcat gatcctcaga aggagctttt ggatcctgca attaaaggga
420

ctttgaatgt gcttactgca gctaaggaag taggggtgaa gcgtgtggtt gttacctcgt
480

ctgtctcggc gattactcct agtcctgatt ggccttctga tgttggttaa agagaggatt
540

gttgactga tgttgaatat tgcaagaaaa aagagttgtg gtatccgttg tccaaaacat
600

tggtgagaa agctgctgg gatttttcca aagaaaatgg tttggatgtt gttgtggtga
660

atcccggtac tgtgatgggt cctgttattc caccacggca taatgcaagc atgctcatgc
720

ttgtgagact tcttgaaggc tgcgctgaaa catttgaaga ctattttatg ggattggtcc
780

acttcaaaga tgtagcattg gcgcataatgt tgggtgatga gaacaaagaa gcatctggta
840

gacatgtgtg tgttgaaact atctctcact acggtgattt tgtggcaaaa gttgctgaac
900

tttatccaga atatagtgtt cctaggatgc agcgagatac gcaacctgga ttgttgagag
960

cgaatgatgg atcaaagaag ctcatagatt tgggttttga attcattcca atggagcaaa
1020

ttatcaagga tgctgtagag agtttgaaga acaaaggatt catttcttga atgatgttac
1080

tggtcttttg agaaccctat agttaccaga gtatagacta aataatatat aggtgatggg
1140

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1200

tatgttaaata tgctaattgtt aacttcaata ttatcagcc agtattgttt ttttaataaa
1260

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1320

cttaatcgaa ttc
1333

<210> 326
<211> 320
<212> PRT
<213> Trifolium repens

<400> 326

Met Ser Lys Leu Val Cys Val Thr Gly Gly Ser Gly Cys Ile Gly Ser
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Trp Leu Val His Leu Leu Leu Leu Arg Gly Tyr Thr Val His Ala Thr
20 25 30

Val Gln Asn Leu Asn Asp Glu Asn Glu Thr Lys His Leu Glu Ala Leu
35 40 45

Glu Gly Ala Gln Thr Asn Leu Arg Leu Phe Gln Ile Asp Leu Leu Asn
50 55 60

Tyr Asp Thr Ile Leu Ala Ala Val Arg Gly Cys Val Gly Ile Phe His
65 70 75 80

Leu Ala Ser Pro Cys Thr Val Asp Lys Val His Asp Pro Gln Lys Glu
85 90 95

Leu Leu Asp Pro Ala Ile Lys Gly Thr Leu Asn Val Leu Thr Ala Ala
100 105 110

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Lys Glu Val Gly Val Lys Arg Val Val Val Thr Ser Ser Val Ser Ala
 115 120 125

Ile Thr Pro Ser Pro Asp Trp Pro Ser Asp Val Val Lys Arg Glu Asp
 130 135 140

Cys Trp Thr Asp Val Glu Tyr Cys Lys Lys Lys Glu Leu Trp Tyr Pro
 145 150 155 160

Leu Ser Lys Thr Leu Ala Glu Lys Ala Ala Trp Asp Phe Ser Lys Glu
 165 170 175

Asn Gly Leu Asp Val Val Val Val Asn Pro Gly Thr Val Met Gly Pro
 180 185 190

Val Ile Pro Pro Arg His Asn Ala Ser Met Leu Met Leu Val Arg Leu
 195 200 205

Leu Glu Gly Cys Ala Glu Thr Phe Glu Asp Tyr Phe Met Gly Leu Val
 210 215 220

His Phe Lys Asp Val Ala Leu Ala His Ile Leu Val Tyr Glu Asn Lys
 225 230 235 240

Glu Ala Ser Gly Arg His Val Cys Val Glu Thr Ile Ser His Tyr Gly
 245 250 255

Asp Phe Val Ala Lys Val Ala Glu Leu Tyr Pro Glu Tyr Ser Val Pro
 260 265 270

Arg Met Gln Arg Asp Thr Gln Pro Gly Leu Leu Arg Ala Asn Asp Gly
 275 280 285

Ser Lys Lys Leu Ile Asp Leu Gly Leu Glu Phe Ile Pro Met Glu Gln
 290 295 300

Ile Ile Lys Asp Ala Val Glu Ser Leu Lys Asn Lys Gly Phe Ile Ser
 305 310 315 320

<210> 327
 <211> 1470
 <212> DNA
 <213> Trifolium repens

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 120

ccatcatcaa acaatggcac cagccaaaac tctaagttat ctctcacaac aaaacactct
 180

cgagtcaagt ttcgtaggg aagaagatga gcgtccaaaa gttgcctaca ataacttcag
240

caacgagatt ccaatcattt ctcttgctgg aattgatgag gttgatggtc gtagaacaga
300

gatatgtaac aagattggtg aagcttggtga gaattggggg atttttcagg ttgttgatca
360

tggtggtgat acaaaacttg tttctgagat gaccggtttt gctagagagt tttttgcttt
420

gccaccgga gagaagctcc ggtttgacat gtccgggtgg aaaaagggtg gtttcattgt
480

ctctagtcac cttcaaggag aagcagtga ggattggaga gagctagtga catatttttc
540

ataccaatt aaacaaagag attattcaag gtggccagac aagccagaag gatggaaaga
600

ggtaacagaa aaatacagtg aaacctaata gaatttagct tgcaagctat tggaagtttt
660

atcagaagca atgggttttag aaaaagaagc tctaacaaaa gcatgtgttg atatggatca
720

aaaagttggt ataaattatt acccaaatg cctgaacct gacctcacac ttggccttaa
780

acgtcacact gaccctggca caattactct tttgcttcaa gatcaagttg gtggtcttca
840

agctaccaa gataatggta agacgtggat tacagttcaa ccagttgaag gtgcttttgt
900

tgtaatactt ggagaccatg gtcactatct aagtaatgga cggttcaaaa atgctgacca
960

tcaagcagtg gtgaattcga actacagccg tttatcaata gcaacatttc aaaatccagc
1020

tccagatgca actgtgtacc ctttgaagat tagagatggg gaaaaatctg tggttgaaga
1080

accaatcact tttgctgaaa tgtatagaag gaagatgacc aaagaccttg aaattgctag
1140

gatgaagaag ttggctaagg aacaacaact tagggacttg gaggagaaca agactaaata
1200

tgaggccaaa cttttgaatg agatctttgc ttaattaatt agtcttaatt taaataataa
1260

attttagact taatttacat ataataattt taattttttg ttcaattaat ctatgtttta
1320

tttgtcgta ttgtccacgt gtattaagct gcttggttgt gtgtgccttg gagaataatc
1380

aataatatta catctatggt taattataaa aaaaaaaaaa aaaaaaaaaa gtatctgcgt
1440

tgttaccact gcttaatcac tagtgaattc
1470

<210> 328
 <211> 366
 <212> PRT
 <213> Trifolium repens

<400> 328

Met Ala Pro Ala Lys Thr Leu Ser Tyr Leu Ser Gln Gln Asn Thr Leu
 1 5 10 15

Glu Ser Ser Phe Val Arg Glu Glu Asp Glu Arg Pro Lys Val Ala Tyr
 20 25 30

Asn Asn Phe Ser Asn Glu Ile Pro Ile Ile Ser Leu Ala Gly Ile Asp
 35 40 45

Glu Val Asp Gly Arg Arg Thr Glu Ile Cys Asn Lys Ile Val Glu Ala
 50 55 60

Cys Glu Asn Trp Gly Ile Phe Gln Val Val Asp His Gly Val Asp Thr
 65 70 75 80

Lys Leu Val Ser Glu Met Thr Arg Phe Ala Arg Glu Phe Phe Ala Leu
 85 90 95

Pro Pro Glu Glu Lys Leu Arg Phe Asp Met Ser Gly Gly Lys Lys Gly
 100 105 110

Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Ala Val Lys Asp Trp
 115 120 125

Arg Glu Leu Val Thr Tyr Phe Ser Tyr Pro Ile Lys Gln Arg Asp Tyr
 130 135 140

Ser Arg Trp Pro Asp Lys Pro Glu Gly Trp Lys Glu Val Thr Glu Lys
 145 150 155 160

Tyr Ser Glu Asn Leu Met Asn Leu Ala Cys Lys Leu Leu Glu Val Leu
 165 170 175

Ser Glu Ala Met Gly Leu Glu Lys Glu Ala Leu Thr Lys Ala Cys Val
 180 185 190

Asp Met Asp Gln Lys Val Val Ile Asn Tyr Tyr Pro Lys Cys Pro Glu
 195 200 205

Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp Pro Gly Thr Ile
 210 215 220

Thr Leu Leu Leu Gln Asp Gln Val Gly Gly Leu Gln Ala Thr Lys Asp

225 230 235 240
 Asn Gly Lys Thr Trp Ile Thr Val Gln Pro Val Glu Gly Ala Phe Val
 245 250 255
 Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn Gly Arg Phe Lys
 260 265 270
 Asn Ala Asp His Gln Ala Val Val Asn Ser Asn Tyr Ser Arg Leu Ser
 275 280 285
 Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Thr Val Tyr Pro Leu
 290 295 300
 Lys Ile Arg Asp Gly Glu Lys Ser Val Leu Glu Glu Pro Ile Thr Phe
 305 310 315 320
 Ala Glu Met Tyr Arg Arg Lys Met Thr Lys Asp Leu Glu Ile Ala Arg
 325 330 335
 Met Lys Lys Leu Ala Lys Glu Gln Gln Leu Arg Asp Leu Glu Glu Asn
 340 345 350
 Lys Thr Lys Tyr Glu Ala Lys Pro Leu Asn Glu Ile Phe Ala
 355 360 365

 <210> 329
 <211> 2515
 <212> DNA
 <213> Trifolium repens

 <400> 329
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 tattccttta attctttcat ataatcattt gaatttccat tctccctaaa aattctatag
 120
 ctaccacatc acacaacata acaaattaag aaatatttat tactatatta agatatggaa
 180
 gtagtagcag cagcaatcac aaaaaacaat ggcaagattg attcattttg cttgaatcat
 240
 gctaattgcta ataacatgaa agtgaatggg gctgatacctt tgaattgggg tgtggctgct
 300
 gaggcaatga aggggaagtca cttggatgag gtgaagcgta tgggtggagga ataccggaaa
 360
 ccggttgctc gtcttggtgg cgagacacta accatttctc aggtggctgc cattgctgca
 420
 cacgatgggtg caacgggtgga gctatcggaa tctgctagag ccggcggttaa ggcaagcagt
 480
 gactgggtta tggagagtat gaacaaagggt accgacagct acggtgtccc aacagggttc

540

ggcgctacct cgcaccgccg aaccaaacaa ggtggtgctt tgcagaaaga gtcataagg
600

tttttgaatg ctggaatatt tggaaatgga actgagtcaa gccacacact accacacaca
660

gccacaagag ctgccatgct agtgagaatc aacacacttc tccaaggcta ttcaggaatt
720

agatttgaaa tcttagaagc tatcaccaag cttcttaaca acaatgtcac cccatgttta
780

ccgcttcgcy gtacaatcac agcttcagga gatttagtcc ctctttctta cattgctggt
840

ttactaaccg gacgaccaa ttccaaggct catggacctt ctggagaagt acttaatgca
900

aaacaagctt ttcaatcagc tggaatcgat gccgagttct ttgaattaca accaaaagaa
960

ggccttgccc ttgttaacgg aaccgctggt gggtctgggt tagcttctat tggtcttttt
1020

gaggctaata tattggcggc gttgtctgaa gttctatctg caattttcgc tgaagttatg
1080

caagggaagc ccgaatttac cgatcatttg acacataagt tgaaacatca ccttggtcaa
1140

attgaggctg ctgctattat ggaacacatt ttggatggga gtgcttatgt taaagacgct
1200

aagaagttgc atgagatgga tcctttacag aagccaaaac aagatagata tgcacttagg
1260

acttcgccac aatggcttgg tcctttgatt gaagtgatta gattctctac caagtcaatt
1320

gagagagaga tcaactctgt caatgacaat cctttgattg atgtttcaag gaacaaggct
1380

ttgcatggtg gaaattttca aggaacacct atcggagtat ccatggataa tacacgtttg
1440

gctcttgcat caattggcaa acttatgttt gctcaattct ctgagcttgt caatgatttt
1500

tacaacaatg gattgccatc aaatctctct gctagtagaa atccgagctt ggattatggg
1560

ttcaagggat ccgaaattgc catggcttct tattgttccg agttgcaata tcttgcaaat
1620

ccggttacia ctcattgtcca aagtgcggaa caacacaacc aagatgtcaa ctctttgggt
1680

ttgatttctt ctagaaaaac ttatgaagca attgagatcc ttcaattgat gtcttcaca
1740

ttcttgattg cactttgtca agcaattgat ttaagacatt tggaggagaa tttgaaaaac
1800

tcgggtcaaaa ataccgtaag ccaagtggcc aaaaagacac taaccatagg tgtcaatgga

1860

gaacttcac cttcaagatt ttgtgaaaaa gacttattga aagtgggtga tagggaacat
1920

gtctttgcct acattgatga tccttgtagt gctacatacc cattgatgca aaaactcagg
1980

caagtactag tggatcatgc attagttaat ggagaaagtg agaagaattht gaacacatca
2040

atctttccaaa agattgcaac ttttgaggaa gagttgaaaa acctttgccca aaagagggtg
2100

aaagtgcaag gattgcatat gaaagtggaa attcaacaat tccaaacaag atcaatggat
2160

gcagatctta tccactctac aattttgtga gaaaggagtt gggaactggt ttgctaactg
2220

gagaaaatgt catttcaccg ggtgaagagt gtgacaaact attcacagct atgtgtcaag
2280

gaaaaatcat tgatcctctt cttgaatgct tgggagagtg gaacgggtgct cctcttccaa
2340

tttgtttaact ttgattgtta gttcataaaa tgttttattt gtatttatca tttgtattta
2400

tgcgagtgtg gtaataatga ttaggtgttt tgtgccttta atgaaaaaaaa aaaaaaaaaa
2460

aaaaaaaaaa aaaagtactc tgcgttggtta ccaactgctta atcactagtg aattc
2515

<210> 330

<211> 671

<212> PRT

<213> Trifolium repens

<400> 330

Met	Glu	Val	Val	Ala	Ala	Ala	Ile	Thr	Lys	Asn	Asn	Gly	Lys	Ile	Asp
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Ser	Phe	Cys	Leu	Asn	His	Ala	Asn	Ala	Asn	Asn	Met	Lys	Val	Asn	Gly
			20					25					30		

Ala	Asp	Pro	Leu	Asn	Trp	Gly	Val	Ala	Ala	Glu	Ala	Met	Lys	Gly	Ser
		35					40					45			

His	Leu	Asp	Glu	Val	Lys	Arg	Met	Val	Glu	Glu	Tyr	Arg	Lys	Pro	Val
	50					55					60				

Val	Arg	Leu	Gly	Gly	Glu	Thr	Leu	Thr	Ile	Ser	Gln	Val	Ala	Ala	Ile
65					70					75					80

Ala	Ala	His	Asp	Gly	Ala	Thr	Val	Glu	Leu	Ser	Glu	Ser	Ala	Arg	Ala
				85					90					95	

Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met Asn Lys Gly
 100 105 110

Thr Asp Ser Tyr Gly Val Pro Thr Gly Phe Gly Ala Thr Ser His Arg
 115 120 125

Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu Ile Arg Phe Leu
 130 135 140

Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Ser Ser His Thr Leu Pro
 145 150 155 160

His Thr Ala Thr Arg Ala Ala Met Leu Val Arg Ile Asn Thr Leu Leu
 165 170 175

Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu Ala Ile Thr Lys
 180 185 190

Leu Leu Asn Asn Asn Val Thr Pro Cys Leu Pro Leu Arg Gly Thr Ile
 195 200 205

Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile Ala Gly Leu Leu
 210 215 220

Thr Gly Arg Pro Asn Ser Lys Ala His Gly Pro Ser Gly Glu Val Leu
 225 230 235 240

Asn Ala Lys Gln Ala Phe Gln Ser Ala Gly Ile Asp Ala Glu Phe Phe
 245 250 255

Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly Thr Ala Val
 260 265 270

Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu Ala Asn Ile Leu Ala
 275 280 285

Val Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val Met Gln Gly
 290 295 300

Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys His His Pro
 305 310 315 320

Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile Leu Asp Gly Ser
 325 330 335

Ala Tyr Val Lys Asp Ala Lys Lys Leu His Glu Met Asp Pro Leu Gln
 340 345 350

Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro Gln Trp Leu

377/390

355	360	365
Gly Pro Leu Ile Glu Val	Ile Arg Phe Ser Thr	Lys Ser Ile Glu Arg
370	375	380
Glu Ile Asn Ser Val	Asn Asp Asn Pro Leu Ile	Asp Val Ser Arg Asn
385	390	395
Lys Ala Leu His	Gly Gly Asn Phe Gln Gly Thr	Pro Ile Gly Val Ser
	405	410
Met Asp Asn Thr Arg	Leu Ala Leu Ala Ser Ile	Gly Lys Leu Met Phe
	420	425
Ala Gln Phe Ser Glu Leu Val	Asn Asp Phe Tyr Asn Asn	Gly Leu Pro
	435	440
Ser Asn Leu Ser Ala Ser	Arg Asn Pro Ser Leu Asp	Tyr Gly Phe Lys
	450	455
Gly Ser Glu Ile Ala Met	Ala Ser Tyr Cys Ser	Glu Leu Gln Tyr Leu
	465	470
Ala Asn Pro Val Thr Thr His Val	Gln Ser Ala Glu Gln His	Asn Gln
	485	490
Asp Val Asn Ser Leu Gly Leu Ile	Ser Ser Arg Lys Thr Tyr	Glu Ala
	500	505
Ile Glu Ile Leu Gln Leu Met	Ser Ser Thr Phe Leu Ile	Ala Leu Cys
	515	520
Gln Ala Ile Asp Leu Arg His	Leu Glu Glu Asn Leu Lys	Asn Ser Val
	530	535
Lys Asn Thr Val Ser Gln Val Ala Lys Lys	Thr Leu Thr Ile Gly Val	
	545	550
Asn Gly Glu Leu His Pro Ser Arg Phe	Cys Glu Lys Asp Leu Leu Lys	
	565	570
Val Val Asp Arg Glu His Val Phe Ala Tyr Ile	Asp Asp Pro Cys Ser	
	580	585
Ala Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val	Leu Val Asp His	
	595	600
Ala Leu Val Asn Gly Glu Ser Glu Lys Asn Leu Asn Thr	Ser Ile Phe	
	610	615

Gln Lys Ile Ala Thr Phe Glu Glu Glu Leu Lys Asn Leu Cys Gln Lys
625 630 635 640

Arg Leu Lys Val Gln Gly Leu His Met Lys Val Glu Ile Gln Gln Phe
645 650 655

Gln Thr Arg Ser Met Asp Ala Asp Leu Ile His Ser Thr Ile Leu
660 665 670

<210> 331
<211> 2667
<212> DNA
<213> Trifolium repens

<400> 331
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120
attactttct acaccccccc ctctcaacta ttattaacta acataatgga gggaattacc
180
aatggccatg ctgaagcaac tttttgcgtg accaaaagtg ttggtgatcc actcaactgg
240
ggtgcagccg cggagtcgtt gatggggagt catttgatg aggtgaagcg tatggtggag
300
gaataccgta atccattggg taaaattggc ggcgagacgc ttaccattgc tcaggtggct
360
ggaattgctt ctcattgatg tgggtgtgagg gtggagctgt ctgagtcgcg cagggccggc
420
gttaaggcga gtagtggttg ggtgatggac agcatgaaca atgggactga tagttatggt
480
gttaccactg gtttcggcgc cacctctcac cggagaacca agcaggggtg tgccttgcat
540
aaggagctaa ttaggttttt gaatgccgga atatttggca atggtacaga atctaactgt
600
acactaccac acacagcaac cagagctgca atgcttgtga gaatcaaac tcttcttcaa
660
ggatattctg gaattagatt tgaaattttg gaagctatca caaagcttct aaacaacaac
720
attaccccat gtttaccact tcgtggtaca atcacggctt ccggtgatct cgttccgctt
780
tctacattg ccggtttggt aaccggtaga ccgaactcca aagccgttgg accctccgga
840
gaaattctca atgcaaaaaga agcttttcaa cttgccggca ttggttctga gttttttgaa
900
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960

tctattgttc tgtttgaagc aaatgtacta gctgttttgt ctgaagttat gtcggcgatt
1020

ttcgctgaag ttatgcaagg gaaaccagaa ttcactgac atttgactca taagttgaaa
1080

catcacctg gtcaaattga agctgctgca attatggaac atattttgga tggaagtgc
1140

tatgttaaag cagctaagaa attacacgaa accgatcctt taaaaagcc gaaacaagat
1200

cgttatgcac ttagaacttc acctcaatgg cttggtcctt tgattgaagt gataagattt
1260

tcaactaagt caattgagag agaaattaac tctgtcaatg ataacccttt gattgatgtt
1320

tcaaggaaca aggccattca cggtggtaat tttcaaggaa cacctattgg agtttcaatg
1380

gataacacac gtttagctct tgcttcaatt ggtaaactca tgtttgctca attctctgaa
1440

cttgттаатg atttttacaa caacgggtta ccttcgaatc ttactgctag taggaacca
1500

agcttgгatt acggtttcaa gggatcgгaa attgccatgg cttcttattg ttctgagtta
1560

caatatcttg ctaatcctgt caccacccat gtccaaagtг cggagcaaca caatcaagat
1620

gttaactctt tgggtttgat ttcttcaaga aaaacaaatg aagctattga gatcctaaag
1680

ctcatgtctt cgacatttct gattgcactt tgtcaagcaa ttgatttaag gcatttgгag
1740

gaaaatctga ggaacactgt caagaacacg gtaagccaag tagcgaagag aacactcacc
1800

accggtgtta atggagaact tcatccttct agattttgtg agaaagattt gctcaaagtt
1860

gttgataggг agtatgtatt tgctatgtc gacgatcctt gtctagctac atacccttg
1920

atgcaaaagt tgagacaagt gcttgгgat catgcattgg taaatgctga tggagagaag
1980

aatttgaaca catcaatctt tcaaaagatt gcaacttttg aggatgaatt gaaagctatc
2040

ttgccaaagg aagttgaaг tacaagaact gcatatgaaa atggacaatg tggaatttca
2100

aacaagatta aggaatgcag gtcttatcca ttgtacaagt ttgttagaga ggagttagga
2160

accgгttgc taaccgгaga aaaaacgata tcgctggгcг aagagtgtga caaattgttc
2220

acagctatgt gccaaгtaa aattgttgat cctcttttgг aatgccttgг agagtгgaat
2280

ggtgctcctc taccaatatg ttaattagca gaattaatat gtttctttga gaagtgattt
2340

ctttatatat ttgtagtata ctatagtagt tgcattgaga agcaattggg ttgtctataa
2400

gcctatggaa aatggcaaaa caattttctg ctcaaagcat cgtttattaa gttttcctta
2460

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2520

gggtgcaa atcacgtgat acatgtgggtg tttgatgtaa atgggtgttt ctcaattaat
2580

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2640

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2667

<210> 332

<211> 712

<212> PRT

<213> Trifolium repens

<400> 332

Met Glu Gly Ile Thr Asn Gly His Ala Glu Ala Thr Phe Cys Val Thr
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Lys Ser Val Gly Asp Pro Leu Asn Trp Gly Ala Ala Ala Glu Ser Leu
20 25 30

Met Gly Ser His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg
35 40 45

Asn Pro Leu Val Lys Ile Gly Gly Glu Thr Leu Thr Ile Ala Gln Val
50 55 60

Ala Gly Ile Ala Ser His Asp Ser Gly Val Arg Val Glu Leu Ser Glu
65 70 75 80

Ser Ala Arg Ala Gly Val Lys Ala Ser Ser Gly Trp Val Met Asp Ser
85 90 95

Met Asn Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala
100 105 110

Thr Ser His Arg Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu
115 120 125

Ile Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Ser Asn
130 135 140

381/390

Cys Thr Leu Pro His Thr Ala Thr Arg Ala Ala Met Leu Val Arg Ile
 145 150 155 160

Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu
 165 170 175

Ala Ile Thr Lys Leu Leu Asn Asn Asn Ile Thr Pro Cys Leu Pro Leu
 180 185 190

Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile
 195 200 205

Ala Gly Leu Leu Thr Gly Arg Pro Asn Ser Lys Ala Val Gly Pro Ser
 210 215 220

Gly Glu Ile Leu Asn Ala Lys Glu Ala Phe Gln Leu Ala Gly Ile Gly
 225 230 235 240

Ser Glu Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn
 245 250 255

Gly Thr Ala Val Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu Ala
 260 265 270

Asn Val Leu Ala Val Leu Ser Glu Val Met Ser Ala Ile Phe Ala Glu
 275 280 285

Val Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu
 290 295 300

Lys His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile
 305 310 315 320

Leu Asp Gly Ser Ala Tyr Val Lys Ala Ala Lys Lys Leu His Glu Thr
 325 330 335

Asp Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser
 340 345 350

Pro Gln Trp Leu Gly Pro Leu Ile Glu Val Ile Arg Phe Ser Thr Lys
 355 360 365

Ser Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp
 370 375 380

Val Ser Arg Asn Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr Pro
 385 390 395 400

Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Leu Ala Ser Ile Gly
 405 410 415

Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn
 420 425 430

Asn Gly Leu Pro Ser Asn Leu Thr Ala Ser Arg Asn Pro Ser Leu Asp
 435 440 445

Tyr Gly Phe Lys Gly Ser Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu
 450 455 460

Leu Gln Tyr Leu Ala Asn Pro Val Thr Thr His Val Gln Ser Ala Glu
 465 470 475 480

Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg Lys
 485 490 495

Thr Asn Glu Ala Ile Glu Ile Leu Lys Leu Met Ser Ser Thr Phe Leu
 500 505 510

Ile Ala Leu Cys Gln Ala Ile Asp Leu Arg His Leu Glu Glu Asn Leu
 515 520 525

Arg Asn Thr Val Lys Asn Thr Val Ser Gln Val Ala Lys Arg Thr Leu
 530 535 540

Thr Thr Gly Val Asn Gly Glu Leu His Pro Ser Arg Phe Cys Glu Lys
 545 550 555 560

Asp Leu Leu Lys Val Val Asp Arg Glu Tyr Val Phe Ala Tyr Val Asp
 565 570 575

Asp Pro Cys Leu Ala Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val
 580 585 590

Leu Val Asp His Ala Leu Val Asn Ala Asp Gly Glu Lys Asn Leu Asn
 595 600 605

Thr Ser Ile Phe Gln Lys Ile Ala Thr Phe Glu Asp Glu Leu Lys Ala
 610 615 620

Ile Leu Pro Lys Glu Val Glu Ser Thr Arg Thr Ala Tyr Glu Asn Gly
 625 630 635 640

Gln Cys Gly Ile Ser Asn Lys Ile Lys Glu Cys Arg Ser Tyr Pro Leu
 645 650 655

Tyr Lys Phe Val Arg Glu Glu Leu Gly Thr Ala Leu Leu Thr Gly Glu
 660 665 670

Lys Thr Ile Ser Leu Gly Glu Glu Cys Asp Lys Leu Phe Thr Ala Met
 675 680 685

Cys Gln Gly Lys Ile Val Asp Pro Leu Leu Glu Cys Leu Gly Glu Trp
 690 695 700

Asn Gly Ala Pro Leu Pro Ile Cys
 705 710

<210> 333
 <211> 2664
 <212> DNA
 <213> Trifolium repens

<400> 333
 gaattcacta gtgattaagc agtggttaaca acgcagagta cgcggggagg aaataaattc
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atcattgttc attattttccc acccaacaca acataacaaa tacattattc tctcctctga
 120

tcacaattat tactttctac accctcctct caactattat taactagcat aatggaggga
 180

attaccaatg gccatgctga aacaactttt tgcgtgacca aaagtgttg tgatccactc
 240

aactgggggtg cagccgcgga gtcgttgacg gggagtcatt tggatgaggt gaagcgtatg
 300

gtggaggagt accgtaatcc gttggctaaa attggcggcg agacgcttac cattgctcag
 360

gtggctggaa ttgcttctca tgatagtgggt gtgaggggtgg agctgtccga gtcgcgaagg
 420

gccggcggtta aggcgagtag tgattgggtg atggatagca tgaacaatgg gactgatagt
 480

tacgggtgta ccaccggttt tgggtgccacc totcaccgga gaaccaagca ggggtgggtgct
 540

ttgcagaagg agctaattag gtttttgaat gctggaatat ttggcaatgg tacagaatct
 600

aactgtacac taccacacac agcaactaga gctgcaatgc ttgtgagaat caacactctt
 660

cttcaagggt actctggtat tagatttgaa attttggag ctatcacaaa gcttccaaac
 720

aacaacatta ccccatgttt accacttcgt ggtacaatca cggcttccgg tgatcttggt
 780

ccgctttcct acattgccgg tttgttaacc ggaagacca actccaaagc agttggacct
 840

tccggagaaa ttttgagtgc taaagaagct tttcaactcg ccggcattgg ttctgagttt
 900

tttgaattgc aacccaaaaga aggtcttgct cttgttaatg gtactgctgt tggctctgggt
 960

ttagcttcta ttgttctgtt tgaagcaa at gtactagctg ttttatccga agttatgtcg
1020

gcgatttttcg ctgaagttat gcaaggga ccggaattta cggatcattt gactcataag
1080

ttgaaacatc accctgggtca aattgaagct gctgcaatta tggaacatat tttggatgga
1140

agtgccttatg ttaaagcagc taagaagtta cacgaaaccg atcctttaca aaaaccgaaa
1200

caagatcggt atgcacttag aacttcacct caatggcttg gtcctttgat tgaagtgata
1260

agattttcaa ccaaatcgat tgaaagagaa attaactcgg tcaacgacaa ccctttgatc
1320

gatgtttcaa ggaacaaggc cattcatggt ggtaactttc aaggaacacc tattggagtt
1380

tcaatggata acacacgttt agctcttgct tcaattggta aactcatggt tgctcaattc
1440

tctgaacttg ttaatgattt ttacaacaac gggttgcctt cgtatcttac tgctagtagg
1500

aacccgagct tggactatgg tttcaaggga tcggaaattg ccatggcttc gtattgttcc
1560

gagttacaat atcttgctaa tcctgtcacc acccatgtcc aaagtgccga gcaacacaac
1620

caagatgtta actctttggg ttgattttct tctagaaaaa caaatgaagc tattgagatt
1680

ctcaagctca tgtcttccac tttcttgatt gcattatgtc aagcaatcga ctttaaggcac
1740

ttggaggaaa atctcaggaa caccgtcaag aacacggtaa gccaaagtagc gaagagaaca
1800

ctcaccaccg gcgtcaacgg agaacttcat tcttctagat tttgtgagaa agatttgctt
1860

aaagttgttg ataggagta tgtatttgcc tatgccgacg atccttgtct agctacatac
1920

cctttgatgc aaaagttgag acaagtgcct gtggatcatg cattggtaaa tgttgatgga
1980

gagaagaatt tgaacacatc aatctttcaa aagattgcaa cttttgagga tgagttgaaa
2040

gctattttgc caaaggaggt tgaaagtaca agaactgcat atgaaaatgg acaatgtgga
2100

atttcaaaca agattaagga atgcaggtct tatccattgt acaagtttgt tagagaggag
2160

ttaggaaccg cgttgctaac cggagaaaaa actatatcgc cgggcgaaga gtgcgataaa
2220

ttgttcacag ctatgtgcc aagtaaaatt gttgatcctc ttatggaatg cctcggagag
2280

tggaatggtg ctcctctacc aatatgttaa ttagcataat atgttttctt tgagaagtga
2340

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2400

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Asn	Pro	Leu	Ala	Lys	Ile	Gly	Gly	Glu	Thr	Leu	Thr	Ile	Ala	Gln	Val
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Ala	Gly	Ile	Ala	Ser	His	Asp	Ser	Gly	Val	Arg	Val	Glu	Leu	Ser	Glu
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Ser	Ala	Arg	Ala	Gly	Val	Lys	Ala	Ser	Ser	Asp	Trp	Val	Met	Asp	Ser
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Cys	Thr	Leu	Pro	His	Thr	Ala	Thr	Arg	Ala	Ala	Met	Leu	Val	Arg	Ile
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Gly Trp Ser Tyr Gly Val Ser Lys Thr Leu Ala Glu Lys Ala Val Leu

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[illegible]

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU02/01345

A. CLASSIFICATION OF SUBJECT MATTER												
Int. Cl. ⁷ : C12N 15/29, 15/52, 15/53, 15/55, 15/60, 15/61; A01H 5/00												
According to International Patent Classification (IPC) or to both national classification and IPC												
B. FIELDS SEARCHED												
Minimum documentation searched (classification system followed by classification symbols) SEE ELECTRONIC DATABASE BOX BELOW												
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched SEE ELECTRONIC DATABASE BOX BELOW												
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) PEPTIDE DATABASES (SWISSPROT, GENBANK, EMBL, PIR) DGENE: SEQ ID NOS 2,9,14,18,24,65,70,79,92,96,109,111,118,136,148,154,156,160,162,164,169,186,195,197,203,246,248,250,279,287,29 4,299,304,308,310,312,314,318,320,322,324,326,328,334												
C. DOCUMENTS CONSIDERED TO BE RELEVANT												
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.										
PX	WO 02 18604 A (THE SALK INSTITUTE FOR BIOLOGICAL STUDIES) 7 March 2002 Fig 1D shares ~92% identity with SEQ ID NOS 2, 9, 14, 308	1-3, 13-19, 25, 27										
X	US 6 054 636 A (FADER GM) 25 April 2000 Fig 2 shares ~81% identity with SEQ ID NOS 2, 9, 14, 308	1-3, 13-27										
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input checked="" type="checkbox"/> See patent family annex												
<p>* Special categories of cited documents:</p> <table border="0"> <tr> <td>"A" document defining the general state of the art which is not considered to be of particular relevance</td> <td>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td> </tr> <tr> <td>"E" earlier application or patent but published on or after the international filing date</td> <td>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td> </tr> <tr> <td>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td> <td>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td> </tr> <tr> <td>"O" document referring to an oral disclosure, use, exhibition or other means</td> <td>"&" document member of the same patent family</td> </tr> <tr> <td>"P" document published prior to the international filing date but later than the priority date claimed</td> <td></td> </tr> </table>			"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	"E" earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family	"P" document published prior to the international filing date but later than the priority date claimed	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention											
"E" earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone											
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art											
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family											
"P" document published prior to the international filing date but later than the priority date claimed												
Date of the actual completion of the international search 28 November 2002		Date of mailing of the international search report 05 DEC 2002										
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustrialia.gov.au Facsimile No. (02) 6285 3929		Authorized officer TERRY MOORE Telephone No : (02) 6283 2632										

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU02/01345

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 36543 A (PIONEER HI-BRED INTERNATIONAL, INC.) 22 July 1999 SEQ ID NO 2 shares ~81% identity with SEQ ID NOS 2, 9, 14, 308	1-3, 13-17, 21, 22, 24-27
X	Genbank Acc No AAB41524 chalcone isomerase (<i>Medicago sativa</i>) 29 January 1997 (See also Medline Abstract 8193301) 92% identity with SEQ ID NOS 18, 310	1-3, 13-18, 24-27
X	Genbank Acc No CAA74847 anther-specific protein (<i>Nicotiana sylvestris</i>) (See also Medline Abstract 99084767) 83% identity with SEQ ID NOS 96, 322 and 67% identity with SEQ ID NOS 318, 70	1, 2, 4, 13-18, 24-26, 28
X	Genbank Acc No CAC14061 chalcone synthase (<i>Ruta graveolens</i>) 27 October 2000 ~87% identity with SEQ ID NOS 24, 65, 79, 92, 102, 107, 314, 316, 320, 324	1, 2, 4, 13-18, 24-26, 28
X	Genbank Acc No AAB41556 chalcone reductase (<i>Medicago sativa</i>) 30 January 1997 ~95% identity with SEQ ID NOS 109, 118, 312	1, 2, 5, 13-18, 20, 24-26, 29
X	Genbank Acc No CAA11226 chalcone reductase (<i>Sesbania rostrata</i>) 3 July 2001 90% identity with SEQ ID NO 111	1, 2, 5, 13-18, 24-26, 29
X	Genbank Acc No AAK52955 dihydro-flavonoid reductase-like protein (<i>Zea mays</i>) 14 May 2001 69% identity with SEQ ID NOS 287, 160 and 53% identity with SEQ ID NO 148	1, 2, 6, 13-18, 24-26, 30
PX	WO 02 063021 A (PIONEER HI-BRED INTERNATIONAL, INC.) 15 August 2002 SEQ ID NO 1 shares 74% identity with SEQ ID NOS 148, 160, 287	1, 2, 6, 13-18, 24-26, 30
X	Genbank Acc No AAD54273 dihydroflavonol-4-reductase DFR1 (<i>Glycine max</i>) 10 September 1999 81 % identity with SEQ ID NO 169	1, 2, 6, 13-18, 24-26, 30
X	WO 95 27790 A (CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE) 19 October 1995 SEQ ID NO 1 shares 43% identity with SEQ ID NOS 136, 156, 326, 39% identity with SEQ ID NO 154 and 51% identity with SEQ ID NO 294.	1, 2, 6, 13-18, 24-26, 30
PX	WO 02 10210 A (BAYER AKTIENGESELLSCHAFT) 7 February 2002 SEQ ID NO 2329 shares 51% identity with SEQ ID NO 164, SEQ ID NO 636 shares 62% identity with SEQ ID NO 186, SEQ ID NO 1573 shares 49% identity with SEQ ID NOS 246, 248, SEQ ID NO 2091 shares 57% identity with SEQ ID NOS 304, 299	1, 2, 7, 9, 13- 17, 24-26, 31, 32
X	WO 99 14351 (E.I. DU PONT DE NEMOURS AND COMPANY) 25 March 1999 SEQ ID NO 1 shares 56% identity with SEQ ID NO 162	1, 2, 6, 13-17, 21, 22, 24-26, 30

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU02/01345

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
PX	WO 02 26994 A (AGRICULTURE VICTORIA SERVICES PTY LTD) 4 April 2002 Fig 39 shares 72% identity with SEQ ID NO 294	1, 2, 6, 13-18, 21, 22, 24-26, 30
X	WO 97 12982 A (CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE) 10 April 1997 SEQ ID NO 5 shares 55% identity with SEQ ID NO 294	1, 2, 6, 13-17, 24-26, 30
X	Genbank Acc No CAA80265 flavonoid 3',5'-hydroxylase (<i>Petunia x hybrida</i>) 7 December 1993 70% identity with SEQ ID NO 197	1, 2, 8, 13-18, 24-26, 32
X	EP 1 033 405 (CERES INCORPORATED) 6 September 2000 SEQ ID NO 49742 shares 57% identity with SEQ ID NO 195	1, 2, 8, 13-18, 24-26, 32
X	Genbank Acc No AAF23859 DFR-like protein (<i>Arabidopsis thaliana</i>) 11 January 2000 61% identity with SEQ ID NO 186	1, 2, 7, 13-18, 24-26, 31
X	Genbank Acc No BAB01697 oxidase-like protein (<i>Arabidopsis thaliana</i>) 27 December 2000 50% identity with SEQ ID NOS 246, 248	1, 2, 9, 13-18, 24-26, 33
X	TREMBL Acc No CAB63776 F3'H1 protein (<i>Glycine max</i>) 1 May 2000 85% identity with SEQ ID NO 328, 203	1, 2, 9, 13-18, 24-26, 33
X	Genbank Acc No CAB78172 flavanone 3-beta-hydroxylase (<i>Arabidopsis thaliana</i>) 16 March 2000 57% identity with SEQ ID NOS 304, 299	1, 2, 9, 13-17, 24-26, 33
X	Genbank Acc No AAG49298 Flavonoid 3'-hydroxylase (<i>Callistephus chinensis</i>) 16 January 2001 68% identity with SEQ ID NO 250	1, 2, 10, 13- 18, 20, 24-26, 34
X	Genbank Acc No AAA99500 Phenylalanine ammonia lyase (<i>Stylosanthes humilis</i>) 15 May 1996 88% identity with SEQ ID NOS 254, 259, 269, 271, 273, 275, 330, 332, 334	1, 2, 11, 13- 18, 24-26, 35
X	Genbank Acc No CAA41169 phenylalanine ammonia lyase (<i>Medicago sativa</i>) 5 May 1995 87% identity with SEQ ID NOS 254, 259, 269, 271, 273, 275, 330, 332, 334	1, 2, 11, 13- 18, 24-26, 35
X	Genbank Acc No AAB41550 vestitone reductase (<i>Medicago sativa</i>) 30 January 1997 (See also Medline abstract 7625843) 95% identity with SEQ ID NOS 336, 279	1, 2, 12-18, 21, 22, 24-26, 36

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU02/01345

Box I Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos :
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos :
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See supplemental Box

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.

☒ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU02/01345

Supplemental Box 1

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II (lack of unity)

The international application does not comply with the requirements of unity of invention because it does not relate to one invention or to a group of inventions so linked as to form a single general inventive concept. The fundamental test for unity of invention is specified in Rule 13.2 of the Regulations under the PCT.

"Where a group of inventions is claimed in one and the same international application, the requirement of unity of invention referred to in Rule 13.1 shall be fulfilled only where there is a technical relationship among those inventions involving one or more of the same or corresponding special technical features. The expression "special technical feature" shall mean those technical features that define a contribution which each of the claimed inventions, considered as a whole, make over the prior art."

The problem addressed by the application is the modification of flavonoid biosynthesis (see page 2, line 29-page 3, line 7). The solution provided by the claims resides in the use of 56 specific polypeptides from clover, medic, ryegrass or fescue species (claim 25) and the nucleic acids or fragments coding for these polypeptides (claim 1). These 56 specific polypeptides fall within the following ten groups:

- | | | |
|-----|------------------------------------|---|
| 1. | Chalcone isomerase (CHI) | (SEQ IDS 2,9,14,18,308,310) |
| 2. | Chalcone synthase (CHS) | (SEQ IDS 24,65,70,79,92,96,102,107,314,316,318,322,324) |
| 3. | Chalcone reductase (CHR) | (SEQ IDS 109,111,118,312) |
| 4. | Dihydroflavonol 4-reductase (DFR) | (SEQ IDS 136,148,154,156,160,162,164,169,287,294,326) |
| 5. | Leucoanthocyanidin reductase (LCR) | (SEQ ID 186) |
| 6. | Flavonoid 3',5' hydrolase (F3'5'H) | (SEQ IDS 195,197) |
| 7. | Flavanone 3-hydrolase (F3H) | (SEQ IDS 203,246,248,299,304,328) |
| 8. | Flavonoid 3'-hydroxylase (F3'H) | (SEQ ID 250) |
| 9. | Phenylalanine ammonia-lyase (PAL) | (SEQ IDS 254,259,269,271,273,275,330,332,334) |
| 10. | Vestitone reductase (VR) | (SEQ IDS 279,336) |

The application acknowledges that representatives of these enzyme species, and the nucleotides that encode them, are known and have been isolated from other plant species (see page 2 lines 29-31). This is supported by the following documents, which disclose the isolation and characterisation of a number of these enzymes from a range of species, including clover and medic and rye.

EMBL CAA63306	<i>Secale cereale</i> chalcone synthase (CHS) (5 March 1999)
GENBANK AAA17993	<i>Trifolium subterraneum</i> phenylalanine ammonia-lyase (PAL) (10 May 1994)
PIR S66262	<i>Medicago sativa</i> vestitone reductase (VS) (12 November 1999)
SWISSPROT P51109	<i>Medicago sativa</i> dihydroflavonol 4-reductase (DHR) (1 October 1996)
SWISSPROT P51088	<i>Trifolium subterraneum</i> chalcone synthase (CHS) (15 July 1999)
PIR S44371	<i>Medicago sativa</i> chalcone isomerase (CHI) (16 July 1999)
Medline Abstract 11164576	altered pigmentation using CHS and DFR
Medline Abstract 7981963	altered plant stress response using CHS and PAL

These documents disclose not only flavonoid biosynthesis enzymes in a range of plant species they also disclose manipulation of these sequences to modify features such as pigmentation and stress responses. Thus features such as the 10 listed enzyme families, the isolation of representative of these families from a range of plant species and modification of flavonoid pathway enzymes are known. Furthermore, the enzymes isolated from the 4 specific species: clover, medic, ryegrass and fescue, do not appear to contribute any advantage or produce any unexpected result in comparison to known members of the same families isolated from other species. Thus these features are known or are obvious and cannot be regarded as "special technical features" conferring unity on the separate inventions.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU02/01345

Supplemental Box 1

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II (lack of unity)

In the absence of an obvious special technical feature, it is appropriate to use the Markush approach.

Claims 1 and 26 are written as claims directed to alternatives, in a so-called Markush style of drafting. The application of the test for Markush claims gives the following result:

(A) the common property is modification of the flavonoid biosynthesis pathway.

(B) (1) no common structure is evident as the structures of the polypeptides are not revealed

(B) (2) there is no single recognised class of compounds embracing all the polypeptides, as the polypeptides belong to different classes ie CHI, CHS, CHR, DFR, LCR F3'5'H, F3H, F3'H, PAL, VR, each carrying out different biological functions.

The species of origin of the polypeptides does not provide a legitimate classification as proteins are primarily classified by their activity not their origin. Thus the polypeptides can be grouped into 10 classes CHI, CHS, CHR, DFR, LCR F3'5'H, F3H, F3'H, PAL, VR, based on their activities, and represent 10 different inventions. Each of these inventions can only be searched using independent search strategies and thus each search requires significant additional effort.

As a service to the Applicant, multiple inventions, as specified by the Applicant, were searched for a single search fee with the proviso that the total number of amino acid sequences associated with the combination of inventions was no greater than 10. This offer was independent of unity consideration and was provided solely as a service to the Applicant. For five additional search fees all the inventions, totalling 56 sequences were searched.

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report				Patent Family Member			
US	6 054 636	AU	94934/98	EP	1 015 614	WO	99 14351
WO	99 36543	AU	22321/99	EP	1 045 909		
WO	99 14351	AU	94934/98				
WO	97 12892	EP	0 853 672	FR	2739395		
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